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(54) Title: ANTIFUNGAL COMPOUNDS AND METHODS OF USE

(57) Abstract: The invention provides screening methods for detecting and identifying compounds that bind to fungal specific target proteins and nucleic acids, as well as compounds which, upon binding or otherwise interacting with the target protein, can inhibit fungal growth, a method of preventing or inhibiting fungal growth in culture, a method of preventing or inhibiting fungal growth in a mammal and a method of studying pathogenic mycetes using such nucleic acid and/or protein sequences. Particularly preferred is the inhibition of the fungus Candida albicans.

ANTIFUNGAL COMPOUNDS AND METHODS OF USE

PRIORITY

This application claims priority under 35 U.S.C. § 119 from Provisional Patent Application Serial Number 60/215,164, filed June 29, 2000, and Provisional Patent Application Serial Number 60/224,457, filed August 10, 2000, which are hereby incorporated by reference in their entireties.

FIELD OF THE INVENTION

The invention encompasses the use of fungal cidal targets in the screening for, isolation and development of antifungal chemicals and drugs to be used in the treatment of fungal infections, such as infections with *Candida albicans*. The invention encompasses methods of determining fungal cidal targets. Such fungal cidal targets are encompassed by nucleic acid and protein sequences encoded by such nucleic acid sequences which are isolated from *S. ceriviseae*, shown to be present in other fungi such as *Candida albicans*, and are shown to be both essential and fungal specific in both *Sacchromyces ceriviseae* and *Candida albicans*. The essential fungal specific nucleic acid and protein sequences may also be used in studying pathogenic mycetes or fungi.

BACKGROUND OF THE INVENTION

Fungi are a distinct class of microorganisms, of which most are free-living. They are eukaryotic organisms containing a nuclear membrane, mitochondria and endoplasmic reticulum. In addition, they are non-motile, do not contain chlorophyl and develop from spores (*i.e.* yeasts, molds, mushrooms and rusts). The cell structure usually includes a rigid cell wall of mannan, glucan and chitin and a cytoplasmic membrane with a large percentage of ergosterol. The size and morphology of fungi vary from monomorphic yeasts like *Cryptococcus* and *Saccharomyces* species and dimorphic fungi like *Candida albicans* to filamentous fungi like *Aspergillus* species.

In contrast to bacteria, which are generally considered mammalian pathogens, fungi tend to be plant pathogens. However, in addition to the well recognized group of dermatophytes (*e.g.* cause of "athlete's foot"), an increasingly large group of fungi turn out to be able to act as opportunistic human pathogens producing disease only in compromised individuals. As the result of an aging population as well as an increase in the number of immunocompromised patients, *e.g.*, patients with acquired immunodeficiency syndrome (AIDS), patients undergoing cancer chemotherapy, or immunosuppressive therapy (*e.g.* treatment with corticosteroids) and patients undergoing organ transplantation, the incidence of fungal infections is increasing rapidly.

Fungi parasitize many different tissues. Most infections begin by colonization of the skin, a mucosal membrane or the respiratory epithelium. Superficial fungi and subcutaneous pathogens cause indolent lesions of the skin. Passage through the initial surface barrier is accomplished through a mechanical break in the epithelium. Although most fungi are readily killed by neutrophils, some species are resistant to phagocytic killing and can infect otherwise healthy individuals. The most virulent fungi cause systemic infections, a progressive disease leading to deep seated visceral infections in otherwise healthy individuals (see *e.g. Sherris Medical Microbiology, Third Edition*, Kenneth J. Ryan, ed., Appleton & Lange, Norwalk, CT, 1994).

The major fungal pathogens in North America are *Histoplasma capsulatum*, *Coccidioides immitis*, *Blastomyces dermatitidis*, *Cryptococcus neoformans*, *Candida* species, such as but not limited to *Candida albicans* and *Aspergillus* species (*Medically Important Fungi, Second Edition*, Davise H. Larone, Ed., American Society for Microbiology, Washington, D.C.). The yeast *C. albicans* (*C. albicans*) is one of the

most pervasive fungal pathogens in humans. It is the cause of an increasing financial and logistic burden on the medical care system and its providers due to its ability to opportunistically infect a diverse spectrum of immunocompromised hosts, which are a quickly growing population of patients in today's society. Although *C. albicans* is a member of the normal flora of the mucous membranes in the respiratory, gastrointestinal, and female genital tracts, it may gain dominance in such locations (*e.g.* upon treatment with antibacterial antibiotics, in patients with diabetes or in patients using corticosteroids) and be associated with pathologic conditions. In addition, almost all HIV-positive individuals suffer from a *Candida* infection prior to the onset of developing full-blown AIDS.

Sometimes *C. albicans* produces progressive systemic disease, particularly if cell-mediated immunity is impaired. In 1994, about thirty percent of patients suffering from leukemia or undergoing organ transplants developed a systemic *Candida* infection of which thirty percent have been estimated to have succumbed to the infection.

Only a handful of agents are active against fungi. For life threatening disease caused by any of the pathogenic fungi, amphotericin B is the agent of choice. This drug, however, is associated with numerous severe side effects such as fever, dyspnea and tachycardia, and dosage is limited over the lifetime of the patient because of renal toxicity. An agent frequently used concurrently is flucytosine, a nucleoside analog, which cannot be used independently of other agents because of the rapid appearance of resistance. Untoward effects of treatment with flucytosine include leukopenia, thrombocytopenia, rash, nausea, vomiting, diarrhea, and severe enterocolitis.

In conditions where the patient's life is not threatened, ketoconazole can be used as a long-term therapy for blastomycosis, histoplasmosis, or coccidioidomycosis. Fluconazole also has a significant role in the treatment of superficial fungal infections. Both compounds are from the same class, the triazoles, and are cytostatic. The emergence of resistance and hepatic toxicity limits the use of triazoles such as fluconazole and ketoconazole. The newest triazole, itraconazole, has similar pharmacokinetics and spectrum of activity as fluconazole. None of the azoles can be used for life threatening or deep seated fungal infections. They are only effective in reducing colonization of fungi such as *Candida* species and for treating superficial mycoses.

All major antifungal agents function by attacking, either directly or

indirectly, ergosterol, a component of the cell wall. Amphotericin B and other polyene macrolide compounds like nystatin interact with ergosterol in the cell membrane and form pores or channels that increase the permeability of the membrane. Resistance to amphotericin B in mutant strains is accompanied by decreased concentrations of ergosterol in their cell membranes. Imidazoles and triazoles inhibit sterol 14-"-demethylase, a microsomal cytochrome P_{450}-dependent enzyme system. Imidazoles and triazoles thus impair the biosynthesis of ergosterol for the cytoplasmic membrane, leading to the accumulation of 14-"-methyl sterols, which impair certain membrane-bound enzyme systems (see, *The Pharmacological Basis of Therapeutics, Eighth Edition*, Goodman and Gilman, Pergamon Press, 1990).

Nystatin, amphotericin B, flucytosine and the various azoles have all been used to treat oral and systemic *Candida* infections. However, orally administered nystatin is limited to treatment within the gut and is not applicable to systemic treatment, and resistance to flucytosine is so widespread that it is only used in combination with other drugs. Some life-threatening systemic infections are susceptible to treatment with the azoles or amphotericin B. Azoles have been the most successful drugs used for treatment of such infections in the last few years but they work relatively slowly, have to be taken for months, and are fungistatic rather than fungicidal. While such azole antifungal agents exhibit significantly lower toxicity compared to amphotericin B, their mechanism of action and inactivation of cytochrome P_{450} prosthetic groups in certain enzymes preclude their use in patients that are simultaneously receiving other drugs that are metabolized by the body's cytochrome P_{450} enzymes.

Widespread use of azoles has also resulted in an important change in the spectrum of *Candida* infections. Whereas *C. albicans* used to be the common cause of *Candidosis*, 50% of these infections are now caused by non-*albicans* species which tend to be less susceptible to azole treatment. In addition, a quickly rising percentage of *C. albicans* isolates obtained from infected patients have been found to be resistant to azoles.

There is thus an immediate need for an effective treatment of opportunistic infections caused by *C. albicans* and other fungi. Although the majority of life-threatening fungal infections are caused by *C. albicans*, infections caused by other less common fungi as discussed above, *e.g.*, *Aspergillus fumigatus* have a worse prognosis. In large part this is due to the absence of diagnosis until a very late stage of infection, usually post-mortem.

Therefore it is desirable that novel compounds be able to act against all pathogenic fungi, preventing the need for precise, time-consuming diagnosis.

Development of an effective method and composition for treatment of fungal infections is a critical goal of the pharmaceutical industry. The industry has made numerous efforts to identify fungal-specific drugs, with only limited success. It would be of great value to identify a new class of antifungal drugs that block a fungal target other than ergosterol. This target should be fungal-specific and should lead to development of a drug that is effective in preventing or inhibiting the growth of, and preferentially killing, the organisms that are resistant to current therapy.

Antifungal drug development often relies on the screening of a large number of compounds before one or more lead compounds are found that are effective against the target fungi. Thus, it is critical for the development of these screens to define proteins essential for survival or growth of the target fungi and to discover means of purifying or producing such proteins. Therefore, there is a need in the art to identify essential fungal structural or functional elements that can serve as targets for drug intervention, and for methods and compositions for identifying useful anti-fungal agents that interact with or inhibit essential fungal elements that can be used to treat fungal infections by preventing or inhibiting the growth of, and preferentially killing, the fungi.

SUMMARY OF THE INVENTION

The present invention is based on the determination of *Saccharomyces cerevisiae* proteins which are potential targets to kill *S. cerevisiae* cells. The invention provides a screening method for detecting and identifying a compound that binds to a homologous target protein isolated from *C. albicans*, as well as compounds which can inhibit *C. albicans* and other fungal growth. The invention also provides a method for evaluating the toxicity of such a fungal inhibitor in mammalian cells.

The invention utilizes target proteins involved in such processes as DNA synthesis, DNA replication, DNA transcription, mRNA translation, post-translational modification of proteins, and intracellular transport of proteins, as well as target proteins whose exact cellular functions are unknown. In preferred embodiments, the invention provides for the use of *S. cerevisiae* target proteins listed in Table 1 together with *C. albicans* and human homologs, depicted therein by their respective amino acid sequences

which are provided in Figure 79. The nucleic acid sequences corresponding to these amino acid sequences are depicted in Figure 80.

Each of the *S. cerevisiae* DNA sequences, and their predicted target protein sequences, which are utilized in practicing the invention are publicly available. The essentiality of each of such *S. cerevisiae* genes may already be known or may be determined and/or corroborated through the analysis of the ability to knock out the gene's function in *S. cerevisiae*. The present invention thus provides a method of determining and/or validating the essentiality of the *S. ceriviseae* gene and the target protein encoded by that gene. More specifically, the invention is directed to the determination of the *S. ceriviseae* protein as a cidal target to be used in the determination and isolation of a homologous target in *C. albicans*. The *C. albicans* target may then be used in the screening of compounds which can inhibit *Candida albicans* and other fungal growth.

Following the determination of the essentiality of the *S. cerevisiae* gene, the *S. ceriviseae* DNA sequence may be used to isolate a homologous fungal gene. Thus, in another aspect, the invention is based on the determination of a *C. albicans* nucleic acid encoding the *C. albicans* protein as a target which is essential for the growth of *C. albicans*.

In a still further aspect, the invention provides for producing a recombinant target *C. albicans* target protein, comprising culturing a host cell transformed with a nucleic acid encoding the *C. albicans* target protein under conditions sufficient to permit expression of the nucleic acid encoding the *C. albicans* target protein and isolating the *C. albicans* target protein to be used in assays described below.

Sequence alignments utilizing the *S. cerevisiae* nucleic acid or protein sequences and/or the *C. albicans* nucleic acid or protein sequences in combination with known sequences available in Genbank may be carried out in order to demonstrate any similarity or differences between different fungi, *i.e.*, *S. cerevisiae, C. albicans*, and *Aspergillus,* and mammals. In this manner, homologous genes can be isolated. One example of such analysis would be BLAST™ analysis.

In a further embodiment, following the determination that the target protein in *Saccharomyces cerevisiae* is a cidal target, and that the homologous protein in *Candida albicans* is essential for growth, the *C. albicans* protein may be used as a target to isolate candidate inhibitors of fungal growth and/or infection. Detection and identification of

compounds that bind to the essential protein may be performed in the presence of a plurality of candidate inhibitor compounds. In carrying out the screening methods of the invention which involve screening a plurality of candidate inhibitor compounds, the plurality of inhibitor compounds may be screened together in a single assay or individually using multiple simultaneous individual detecting steps.

In another aspect, the invention provides a method of preventing or inhibiting fungal, particularly *C. albicans*, growth in culture, by contacting the culture with an inhibitor compound that selectively inhibits the biological activity of a fungal target protein, particularly a *C. albicans* target protein.

In a further aspect, the invention provides a method of preventing or inhibiting fungal, particularly *C. albicans*, growth in a mammal, comprising administering to the mammal an effective amount of an inhibitor compound that selectively inhibits the biological activity of a fungal, particularly *C. albicans,* target protein.

In a still further aspect, the invention provides a method of preventing or inhibiting fungal, particularly *C. albicans*, growth in a mammal, comprising administering to the mammal an effective amount of an inhibitor compound, wherein the inhibitor selectively inhibits the biological activity of a fungal, particularly *C. albicans,* target protein, but inhibits the biological activity of the homologous mammalian protein to a lesser degree, or not at all.

In yet another aspect, the invention provides a method of preventing or inhibiting fungal growth, comprising administering to a fungal infection an effective amount of an inhibitor compound that selectively inhibits the biological activity of a fungal target protein.

In still another aspect, the invention provides a method of studying pathogenic mycetes using such nucleic acid and/or protein sequences.

Other features and advantages of the invention will be apparent from the description, preferred embodiments thereof, the drawings, and from the claims.

TABLE 1 - Preferred target proteins

S. cerevisiae			*C. albicans*	Human	
Gene name	ORF name [1]	Sequence	Sequence	Sequence	Genbank Acc# [2]
RPC34	YNR003C	SEQ ID NO:1	SEQ ID NO:	SEQ ID NO:3	U93869

			2		
POP3	YNL282W	SEQ ID NO:4	SEQ ID NO: 5	-	n/a
TFA2	YKR062W	SEQ ID NO: 6	SEQ ID NO: 7	SEQ ID NO: 8	NP_002086
NAB2	YGL122C	SEQ ID NO: 9	SEQ ID NO: 10	SEQ ID NO: 11	AAD42873
MPT1	YMR005W	SEQ ID NO: 12	SEQ ID NO: 13	SEQ ID NO: 14	CAA72189
MTR2	YKL186C	SEQ ID NO: 15	SEQ ID NO: 16	-	n/a
BOS1	YLR078C	SEQ ID NO: 17	SEQ ID NO: 18	SEQ ID NO: 19	NP_003560
POL30	YBR088C	SEQ ID NO: 20	SEQ ID NO: 21	SEQ ID NO: 22	P12004
RSA2	YMR131C	SEQ ID NO: 23	SEQ ID NO: 24	SEQ ID NO: 25	NP_005601
SQT1	YIR012W	SEQ ID NO: 26	SEQ ID NO: 27	SEQ ID NO:28	NP_001078
MTW1	YAL034W-A	SEQ ID NO: 29	SEQ ID NO: 30	-	n/a
TFB1	YDR311W	SEQ ID NO: 31	SEQ ID NO: 32	SEQ ID NO: 33	W19128
SPC98	YNL126W	SEQ ID NO: 34	SEQ ID NO: 35	SEQ ID NO: 36	AAC39727
BFR2	YDR299W	SEQ ID NO: 37	SEQ ID NO: 38	SEQ ID NO: 39	NM_000055
RNA1	YMR235C	SEQ ID NO: 40	SEQ ID NO: 41	SEQ ID NO:42	CAA57714
GCD7	YLR291C	SEQ ID NO: 43	SEQ ID NO: 44	SEQ ID NO: 45	AAC42002
SKI6	YGR195W	SEQ ID NO: 46	SEQ ID NO: 47	SEQ ID NO: 48	BAA91279
NIP1	YMR309C	SEQ ID NO: 49	SEQ ID NO: 50	SEQ ID NO: 51	AAD03462
LCP5	YER127W	SEQ ID NO: 52	SEQ ID NO: 53	SEQ ID NO: 54	AL050003
NCE103	YNL036W	SEQ ID NO: 55	SEQ ID NO: 56	-	n/a
ECO1	YFR027W	SEQ ID NO: 57	SEQ ID NO: 58	-	n/a
ORC2	YBR060C	SEQ ID NO: 59	SEQ ID NO: 60	SEQ ID NO: 61	Q13416
CNS1	YBR155W	SEQ ID NO: 62	SEQ ID NO: 63	SEQ ID NO:64	NP_004614
YPD1	YDL235C	SEQ ID NO: 65	SEQ ID NO: 66	SEQ ID NO: 67	CAA78727
TIM10	YHR005C-A	SEQ ID NO: 68	SEQ ID NO: 69	SEQ ID NO:70	NP_036588
SRB4	YER022W	SEQ ID NO: 71	SEQ ID NO: 72	SEQ ID NO: 73	BAA88763

[1] ORF = Open Reading Frame

[2] Acc # = Accession number

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1-26 provide sequence alignments and identity determinations for the target proteins presented herein. Each figure refers to one target protein as identified in Table 2, comparing amino acid sequences from *S. cerevisiae*, *C. albicans*, and, if available, human homologs. Sequence alignment was carried out using Clustal W (Thompson *et al.*, Nucleic Acids Res. 1994;22:4673-80), and percentage identities determined using the Genetics Computer Group ("GCG") GAP Program (Madison, Wisconsin) with a gap creation penalty of 12 and a gap extension penalty of 4.

Figures 27-52 provide *S. cerevisiae* inactivation analyses of the target genes/proteins identified in Table 1. These data show the essentiality of each gene for *S. cerevisiae* growth. Each figure refers to one target protein. Inactivation analyses were conducted by placing the *S. cerevisiae* expression of a target gene under the control of a metal-sensitive element and incubating the yeast cells together with a Cu-salt, as described in the Detailed Description below and in Example 1.

Figures 53-78, A and B for each, provide *C. albicans* deletion analyses of the target genes/proteins identified in Table 1. These data indicate the essentiality of each gene for *C. albicans* growth. Each figure refers to one target protein. Deletion analyses were conducted as described in the Detailed Description, and C. albicans transformation as described in Example 2 below.

Figure 79 provides amino acid sequences for each of the proteins disclosed herein and depicted in Table 1.

Figure 80 provides nucleic acid sequences corresponding to each of the proteins disclosed in Figure 79.

DETAILED DESCRIPTION OF THE INVENTION

All patent applications, patents, and literature references cited in this specification are hereby incorporated by reference in their entirety.

This invention is directed to essential fungal proteins isolated from *S. cerevisiae* to be used in the determination and/or isolation of a homologous protein from

fungi, particularly *C. albicans*. These fungal protcins, each of which described in more detail below, play essential roles in cell viability and/or growth, and are conserved among fungi. Because these fungal proteins are essential for viability and/or growth of fungal cells, a compound that blocks the biological activity of such a target protein would be expected to have fungicidal and/or fungistatic properties. Since amino acid sequences of any such protein from different fungal sources are likely to be more similar to one another than to the corresponding human protein, it is expected that certain compounds that bind to the fungal protein will not bind to the corresponding human protein, and so will be specific inhibitors of fungal cell growth. Therefore, the invention is also directed to assays to screen for inhibitors of these target proteins which are active against fungi.

In general, nucleic acid manipulations and other related techniques used in practicing the present invention employ methods that are well known in the art, as disclosed in, *e.g.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., Sambrook, Fritsch and Maniatis, Cold Spring Harbor) and *Current Protocols in Molecular Biology* (Eds. Ausubel, Brent, Kingston, More, Feidman, Smith and Stuhl, Greene Publ. Assoc., Wiley-Interscience, NY, NY, 1997).

Definitions

1. The terms "Prevention" and "Inhibition" as used herein may be used interchangeably. "Inhibition" as used herein refers to a reduction in the parameter being measured, whether it be fungal growth, DNA transcription, or another parameter related to a selected process relating to the biological activity of a target protein. The amount of such reduction is measured relative to a standard (control). Because of the multiple interactions of various fungal protein in cell division, growth regulation, cell cycle regulation, and other growth and/or metabolic processes, the amount of target product needed to produce a detectable inhibition will vary with respect to the particular screening assay employed. "Reduction" is defined herein as a decrease of at least 25% relative to a control, preferably of at least 50%, and most preferably of at least 75%.

2. "Growth" or "multiplication" as used herein refers to the normal growth pattern of fungi, particularly *S. cerevisiae* and/or *C. albicans*, *i.e.*, to a cell doubling time of 60-90 minutes during the log phase of growth. In rich media, wild-type *S. cerevisiae* strains have a doubling time of 90 minutes, while wild type *C. albicans*

doubling time is closer to approximately 60 minutes. Growth of the cells may be measured by following the optical density of cells in liquid media. An increasing optical density indicates growth. Growth can also be measured by colony formation from single cells on solid media plates.

3. "Viability" as used herein refers to the ability of the *S. cerevisiae* or *C. albicans* cells to resume growth following a treatment of the cells which results in cessation of growth. Examples of such treatments resulting in cessation of growth include, but are not limited to, transient inactivation of a gene product required for growth or treatment with an antifungal drug. One typical means by which viability is measured is by testing the ability of cells to form colonies on solid media plates following removal of the treatment which resulted in a cessation of growth. Cells that fail to form colonies are considered inviable.

4. "Cidal" as used herein is defined as a rapid loss in viability. Rapid is defined as a population of cells losing viability with a measured half-life of at least about 2 hours or less.

5. A "homologous" protein as used herein is defined as any protein which possesses a protein domain with at least about 30% sequence identity or similarity to a given protein, preferably at least about 40% sequence identity, and most preferably at least about 50% sequence identity. Useful sequence comparison algorithms to determine degree of sequence similarity include BLAST™, FASTA, DNA Strider, the GCG pileup program (Wisconsin Package version 10, Genetics Computer Group, Madison, Wisconsin), as well as alignment schemes such as Clustal W (*See* Thompson *et al.*, *supra*), using, *e.g.*, the default parameters provided with these algorithms. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. (*See* "hybridization", below)

6. A "protein domain" as used herein is defined as a region of a protein which is at least about 50 amino acids ranging to the full length of the protein.

7. "Biological activity" as used herein refers to the ability of a protein to promote or sustain cell growth and/or metabolism through a known or unknown cellular mechanism. Biological activity need not be measured in living cells; an *in vitro* system consisting of the protein together with other chosen components, designed to reflect the

ability of the protein to promote or sustain cell growth and/or metabolism, may also be used to evaluate biological activity.

8. "Target protein" or "cidal protein" as used herein refers to an essential protein involved in, *e.g.*, growth and/or metabolism. Inhibition of the biological activity of a fungal target protein results in an inhibition of fungal growth. Target proteins may play essential roles in processes which include, but are not limited to, DNA synthesis, DNA repair, transcription, mRNA transport, mRNA processing, translation, protein transport, protein processing, cell cycle control, cell division, and cell signaling. The term "target protein" also includes fragments and polypeptides, as well as target proteins modified by any means known in the art, *e.g.*, by radiolabeling, conjugation, mutations in amino acid sequence, using chemically modified amino acid residues in the target protein, and so forth.

9. "Mycete" or "fungi" as used herein refers to a eukaryotic organism which carries spores, nutrition of which takes place via absorption, which is deficient in chlorophyll and which reproduces sexually or asexually.

10. "Nucleic acid" or "polynucleotide" as used herein refers to purine- and pyrimidine-containing polymers of any length, either polyribonucleotides or polydeoxyribonucleotides or mixed polyribo-polydeoxyribo nucleotides. This includes single- and double-stranded molecules, *i.e.*, DNA-DNA, DNA-RNA and RNA-RNA hybrids, as well as "protein nucleic acids" (PNA) formed by conjugating bases to an amino acid backbone. This also includes nucleic acids containing modified bases.

11. An "isolated" nucleic acid or polypeptide as used herein refers to a nucleic acid or polypeptide that is removed from its original environment (for example, its natural environment if it is naturally occurring). An isolated nucleic acid or polypeptide contains less than about 50%, preferably less than about 75%, and most preferably less than about 90%, of the cellular components with which it was originally associated.

12. A nucleic acid or polypeptide sequence that is "derived from" a designated sequence refers to a sequence that is related in nucleotide or amino acid sequence to a region of the designated sequence. For nucleic acid sequences, this encompasses sequences that are homologous or complementary to the sequence, as well as "sequence-conservative variants" and "function-conservative variants." For polypeptide sequences, this encompasses "function-conservative variants." Sequence-conservative

variants are those in which a change of one or more nucleotides in a given codon position results in no alteration in the amino acid encoded at that position. Function-conservative variants are those in which a given amino acid residue in a polypeptide has been changed without altering the overall conformation and function of the native polypeptide, including, but not limited to, replacement of an amino acid with one having similar physical and/or chemical properties (such as, for example, acidic, basic, hydrophobic, and the like). "Function-conservative" variants of a designated polypeptide also include any polypeptides that have the ability to elicit antibodies specific to the designated polypeptide.

13. Nucleic acids are "hybridizable" to each other when at least one strand of nucleic acid can anneal to another nucleic acid strand under defined stringency conditions. Stringency of hybridization is determined, *e.g.*, by a) the temperature at which hybridization and/or washing is performed, and b) the ionic strength and polarity (*e.g.*, formamide concentration) of the hybridization and washing solutions, as well as other parameters. Hybridization requires that the two nucleic acids contain substantially complementary sequences; depending on the stringency of hybridization, however, mismatches may be tolerated. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementarity, variables well known in the art.

Hybridizable polynucleotides may be of any length. In one embodiment, such polynucleotides are at least 7, preferably at least 25 and most preferably at least 100 nucleotides long. In another embodiment, the polynucleotide that hybridizes to any of the polynucleotides of the invention is of the same length as the polynucleotide of the invention. Nucleic acids that are hybridizable to other nucleic acids are capable of hybridizing with their complements under the hybridization conditions defined herein as "high stringency" as defined below.

- Prehybridization treatment of the support (nitrocellulose filter or nylon membrane), to which is bound the nucleic acid capable of being hybridized at 65EC for 6 hours with a solution having the following composition: 4 x SSC, 10 x Denhardt (1X Denhardt is 1% Ficoll, 1% polyvinylpyrrolidone, 1% BSA (bovine serum albumin); 1 x SSC consists of 0.15M of NaCl and 0.015M of sodium citrate, pH 7);
- Replacement of the pre-hybridization solution in contact with the support by a buffer solution having the following composition: 4 x SSC, 1 x Denhardt, 25 mM

$NaPO_4$, pH 7, 2 mM EDTA, 0.5% SDS, 100 g/mL of sonicated salmon sperm DNA containing a nucleic acid probe, in particular as radioactive probe, and previously denatured by a treatment at 100EC for 3 minutes;

- Incubation for 12 hours at 65EC;
- Successive washings with the following solutions: (i) four washings with 2 x SSC, 1 x Denhardt, 0.5% SDS for 45 minutes at 65EC; (ii) two washings with 0.2 x SSC, 0.1 x SSC for 45 minutes at 65EC; and (iii) 0.1 x SSC, 0.1% SDS for 45 minutes at 65EC.

14. A "promoter sequence" as used herein is defined as a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence.

15. A "candidate inhibitor," as used herein, is any compound with a potential to inhibit *Candida albicans* or other fungal growth and/or metabolism via an activity mediated by any of the target proteins described in Table 1, and throughout the specification.

16. "ATLAS", an abbreviation of "Any Target Ligand Assisted Screening" as used herein refers to the screening method described in the section entitled "Primary Inhibitor Screening; High-Throughput Methods for Screening Inhibitors."

Target proteins

The present invention is based on the isolation of DNA encoding fungal proteins involved in cellular growth and/or metabolism, particularly those derived from the *S. cerevisiae* and/or *Candida albicans* genes listed in Table 1, and the determination of the essentiality and or cidality of such fungal gene. The discovery and characterization of these *S. cerevisiae* target proteins and/or their *C. albicans* homologs, and the elucidation of differences between the fungal and mammalian target proteins, implicates these protein, particularly the *C. albicans* protein, as an important target for the development of new methods and compositions for the treatment of fungal infections. Agents which selectively interfere the biological activity would likely be candidates for anti-fungal, particularly anti-*C. albicans* and related fungi, therapeutics. The present invention also encompasses methods for identifying compounds that selectively interfere with *C. albicans* target protein activity and thus may comprise useful antifungal agents.

Ideally, an antifungal compound directs its action against a target that is present in fungi but absent in human cells. Such targets, however, are important for cell function and tend to be conserved in evolution and, thus, be present in both human and fungal cells. In such cases, the target protein is present in both cell types, as noted above, but the human homolog of the target protein has an amino acid sequence that distinguishes it from the fungal target protein.

If a human homolog of the target protein has been identified, such a human sequence is considered distinguishable from the fungal sequence if it has less than about 50%, preferably less than about 40%, and even more preferably less than about 30% sequence identity. The lower the sequence similarity, the higher the chance for identifying compounds that act specifically against the fungal target protein but not its human homolog. However, an important factor is also the sequence similarity between different fungal homologs of the target protein. If homologous proteins derived from two different fungal sources such as, *e.g.*, *S. cerevisiae* and *C. albicans*, display a high sequence similarity such as, *e.g.*, higher than 50%, more preferably 70%, and even more preferably higher than 90%, this allows for a higher chance of identifying an inhibitor specific for the fungal target proteins but not their human homolog. Thus, a higher than optimal sequence similarity between the fungal and human target protein homologs does not preclude finding a substance which only inhibits the biological activity of the fungal protein.

Each preferred target protein is described below. Non-limiting examples of some assays for some of the target proteins are also provided. Such assays are useful in identifying and/or measuring the biological activity of target proteins, *e.g.*, in the presence of a potentially inhibitory compound. Amino acid sequences for each target protein in *S. cerevisiae*, *C. albicans*, and, where relevant, human, can be found in Table 1. Sequence identity determinations between the the *S. cerevisiae*, *C. albicans*, and, if available, human homologs, are provided in Table 2.

RPC34

RPC34 (C34) is an essential and specific subunit of RNA polymerase III complex (Stettler, S., *et al.*, J. Biol. Chem., 1992; 267:21390-21395). RNA polymerase III is responsible for transcription of tRNAs, 5S rRNA, and some other small RNAs. Three RNA polymerase III unique subunits, C34, C82, and C31 form a complex that interacts

with 70-kDa component of transcription factor TFIIIB via C34 (Werner, M., *et al.*, J. Biol. Chem., 1993; 268:20721-20724). C34 subunit is a major determinant of pol III recruitment by pre-initiation complex. Interaction between C34 and TFIIIB70 is essential for pre-initiation complex formation and later during promoter opening (Brun, I., *et al.*, EMBO J., 1997; 16:5730-5741). It has been demonstrated that strains carrying temperature-sensitive or cold-sensitive mutations in RPC34 are impaired in tRNA synthesis (Stettler, S., *et al.*, J. Biol. Chem., 1992; 267:21390-21395; Brun, I., *et al.*, EMBO J., 1997; 16:5730-5741). RPC39 human homolog of RPC34 has been identified (Wang, Z. and Roeder, R. Gen. Dev., 1997; 11:327-7949). RPC34 and RPC39 are 27% identical and 50% similar.

RPC34 assays:

(a) ATLAS

(b) Cell-based assays in S. cerevisiae and human cells were developed utilizing the information that in the absence/inability to perform, the function of RPC34 tRNA synthesis decreases (Stettler, S., *et al.*, J. Biol. Chem., 1992; 267:21390-21395; Brun, I., *et al.*, EMBO J., 1997; 16:5730-5741). If the compound specifically binds to Rpc34p, a tRNA level decrease can be detected after addition of the compound to the growing media. Similar assay in human cells can be designed based on the same principle. The level of tRNA can be assayed upon addition of a compound to the cells at different time points.

(c) In vitro assays can be developed using purified RNA polymerase III transcription factors, including RPC34, to assess tRNA and 5S rRNA levels in the presence/absence of a compound (Kassavetis, G., *et al.*, EMBO J., 1999; 18:5042-5051).

(d) A reporter-based assay can be developed utilizing a two-hybrid system, knowing that RPC34 physically interacts with C82, C31, and TFIIIB70. One of the proteins can be fused with a transcriptional activator and the other with a DNA-binding protein. The ability of the two proteins to interact with each other in the presence or absence of a compound can be measured by monitoring enzymatic activity of a reporter gene expressed from the promoter.

POP3

Saccharomyces cerevisiae POP3 is involved in post-transcriptional processing of the large precursor RNAs into the mature functional forms of tRNA and rRNA (Dichtl, B. and D. Tollervey, EMBO Journal, 1997; 16:417-429; Chamberlain, J.R., *et al.*, Genes and Development, 1998; 12:1678-1690). This processing of tRNA and rRNA is carried out by the RNase MRP and RNase P ribonucleoproteins, respectively, but the two complexes are known to have extensive subunit overlap (Chamberlain, J.R., *et al.*, Genes and Development, 1998; 12:1678-1690). Mutations in POP3 result in phenotypes identical to loss of RNase MRP, including interference with the complete processing of tRNA and rRNA (Dichtl, B. and D. Tollervey, EMBO Journal, 1997; 16:417-429; Chamberlain, J.R., *et al.*, Genes and Development, 1998; 12:1678-1690). POP3 is essential for cell growth in Saccharomyces cerevisiae (Dichtl, B. and D. Tollervey, EMBO Journal, 1997; 16:417-429).

POP3 Assays:

(a) ATLAS: CaPop3 protein could be purified and challenged with an environmental condition, such as higher temperature or reduced pH, that unfolds the protein. A compound that binds to CaPop3 protein may stabilize the native conformation of the protein.

(b) Two hybrid interruption screen using another interacting protein: CaPOP3 and a Candida albicans ortholog of another subunit of either the RNase MRP or the RNase P complex could be placed into yeast two-hybrid screening vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a reporter gene. A compound that interferes in the binding of the two proteins should disrupt the induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than those in the RNase MRP or RNase P complex could be used in this format.

TFA2

Saccharomyces cerevisiae TFA2 is a subunit of the general RNA polymerase II transcription initiation factor, TFIIE. The gene product of TFA2 forms a hetero-tetramer with that of TFA1, and both genes are essential for cell viability (Feaver *et al.*, J Biol Chem, 1994, 269:27549-53). The genes for TFA1 and TFA2 were identified from the purified protein shown to have an activity required for accurately initiated

transcription from promoters in vitro, and the gene sequences have significant homology to mammalian TFIIE (Feaver *et al.*, J Biol Chem, 1994, 269:27549-53). The requirement for TFIIE to carry out transcription of a gene varies, depending on the promoter structures, (Sakur *et al.*, J Biol Chem, 1997, 272: 15936-15942). It has been suggested that yeast GAL11 product enhances the interaction between TFIIE and the RNA polymerase II holoenzyme and thus increases transcriptional efficiency (Sakurau *et al.*, PNAS, 1996, 93:9488-9492).

TFA2 Assays:

(a) ATLAS: CaTfa2 protein could be purified and challenged with an environmental condition, such as higher temperature or reduced pH, that unfolds the protein. A compound that binds to CaTfa2 protein may stabilize the native conformation of the protein.

(b) Two-hybrid interruption screen using another interacting protein: CaTfa2 and CaTfa1 could be placed into yeast two-hybrid screening vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a reporter gene. A compound that interferes in the binding of the two proteins should disrupt the induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than CaTfa1p could be used in this format, notably CaGal11 protein.

NAB2

Nascent RNA polymerase II transcripts associate with nuclear ribonucleoproteins and remain associated during the subsequent RNA processing reactions, such as pre-mRNA polyadenylation and splicing and transport to the cytoplasm. *Saccharomyces cerevisiae* NAB2 is one of the major proteins associated with polyadenylated RNA in vivo and is essential for cell growth (Anderson, J.T., *et al.*, Molecular and Cellular Biology, 1993;13:2730-2741). The NAB2 gene product is localized primarily to the nucleus (Anderson, J.T., *et al.*, Molecular and Cellular Biology, 1993;13:2730-2741). Two different RNA-binding motifs are identifiable in the sequence of NAB2: an RGG box observed in a variety of heterogenous nuclear RNA-binding proteins, and CCCH motif repeats related to the zinc-binding motifs of the largest subunit of RNA polymerases (Anderson, J.T., *et al.*, Molecular and Cellular Biology,

1993;13:2730-2741). NAB2 gene product interacts with the product of yeast KAP104, a gene encoding a karyopherin shown to function in the nuclear import of proteins, and has been shown to interact with human transportin1 (hTRN1), the human homolog of yeast KAP104 (Aitchison, J.D., *et al.*, Science, 1996; 274:624-627;Truant, R., *et al.*, Molecular and Cellular Biology, 1998;18:1449-1458; M.C. Siomi, *et al.*, Molecular and Cellular Biology, 1998; 18:4141-4148).

NAB2 Assays:

(a) ATLAS: CaNab2 protein could be purified and challenged with an environmental condition, such as higher temperature or reduced pH, that unfolds the protein. A compound that binds to CaNab2 protein may stabilize the native conformation of the protein.

(b) Two-hybrid interruption screen using another interacting protein: CaNAB2 and CaKAP104 could be placed into yeast two-hybrid screening vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a reporter gene. A compound that interferes in the binding of the two proteins should disrupt the induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than CaKap104p could be used in this format.

(c) RNA-binding screen: Compounds could be screened for their ability to interfere with the binding of RNA by CaNab2 protein. The binding of RNA and CaNab2 protein could be assessed in a variety of ways: 1) through capture on a filter or capture by antibodies; 2) in homogeneous solution using fluorescently-labeled RNA and detection of a change in fluorescence polarization; or 3) detection of a gel shift when RNA is bound by the protein.

MPT1

MPT1 is a target that has been identified in both *S. cerevisiae* and *C. albicans*. MPT1 proteins have not been characterized in detail. ScMPT1 was isolated in a two-hybrid screen using ScPrp9 as bait (Fromont-Racine, M., *et al.*, Nat Genet, 1997; 16:277-82). Prp9 is a subunit of a complex involved in RNA splicing. The fact that ScMPT1 would interact with Prp9 suggests that ScMPT1 would also be involved in RNA splicing. Validation data in *S. cerevisiae* and *C. albicans* indicate that MPT1 is important for fungal cell growth and viability, which may correlate with its putative function in RNA

splicing. A mammalian homolog has been proposed, but the degree of homology is too low to be confident about this. The apparent importance of MPT1 for fungal growth combined with the absence of a highly similar protein in mammalian cells make MPT1 an excellent target for antifungal drug discovery.

MPT1 assays:

(a) ATLAS. (*See* above).

(b) Cell-based assays: Various strains of *S. cerevisiae* could be constructed in which ScMPT1 would be replaced with a functional MPT1 gene (*i.e.*, derived from cDNA when necessary) from different organisms, in particular fungi and mammals. These cells would be grown in individual wells containing defined number and mixtures of compounds, which potentially could inhibit growth. Differences in degrees of inhibition by compounds between above-mentioned strains may suggest that a compound may inhibit growth by preferentially inhibiting activity of a class of MPT1.

(c) Protein-protein interaction based assays: (i) Two-hybrid screen (Fromont-Racine, M., *et al.*, Nat Genet, 1997; 16:277-82) using MPT1 and PRP9 (or any other protein found to interact with MPT1); (ii) Direct binding assay: The interacting protein could be fixed onto a carrier an allowed to bind easily detectable MPT1. In the absence of inhibitors, a high signal would result. However, interference with this interaction may reduce signal. The orientation of the assay could also be reversed by fixation of MPT1 and incubation with a interacting protein labeled with a reporter molecule such as, *e.g.*, a radionucleotide or a fluorescent compound.

MTR2

In eukaryotic cells, mRNA transport is an important cellular process for gene expression and regulation. A set of genes were identified through an attempt to isolate Saccharomyces cerevisiae temperature-sensitive mutants that accumulate poly(A) RNA in the nucleus.(Kadowaki, T., *et al.*, J Cell Biol, 1994; 126, 649-59) One of the genes, MTR2 encodes a 21 kD nuclear protein that shows a limited homology to a E. coli protein implicated in plasmid DNA transfer.(Kadowaki, T., *et al.*, J Cell Biol, 1994; 126, 649-59) It has been shown that Mtr2 protein can interact with a nuclei pore associated protein, Mex67p and their interaction appears to be essential for mRNA export.(Santos-Rosa, H., *et al.*, Mol Cell Biol, 1998; 18:6826-38) Genetic and biochemical evidence also indicated

that Mtr2p can interact with Nup85p, suggesting that Nup85p might be the target at nuclei pore complex (NPC) to which Mtr2p and Mex67 bind.(Santos-Rosa, H., *et al.*, Mol Cell Biol, 1998; 18:6826-38) Given all these factors, it was proposed that Mtr2 protein is the key component of mRNA export machinery in yeast.(Santos-Rosa, H., *et al.*, Mol Cell Biol, 1998; 18:6826-38; Schneiter, R., *et al.*, Mol Biol Cell, 1995; 6:357-70)

Recently, a human homolog of Mex67, TAP was identified that can interact with poly(A) RNA and human nucleoporin. However, no Mtr2 human homolog was found so far. Katahira et al (The Mex67p-mediated nuclear mRNA export pathway is conserved from yeast to human. Embo Journal 18, 2593-2609 (1999)) identified a small human protein, p15 that interact with TAP. Interestingly, co-expression of TAP and p15 in yeast can functionally complement Mex67-Mtr2 complex suggesting the existence of the evolutionarily conserved pathway that is involved in mRNA transport.

MTR2 assays:

(a) ATLAS: Mtr2 protein can be purified to homogeneity. Challenging purified Mtr2 protein with different environment conditions such as higher temperature or reduced pH will result in the protein conformation change leading protein to the unfolding state. Any compound that binds to Mtr2 will potentially stabilize protein in the native state. Using ATLAS can help identify compound that binds to Mtr2.

(b) Two hybrid with Mex67. Mtr2 and Mex67 can be used as a pair of genes in yeast with one of them as the bait and the other used as target. Binding of Mtr2 and Mex67 protein in yeast will result in the induction of a reporter gene that can be detected. Any compound that interrupts the interaction of Mtr2pand Mex67p will disrupt the induction of the reporter gene and thus that compound can be identified.

(c) Two hybrid with Nup85p. Mtr2 and Nup85 can be used as a pair of genes in yeast with one of them as the bait and the other used as target. Binding of Mtr2 and Mex67 protein in yeast will result in the induction of a reporter gene that can be detected. Any compound that interrupts the interaction of Mtr2p and Nup85p will disrupt the induction of the reporter gene and thus that compound can be identified.

BOS1

Saccharomyces cerevisiae BOS1 is an essential gene that functions in ER-to-Golgi transport. The protein is a cytoplasmically-oriented type II integral membrane protein of secretory vesicles (Newman *et al.*, Embo J.,1992, 11:3609-3617; Lian *et al.*, Cell, 1993, 73:735-745). Depletion of BOS1 results in a block in ER-to-Golgi protein transport and accumulation of small vesicles (Shim *et al.*, J. Cell Biol., 1991, 13:55-64). The gene was originally isolated as a high copy suppressor of BET1 (Newman *et al.*, Embo J., 1992, 11:3609-3617). BOS1 exhibits genetic and physical interactions with several proteins known to be involved in vesicular transport from the ER to the Golgi. In addition to suppressing BET1 defects, BOS1 overexpression can also overcome defects in SEC22 and YPT1 (Newman *et al.* Embo Journal 11, 3609-17 (1992)). Bos1p has been shown to pair with Sec22p under the influence of Ypt1. Bos1p, Bet1p and Sec22p are V-SNARE proteins (Lian *et al.*, Cell 73, 735-45 (1993); Pfeffer, Annu. Rev. Cell Dev. Biol. 12, 441-461 (1996)) that form a complex involved in transport vesicle docking (Ferro-Novick *et al.*, Cell Biophys 19, 25-33 (1991)). YPT1 is a Rab protein required for SNARE complex formation (Sogaard *et al.*, Cell 78, 937-48 (1994); Lian *et al.*, Nature 372, 698-701 (1994); Lazar *et al.*, Trends Biochem Sci 22, 468-472 (1997)). The V-SNAREs Bos1p and Sec22p cooperatively interact with the t-SNARE Sed5p prior to membrane fusion (Sacher *et al.*, J Biol Chem 272, 17134-8 (1997)).

BOS1 assays:

(a) BOS1 is a good ATLAS assay target. In addition, defects in BOS1 function could be assessed in a reconstituted transport system (Lian, J. P., and Ferro-Novick, S. Bos1p, Cell, 1993; 73:735-45) or in a cell-based assay of invertase secretion (Johnson, L.M., *et al.*,Cell, 1987; 48:875-885) that monitors the inefficient transport of secreted protein from the ER to the Golgi (Shim, J., *et al.*, J Cell Biol, 1991;113:55-64).

(b) In vitro transport system (Lian *et al.*, Cell 73, 735-45 (1993)).

(c) Cell-based assay of invertase secretion (Johnson *et al.*, 1987) that monitors the inefficient transport of secreted protein from the ER to the Golgi (Shim *et al.*, 1991).

(d) Protein:protein interactions. BOS1 has multiple protein partners (see above) whose interactions can be monitored by assayed by two-hybrid analysis or in vitro protein binding assays.

POL30

References for this section are numbered at the end of the section.

Saccharomyces cerevisiae POL30 is an essential gene and encodes the yeast proliferating cell nuclear antigen (PCNA) (Bauer *et al.*, NAR, 1990, 18: 261-5). The structure of yeast PCNA has been determined, and it appears to function as a trimer that forms a sliding clamp around the DNA double helix (Krishna *et al.*, J Mol Biol, 1994, 241: 265-8). PCNA can load onto the ends of linear DNA molecules in vitro, but efficient loading of PCNA onto DNA requires ATP and the product of RFC1 (McAlear *et al.*, Genetics, 1996, 142:65-78, Burgers *et al.*, J Biol. Chem., 1993, 268: 19923-19926).

PCNA is required for both DNA synthesis and DNA repair in mammals and yeast. PCNA interacts with DNA polymerase delta or epsilon to enhance processive replication of DNA (Holmes *et al.*, Cell, 1999, 96: 415-424). PCNA interacts with FEN-1, the product of the mammalian homolog of RAD27, a protein required for Okazaki fragment processing (Ishimi *et al.*, J. Biol.Chem., 1988, 263: 19723-19733; Li *et al.*, J. Biol. Chem., 1995, 270:22109-22112; Turchi *et al.*, PNAS, 1995, 91:9803-9807). PCNA is required in vitro for reconstitution of nucleotide excision repair and base excision repair reactions. (Ayyagari *et al.*, Mol Cell Biol, 1995, 15:4420-0; Umar *et al.*, Cell, 1996, 87:65-73; Johnson et al, J Biol Chem, 1996, 271:27987-90; Matsumoto *et al.*, Mol Cell Bio., 1994, 14:6187-97; Nichols *et al.*, NAR, 1992 10:2441-2446; Shivji *et al.*, Cell, 1992, 69:367-374). Transcription silencing may also involve PCNA (Ehrenhofer-Murray *et al.*, Genetics, 1999, 153:1171-82).

POL30 assays:

(a) ATLAS: CaPol30 protein could be purified and challenged with an environmental condition, such as higher temperature or reduced pH, that unfolds the protein. A compound that binds to CaPol30 protein may stabilize the native conformation of the protein.

(b) Two-hybrid interruption screen using CaRad27 protein or another interacting protein: CaPol30 and CaRad27 could be placed into yeast two-hybrid screening

vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a reporter gene. A compound that interferes in the binding of the two proteins should disrupt the induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than CaRad27p could be used in this format. A screen could be designed to interfere with the multimerization of CaPol30 by using the gene as both bait and prey.

(c) DNA-binding screen: Compounds could be screened for their ability to interfere with the binding of DNA to CaPol30 protein. The binding of DNA and CaPol30 protein could be assessed in a variety of ways: 1) through capture on a filter or capture by antibodies; 2) in homogeneous solution using fluorescently-labeled DNA and detection of a change in fluorescence polarization; or 3) detection of a gel shift when DNA is bound by the protein.

YMR131C

YMR131C is an essential gene in *C. albicans*. Nearest human match is a 25% identity to human retinoblastoma protein RBBP4. YMR131C protein has WD40 repeats suggesting that it may physically interact with other proteins. Recent report suggests that the protein may be involved in the nucleopore complex formation (Rout, M., *et al.*, J. Cell Biol., 2000; 148:635-652).

YMR131C assays:

(a) ATLAS

(b) If a mammalian YMR131C Homolog is found that complements C albicans YMR131C, a cell-based assay could be set up to measure cell growth in the presence/absence of a compounds comparing strains with C. albicans YMR131C and human YMR131C Homolog.

(c) If proteins that physically interact with YMR131C are identified, two-hybrid system based assay can be developed to monitor interaction between YMR131C and another protein.

(d) If YMR131C is essential for nuclear pore transport, an assay can be set up to monitor efficiency of transport through nuclear pores.

SQT1

Saccharomyces cerevisiae SQT1 is an essential gene, which encodes a 60S ribosomal subunit protein required for joining of 40S and 60S subunits (Eisinger *et al.*, MCB, 17:5146-5155, 1997). SQT1 was isolated as a suppressor of dominant-negative truncation mutations of ribosomal protein QSR1 (Eisinger *et al.*, MCB, 17:5136-5145, 1997; Eisinger *et al.*, MCB, 17:5146-5155, 1997). The loss of SQT1 function results in the formation of half-mer polysomes whereby the 40S and 60S subunits fail to join. SQT1 may be required for the assembly of QSR1 onto the 60S ribosomal subunit (Eisinger *et al.*, MCB, 17:5146-5155, 1997). The protein may be part of an oligomeric complex and is localized to the cytoplasm where it is loosely associated with ribosomes (Eisinger *et al.*, MCB, 17:5146-5155, 1997).

SQT1 assays:

(a) SQT1 is a good candidate for an ATLAS assay. In addition, polysome and ribosome subunit analysis could be carried out in a low-throughput secondary assay. Interference with SQT1 function should result in half-mer polysome profiles. This type of assay would involve isolation and fractionation of ribosomal subunits, 80S ribosomes and polysomes on sucrose velocity gradients (Eisinger *et al.*, MCB, 17:5136-5145, 1997).

(b) Polysome and ribosome subunit analysis could be carried out in a low-throughput secondary assay. Interference with SQT1 function should result in half-mer polysome profiles. This type of assay would involve isolation and fractionation of ribosomal subunits, 80S ribosomes and polysomes on sucrose velocity gradients (Eisinger *et al.*, 1997a).

MTW1

MTW1 is an essential protein in *C. albicans* with unknown function. Mtw1p (Mis twelve-like protein) is 33% identical to *S. cerevisiae* Mis12p. The published data suggests that *S. pombe* Mis12p is required for centromere structure maintenance and correct spindle morphogenesis during chromosomal segregation (Goshima *et al.*, Gen. Dev., 13:1664-1677, 1999). It is possible that *C. albicans* Mtw1p has DNA-binding motifs. No true human homolog has been identified so far.

MTW1 assays:

(a) ATLAS

(b)If MTW1 binds to DNA, an assay for DNA-binding activity can be set up.

(c) If a mammalian MTW1 homolog is found which complements *C albicans* MTW1, a cell-based assay can be set up to measure cell growth in the presence/absence of a compound, comparing strains with *C. albicans* MTW1 and the human MTW1 homolog.

(d) If proteins that physically interact with MTW1 are identified, two-hybrid system based assays can be developed to monitor interaction between MTW1 and other proteins.

TFB1

RNA polymerase II needs five additional general transcription factors for promotor dependent transcription, one of which is TFIIH (Svejstrup *et al.*, J Biol Chem, 269:28044-8, 1994). TFIIH contains DNA-dependent ATPase activity and protein kinase activity directed against the C-terminal Repeat Domain of RNA polymerase II. TFB1 is one of the subunits of TFIIH and is needed for both transcription and nucleotide excision repair.

TFB1 genes have been found in both mammalian and fungal cells. However, the degree of conservation between fungi is higher than that between fungi and mammalian (approximately 40% vs. 20%). This difference combined with the importance for fungal cell viability makes TFB1 an excellent target for antifungal drug discovery.

TFB1 assays:

(a) ATLAS

(b) RNA polymerase II promotor-dependent transcription assay

(c) Cell-based assay: Various strains of S. cerevisiae would be constructed in which ScNIP1 would be replaced with a functional TFB1 gene (*i.e.* derived from cDNA when necessary) from different organisms, in particular fungi and mammals. These cells would be grown in individual wells containing defined number and mixtures of compounds, which potentially could inhibit growth. Differences in degrees of inhibition by compounds between above-mentioned strains suggest that a compound may inhibit growth by preferentially inhibiting activity of a class of TFB1.

(d) Protein-protein/DNA interaction based assay: (i) Two-hybrid screen (Fromont-Racine *et al.*, Nat Genet, 16:277-82, 1997) using TFB1 and any protein (or DNA) found to interact with TFB1 (*e.g.* other TFIIH subunits); (ii) Direct binding assay: The interacting protein or DNA would be fixed onto a carrier an allowed to bind easily detectable TFB1. In the absence of inhibitors a high signal would result. However, interference with this interaction would reduce signal. Orientation of the assay could also be reversed by fixation of TFB1 and incubation with labeled interacting protein/DNA.

SPC98

Saccharomyces cerevisiae SPC98 encodes an essential protein that has a role at the spindle pole body (SPB), the fungal equivalent of the centrosome. SPC98 was identified as a high copy suppressor of a mutation in TUB4, the yeast gene for gamma-tubulin. A conditional mutation in SPC98, when shifted to restrictive conditions, results in a cell-cycle arrest with defective mitotic spindles (Geissler, *et al.*, Embo Journal, 15:3899-911, 1996). SPC97, a gene that has regions of sequence similarity to SPC98, was identified as a high copy suppressor of a mutation in SPC98 (Knop *et al.*, Embo Journal, 16:1550-64, 1997). The products of both SPC97 and SPC98 have been shown to form a complex with gamma tubulin and to be responsible for microtubule nucleation (Knop, M., *et al*, 1997; Pereira *et al.*, Embo Journal, 18:4180-4195, 1999; Chen *et al.*, J Cell Biol, 141:1169-1179, 1998). The human homologs of SPC97 and SPC98 are also in a complex with gamma-tubulin and appear to have the same functions (Tassin *et al.*, J Cell Biol, 141:689-701, 1998; Murphy *et al.*, J Cell Biol, 141:663-74, 1998).

SPC98 Assays:

(a) ATLAS: CaSpc98 protein could be purified and challenged with an environmental condition, such as higher temperature or reduced pH, that unfolds the protein. A compound that binds to CaSpc98 protein may stabilize the native conformation of the protein.

(b) Two hybrid interruption screen using another interacting protein: CaSpc98 and CaSpc97 could be placed into yeast two-hybrid screening vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a reporter gene. A compound that interferes in the binding of the two proteins should disrupt the

induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than CaSpc97 could be used in this format.

BFR2

Saccharomyces cerevisiae BFR2 is an essential gene that was isolated as a high copy suppressor of the growth defects induced by Brefeldin A (BFA), a fungal metabolite that disrupts Golgi structure and function (Chabane *et al.*, Curr. Genet, 33:21-8, 1998; Takatsuki *et al.*, Agric. Biol. Chem., 49:899-902, 1995; Klausner *et al.*, J. Cell Biol., 116:1071-1080, 1992). In addition, BFR2 overproduction was shown to partially suppress the growth defects of four mutants involved in the secretory pathway (Chabane *et al.* 1998). The mutants, sec13-1, sec16-1, sec23-1 and ypt1-1, are each involved in budding and or docking of small vesicles en route to the Golgi. Thus, it was suggested that BFR2 is involved in protein transport (Chabane *et al.* 1998).

BRF2 assays:

(a) BFR2 can be screened in an ATLAS assay format; and

(b) Based on the proposed function of BFR2, compound interference with BFR2 would make cells more highly sensitive to BFA. Therefore, increased cellular sensitivity to BFA is an additional assay that could be used as a secondary screen.

RNA1

Saccharomyces cerevisiae RNA1 gene encodes the Rna1 protein, which is involved in nuclear export of all types of RNA (Sarkar *et al.* Mol Biol Cell, 1998, 9:3041-55). It is required for export of assembled 60S ribosomal subunits from the nucleus to the cytoplasm (Hurt *et al.*, J Cell Biol, 1999, 144:389-401). Rna1p plays a direct role in the import of proteins into the nucleus (Corbett *et al.*, J Cell Biol, 1995, 130:1017-26). GST-Rna1p catalytically stimulates GTP hydrolysis by purified Gsp1p (Corbett *et al.*, J Cell Biol, 1995, 130:1017-26). It does not stimulate GTPase activity of ras or Rab7 (Becket *et al.*, J Biol Chem, 1995, 270:11860-5). RNA1 has extensive homology to S. pombe Rna1p and to the mammalian Ran/TC4 GTPase activating protein (Corbett *et al.*, J Cell Biol, 1995, 130:1017-26; Bischoff *et al.*, PNCAS USA, 1995 92:1749-53; Melchior *et al.*, Mol Biol Cell, 1993 4:569-81). The rna1-1 mutant is complemented by S. pombe rna1. It is a member of superfamily of proteins that have leucine-rich repeat motifs, which

can be up to 29 amino acids in length (Melchior *et al.*, Mol Biol Cell, 1993 4:569-81; Schneider *et al.*, Mol Gen Genet, 1992, 233: 315-8). Cytosolic extracts made from rna1-1 mutants are completely devoid of Rna1p and the protein was found to be localized within the nucleus (Traglie *et al.*, PNCAS USA, 1996, 93:7667-72). The mutant affects RNA processing and export from nucleus although Rna1p is cytoplasmic (Hopper *et al.*, J Cell Biol, 1990, 111:309-21). rna1-1 mutant accumulates intron-less and intron-containing tRNA in the nucleus at the nonpermissive temperature (Sarkar *et al.* Mol Biol Cell, 1998, 9:3041-55). It shows altered export of RNA from nucleus to cytoplasm with RNA accumulating at the nuclear periphery (Amberg *et al.*, GAD, 1992 6:1173-89). The temperature-sensitive mutant has accumulation of 35S pre-rRNA (Venema *et al.*, Yeast, 1995, 11:1629-50). The rna1-1 mutant abolishes nuclear pore complex localization of Cse1p-GFP, which becomes distributed throughout the cell (Hood *et al.*, J Biol Chem, 1998, 273:35142-35146). When the 11 amino acids from the carboxy terminal are removed, the protein retains its function (Traglia *et al.*, Mol Cell Biol, 1989, 9:2989-99). In rna1-1 mutant, export of the small ribosomal subunit from the nucleus is directly inhibited with accompanying secondary defects in processing of pre-rRNA (Moy *et al.*, GAD, 1999, 13:2118-2133).

RNA1 assays:

(a) ATLAS

(b) Mutants of RNA1 accumulates intron-less and intron-containing tRNA (1). This information may be useful in assaying such tRNA in presence/absence of compounds that bind and disrupt Rna1p activity.

(c) The defects in processing of ^{35}S pre-rRNA may be monitored by probing with oligonucleotides near the pre-rRNA cleavage sites by Northern Hybridization and primer extension analysis.

(d) There is accumulation of ^{35}S pre-rRNA in temperature sensitive mutants (11). This effect may be studied in a cell-based assay. Levels of ^{35}S-labeled pre-rRNA may be assayed in presence/absence of a compound.

GCD7

Eukaryotic protein translation is initiated by acquisition of mRNA and Met-tRNAiMet by the 40S ribosomal subunit. These changes are mediated by Initiation

Factors (eIF's). eIF2 forms a complex with Met-tRNAiMet and GTP, which binds to 40S ribosomes (Pavitt *et al.*, Mol Cell Biol, 1997, 17:1298-313). After subsequent binding of mRNA to these 40S ribosomes and recognition of the AUG codon by Met-tRNAiMet, GTP hydrolysis releases eIF2-GDP. eIF2-GDP is converted to eIF2-GTP by eIF2B, a guanine nucleotide exchange factor, as a result of which protein translation can continue. Starvation for amino acids leads to phosphorylation of eIF2, reduction of recycling of eIF2-GDP by eIF2B and preferential translation of GCN4, a transcriptional activator of amino acid biosynthetic enzymes. eIF2B is composed of 5 subunits of which 4, including GCD7, are essential for growth. GCD7 seems to form part of the binding site for phosphorylated-eIF2 thereby mediating inhibition of eIF2B.

GCD7 genes have been found in both mammalian and fungal cells. However, the degree of conservation between fungi is higher than that between fungi and mammalian (approximately 50% vs. 35%). This difference combined with the importance for fungal cell viability makes GCD7 an excellent target for antifungal drug discovery.

GCD7 assays:

(a) ATLAS

(b) Protein translation assay (Colthurst, *et al.*, J Gem Microbiol, 1991, 137:851-857)

(c) Cell-based assays: (i) Various strains of *S. cerevisiae* could be constructed in which ScGCD7 would be replaced with a functional GCD7 gene (*i.e.*, derived from cDNA when necessary) from different organisms, in particular fungi and mammals. These cells would be grown in individual wells containing defined number and mixtures of compounds, which potentially could inhibit growth. Differences in degrees of inhibition by compounds between above-mentioned strains suggest that a compound may inhibit growth by preferentially inhibiting activity of a class of GCD7; (ii) Instead of measuring growth dependent on the presence of inhibitory compounds a more specific assay aimed at expression of GCN4 could be performed. Histidine starvation would be induced with AT thereby making expression of GCN4 required for growth. Alternatively, cells could be grown to higher densities prior to addition of AT and GCN4 activation could be monitored by transcriptional (or translational) fusions of the GCN promotor (plus (part

of) Gcn4p) to a suitable reporter gene/protein (Pavitt *et al.*, Mol Cell Biol, 1997, 17:1298-313).

(d) GDP exchange assays (Cigan *et al.*, PNAS, 1993, 90:5350-5354): eIF2 and eIF2B would be isolated from an appropriate host. eIF2 would complexed with labeled GDP. Incubation of this complex will release labeled GDP, which would be separated from the complex. Compound interference with this liberation would leave high amounts of label.

(e) Protein-protein interaction based assays: (i) A two-hybrid screen (Fromont-Racine *et al.*, Nat Genet, 1997, 16:277-82) using GCD7 and any protein found to interact with GCD7 (*e.g.* other eIF2 subunits); (ii) A direct binding assay. The interacting protein would be fixed onto a carrier an allowed to bind easily detectable GCD7. In the absence of inhibitors, a high signal would result. However, interference with this interaction would reduce the signal. Orientation of the assay could also be reversed by fixation of GCD7 and incubation with labeled interacting protein.

SKI6

Most strains of *Saccharomyces cerevisiae* carry one or more dsRNA viruses. Yeast harboring these viruses are called killer strains and secret toxin which is lethal to most of the ones that carry no viruses. Derepression of toxin expression results in superkiller phenotype (Ridley *et al.*, Mol Cell Biol, 1984, 4:761-70).

SKI6 is one of the many genes that were identified by the superkiller phenotype of mutants. (Masison *et al.*, Mol Cell Biol, 1995, 15:2763-71) It encodes an essential protein that is homologous to bacterial tRNA-processing enzyme, RNase PH. (Lussier *et al.*, Genetics, 1997, 147:435-450;Mitchell *et al.*, Cell, 1997, 91:457-466) Benard et. al. discovered that ski6 mutation bypassed the requirement of polyA tail for efficient mRNA translation, allowing better translation of non-polyA mRNA, including L-A virus mRNA. (Benard *et al.*, Mol Cell Biol, 1998, 18:2688-2696) Later experiments suggested that SKI6 plays an important role in 3'-5' mRNA decay which is consistent with the fact the ski6 mutant derepresses the virus mRNA translation.(Mitchell *et al.*, Cell, 1997, 91:457-466;vanHoof *et al.*, Cell, 1999, 99:347-350)

SKI6 also functions in ribosomal RNA processing. (Allmang *et al.*, GAD, 1999, 13:2148-58) It is a part of exosome complex that functions as 3'-5' exoribonuclease that is required for 5.8S rRNA maturation. (Mitchell *et al.*, Cell, 1997, 91:457-466)

SKI6 Ski6p can be screened by 3'-5' exoribonuclease activities. RNA substrate will be radiolabeled with P-32 and incubated with recombinant purified Ski6p. Loss of TCA precipitable radiolabeled RNA substrate is due to the activity of Ski6 protein, and inhibitors of Ski6p can thereby be screened.

(a) ATLAS: Ski6 protein can be purified to homogeneity. Challenging purified Ski6 protein with different environment conditions such as higher temperature or reduced pH will result in the protein conformation change leading to the unfolding state. Any compound that binds to Ski6 can potentially stabilize protein in the native state. Using ATLAS can help identify compound that binds to Ski6p.

(b) Luciferase assay. Luciferase messenger RNA with or without PolyA tails can be prepared and transfected into yeast through electroporation. Since Ski6p blocks translation of non-polyA mRNA, Luciferase activity will be high with mRNA that contains polyA tails and about 40 times lower with mRNA that has no polyA tails. In the presence of compound that block the activity of Ski6p, luciferase activity in the presence of mRNA that contains polyA tails should remain relatively the same while activity in the absence of polyA tail should increase about 10 times.

NIP1

Eukaryotic protein translation is a initiated by acquisition of mRNA and Met-tRNAiMet by the 40S ribosomal subunit (Hanachi *et al.*, J Biol Chem, 1999, 274:8546-8553). These changes are mediated by Initiation Factors (eIF's). eIF3 is composed of approximately 8-10 subunits, one of which is NIP1. No specific, enzymatic function of NIP1 within eIF3 has been described. However, validation of this gene in C. albicans and S. cerevisiae indicates that the protein is important for cell growth and viability.

NIP1 genes have been found in both mammalian and fungal cells. However, the degree of conservation between fungi is higher than that between fungi

and mammalian (approx. 40% vs. 25%). This difference combined with the importance for fungal cell viability makes NIP1 an excellent target for antifungal drug discovery.

NIP1 assays:

(a) ATLAS

(b) Protein translation assay (Colthurst *et al.*, J Gen Biol, 1991, 137:851-857)

(c) Cell-based assays: Various strains of S. cerevisiae would be constructed in which ScNIP1 would be replaced with a functional NIP1 gene (*i.e.* derived from cDNA when necessary) from different organisms, in particular fungi and mammals. These cells would be grown in individual wells containing defined number and mixtures of compounds, which potentially could inhibit growth. Differences in degrees of inhibition by compounds between above-mentioned strains suggest that a compound may inhibit growth by preferentially inhibiting activity of a class of NIP1.

(d) Protein-protein interaction based assays: (i) A two-hybrid screen (Fromont-Racine *et al.*, Nat Genet, 1997, 16:277-82) using NIP1 and any protein found to interact with NIP1 (*e.g.* other eIF3 subunits); (ii) Direct binding assay: The interacting protein would be fixed onto a carrier an allowed to bind easily detectable NIP1. In the absence of inhibitors a high signal would result. However, interference with this interaction would reduce signal. Orientation of the assay could also be reversed by fixation of NIP1 and incubation with labeled interacting protein

LCP5

LCP5 is an essential *Saccharomyces cerevisiae* gene which encodes a 40.8 Kd protein. LCP5p immunolocalizes to the nucleolus and participates in the early cleavage events at sites A0 to A2 in the pathway of pre-rRNA processing (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372). Depletion leads to reduced levels of 18S ribosomal subunits with concomitant accumulation of 60S ribosomal subunits and a sharp reduction in polysomes (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372). An lcp5-1 mutant shows increased sensitivity to the aminoglycoside antibiotics paromomycin and neomycin, and to cycloheximide, indicating a defect in translation (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372). lcp5-1 mutant, or depletion of Lcp5p, shows sharp

reduction of 18S rRNA, with accumulation of an aberrant 23S pre-rRNA species (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372).

LPC5 assays:

(a) ATLAS

(b) Lcp5 mutant shows predominant processing at site A3 and reduced cleavage at sites A0 and A2 in the 35S pre-rRNA (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372). The defects in processing of ^{35}S pre-rRNA may be monitored by probing with oligonucleotides near the pre-rRNA cleavage sites by Northern Hybridization and primer extension analysis.

(c) The rRNA metabolism may be affected by LCP5 specific compounds and this may be monitored by looking at the total RNA which will show a decrease in the steady state amounts of 18S rRNA (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372).

(d) Compounds may be assayed in presence/absence of aminoglycoside antibiotics paromomycin and neomycin, and to cycloheximide. Since mutant shows an increased sensitivity to these antibiotics (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372), a synergystic effect may be observed.

NCE103

In a search for components of protein export machinery, Cleves et al (Cleves *et al.*, J Cell Biol., 1996, 133(5):1017-26) discovered NCE103 gene that is involved in non-classic export pathway that functions independent of the classical pathway through ER and the Golgi compartments. (Cleves *et al.*, J Cell Biol., 1996, 133(5):1017-26) Even though NCE103 gene appeared to be essential under normal conditions, experiments by Gotz et al suggested that it grew like wild-type under anaerobics conditions. (Gotz, *et al.*, Yeast, 1999, 15:855-864) The predicted amino acid sequence of Nce103p shows high levels of identities to carbonic anhydrase of both prokaryotes and eukaryotes. (Gotz, *et al.*, Yeast, 1999, 15:855-864) Expression of Medicago sativa carbonic anhydrase gene in a high-copy number plasmid complement the growth defects caused by nce103 deletion. (Gotz, *et al.*, Yeast, 1999, 15:855-864) Given that nce103 deletion strain grow like wild-type under anaerobic conditions and null deletion can be complemented by Medicago sativa carbonic anhydrase gene, it was proposed that nce103 functions as an authentic carbonic anhyrase and

is required for protection against certain products of oxidative metabolites under aerobics condition. (Gotz, *et al.*, Yeast, 1999, 15:855-864)

NCE103 assays:

(a) ATLAS: Nce103 protein can be purified to homogeneity. Challenging purified Nce103 protein with different environment conditions such as higher temperature or reduced pH will result in the protein conformation change leading protein to the unfolding state. Any compound that binds to Nce103p can potentially stabilize protein in the native state. Using ATLAS can help identify compound that binds to Nce103p.

ECO1

Saccharomyces cerevisiae ECO1 (also called CTF7) is an essential gene that is required to establish cohesion between sister chromatids during DNA replication. It was isolated as a mutant that can separate sister centromeres in the presence of Pds1p, an anaphase inhibitory protein (Toth *et al.*, Genes and Dev., *13:320*-333, 1999; Skibbens *et al.*, Genes and Dev., 13:307-319, 1999). The protein is essential during S phase to establish sister chromatid cohesion but not during mitosis to maintain it (Skibbens *et al.*, 1999). Cells harboring temperature-sensitive alleles of ECO1 arrest at restrictive temperature predominately as large budded cells with elongated spindles. There is a defect in separation of DNA such that mother cells often contain all the DNA (Skibbens *et al.*, 1999). Some temperature-sensitive mutants display increased chormosome fragment loss at permissive temperature (Toth *et al.*, 1999; Skibbens *et al.*, 1999). The POL30 (DNA replication processivity factor or PCNA) gene in high copy can suppress ctf7 temperature sensitivity and chromosome loss thus lending further support of the hypothesis that CTF1/ECO1 functions in the establishment of sister chromatid cohesion (Skibbens *et al.*, 1999).

ECO1 assays:

(a) ECO1 can be screened in an ATLAS format. Chromosome fragment loss can be assessed in a secondary assay. In this assay, faithful maintenance of a reporter chromosome fragment yields white colonies whereas loss of the reporter chromosome yields red sectored colonies (Toth *et al.*, 1999; Skibbens, *et al.*, 1999). In addition, the DNA content of cells can be analyzed by flow cytometry and in micrographs of cells stained with the nuclear dye, DAPI. (Toth *et al.*, 1999).

(b) Chromosome fragment loss. Faithful maintenance of a reporter chromosome fragment yields white colonies whereas loss of the reporter chromosome yields red sectored colonies (Toth *et al.*, 1999; Skibbens, *et al.*, 1999).

(c) DNA content of cells can be analyzed by flow cytometry and in micrographs of cells stained with the nuclear dye, DAPI. (Toth *et al.*, 1999).

ORC2

Saccharomyces cerevisiae ORC2 is a component of the 6-subunit origin recognition complex (ORC) that acts at the origins of DNA replication distributed throughout the length of chromosomes (Bell *et al.*, Nature, 1992, 357:128-134). ORC2 is required for viability, and temperature sensitive mutations in ORC2 result in cell cycle arrest consistent with defects in DNA replication (Micklem *et al.*, Nature, 1993, 366:87-89; M. Foss *et al.*, Science, 1993, 262:1838-1844; Bell *et al.*, Science, 1993, 262:1844-1849). ORC has been demonstrated to bind origins of replication by DNAse footprinting, and this activity is dependent on ORC2 (Bell *et al.*, Science, 1993, 262:1844-1849; Lee *et al.*, Mol Cell Bio, 1993, 262:1844-1849).The gene has also been shown to be required for transcriptional silencing and telomere silencing (Micklem *et al.*, Nature, 1993, 366:87-89; M. Foss *et al.*, Science, 1993, 262:1838-1844; Bell *et al.*, Science, 1993, 262:1844-1849). These appear to be separable functions for the ORC2 gene product, since the role of ORC2 in silencing can be complemented in yeast by expression of Drosophila ORC2, but its role in replication is not complemented (Ehrenhofer-Murray *et al.*, Science, 1995, 270:1671-1674).

ORC2 assays:

(a) ATLAS: CaOrc2 protein could be purified and challenged with an environmental condition, such as higher temperature or reduced pH, that unfolds the protein. A compound that binds to CaOrc2 protein may stabilize the native conformation of the protein.

(b) Two hybrid interruption screen using another interacting protein: CaOrc2 and a Candida albicans ortholog of another member of the ORC could be placed into yeast two-hybrid screening vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a reporter gene. A compound that interferes in the

binding of the two proteins should disrupt the induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than those in the ORC could be used in this format.

(c) DNA-binding screen: Compounds could be screened for their ability to interfere with the binding of DNA to CaOrc2 protein. The binding of DNA and CaOrc2 protein could be assessed in a variety of ways: 1) through capture on a filter or capture by antibodies; 2) in homogeneous solution using fluorescently-labeled DNA and detection of a change in fluorescence polarization; or 3) detection of a gel shift when DNA is bound by the protein. These screens may be done with other proteins in the ORC present during the assay.

CNS1

Hsp90 chaperone complexes maintain or restore activity in both heat-denatured proteins and signaling proteins prone to deactivation (Dolinski *et al.*, Mol Cell Biol, 1998, 18:7344-7352). In present day models of Hsp90 complex interaction with signaling proteins (*e.g.*, hormone receptors), a cycle is assumed to occur of contruction and degradation of an Hsp90-signaling protein complex into its subunits. When construction of the protein complex is complete, signaling can occur. However, if Hsp90 removal does not occur the signaling protein is degraded.

CNS1 is one of the Hsp90 chaperone complex subunits and is presumably bound via a Tetratrico Peptide Repeat (TPR) domain. CNS1 genes have been found in both mammalian and fungal cells. However, the degree of conservation between fungi is higher than that between fungi and mammalian (approx. 55% vs. 30%). This difference combined with the importance for fungal cell viability makes CNS1 an excellent target for antifungal drug discovery

CNS1 assays:

(a) ATLAS

(b) Cell-based assays: Various strains of *S. cerevisiae* could be constructed in which ScCNS1 would be replaced with a functional CNS1 gene (*i.e.* derived from cDNA when necessary) from different organisms, in particular fungi and mammals. These cells would be grown in individual wells containing defined number and mixtures of compounds, which potentially could inhibit growth. Differences in degrees of inhibition by compounds

between above-mentioned strains suggest that a compound may inhibit growth by preferentially inhibiting activity of a class of CNS1.

(c) Protein-protein interaction based assays: (i) Two-hybrid screen (Fromont-Racine *et al.*, Nat Genet, 1997, 16:277-82) using CNS1 and any protein found to interact with CNS1 (*e.g.* other Hsp90 complex subunits); (ii) Direct binding assay: The interacting protein would be fixed onto a carrier an allowed to bind easily detectable CNS1. In the absence of inhibitors a high signal would result. However, interference with this interaction would reduce signal. Orientation of the assay could also be reversed by fixation of CNS1 and incubation with labeled interacting protein.

YPD1

Saccharomyces cerevisiae YPD1 is an essential gene that functions in a two-component regulatory system in the high-osmolarity sensing MAP kinase pathway. The protein mediates a transfer of a phosphate from Sln1p to Ssk1p under normal osmolarity to inhibit the MAP kinase kinase kinases Ssk2p and Ssk22p (Posas *et al.*, Cell, 86:865-875, 1996). Ypd1 lethality is due to constant activation of the HOG1 pathway (Posas *et al.*, 1996). The structure of Ypd1p has been solved and consists of a four-helix bundle that makes up the central core and contains the active site residue, His64. Residues around the active site are exposed to solvent and are important for phosphotransfer activity (Xu *et al.*, J. Mol. Biol., 292:1039-1050, 1999).

YPD1 assays:

(a) YPD1 is a good candidate for an ATLAS screen. In addition, as a secondary in vitro assay, transfer of radiolabeled phosphate from Sln1p to Ypd1 can be monitored (Li *et al.*, 1998).

(b) Transfer of radiolabeled phosphate from Sln1p to Ypd1 can be monitored in vitro (Li *et al.*, EMBO J., 17:6952-6962, 1998).

TIM10

Tim10 was originally isolated as a suppressor of mrs2 mutant that is defect in mitochondria RNA splicing and respiration. (Jarosch *et al.*, Mol Gen Genet, 1997, 255:157-65) Tim10 belongs to a group of evolutionary conserved protein called TIM family and shares extensive homology with another Tim protein, Tim9. (Bauer, *et al.*, GEBS Lett,

1999, 464:41-47) Located in the mitochondria intermembrane space, it functions to transfer metabolic carrier proteins from cytoplasm to mitochondria. Tim10 is a soluble protein that forms a complex with Tim9 and Tim12 to bind to the precursor protein that is destined to the mitochondria and transfer them to another Tim complex, Tim 54-22-18. (Koehler *et al.*, Science, 279:369-373, 1998; Sirrenberg *et al.*, Nature, 391:912-915, 1998; Adam *et al.*, Embo Journal, 18:313-319, 1999; Koehler *et al.*, Embo J., 17:6477-6486, 1998; Endres *et al.*, Embo J., 18:3214-3221, 1999). Tim 10 is essential for the biogenesis of mitochondria, as well as for viability of yeast cells. (Jarosch *et al.*, Mol Gen Genet, 1997, 255:157-65) As a result of Tim10 depletion, mitochondria undergo dramatic changes in morphology and are unable to assemble cytochrome complexes. (Kubrich *et al.*, J Biol Chem, 1998, 273:16374-16381)

TIM10 assays:

(a) ATLAS: Tim10 protein can be purified to homogeneity. Challenging purified Tim10 protein with different environment conditions such as higher temperature or reduced pH will result in the protein conformation change leading to the unfolding state. Any compound that binds to Tim10p can potentially stabilize protein in the native state. Using ATLAS can help identify compound that binds to Tim10p.

(b) Two-hybrid with Tim9. Even though, Tim10 has been shown to form a complex with Tim9 and Tim 12, only Tim10p direct interaction with Tim9p has been fully addressed. Screening compound that block Tim10 interaction with Tim9 using Two-hybrid will help identify compound that hit Tim10 protein. Tim10 and Tim9 can be used as a pair of genes in yeast with one of them as the bait and the other used as target. Binding of Tim10 and Tim9 protein in yeast will result in the induction of a reporter gene that can be detected. Any compound that interrupt binding of Tim10 protein and Tim9 protein will disrupt the induction of the reporter gene and thus that compound can be identified.

SRB4

SRB4 is an essential component of RNA polymerase II multisubunit complex (Thompson *et al.*, Cell, 1993, 73:1361-75). SRB is known in the art to stand for Suppressor of RNA Polymerase B. SRB4 is required for RNA polymerase II transcription at most of the promoters (Thompson *et al.*, PNAS, 1995, 92:4587-90). It has been recently demonstrated that SRB4 is dispensable for transcriptional activation of some genes

depending on activation mechanism of a particular activator (Lee *et al.*, Gen. Dev., 1999, 13:2934-9). DNA-crosslinking immunoprecipitation assay was used to show that activator-dependent stimulation of TBP binding requires Srb4 (Li *et al.*, Nature, 1999, 399:605-9). *C. albicans* Srb4 protein has an intron and it is about 30% identical to its *S. cerevisiae* Homolog. SRB4 has a potential human homolog which is 20% identical.

SRB4 assays:

(a) ATLAS

(b) Cell-based assays can be set up to monitor transcriptional activation of a reporter gene in wild type strain and SRB4 temperature-sensitive strain.

(c) A two-hybrid system based assay can be developed to monitor interaction between Srb4p and other SRB proteins or RNA polymerase II CTD.

(d) *In vitro* transcription assay (Thompson *et al.*, Cell, 1993, 73:1361-75, Koleske *et al.*, Nature, 1994, 368:466-469).

Sequence identities

The degree of sequence identity between the above *S. cerevisiae* (sc) genes and their *C. albicans* (ca) and, if available, human (hs) homologs are provided in Table 2. (*See* below). Multiple alignments were created using Clustal W (*See* Thompson *et al.*, *supra*), and percentage identities caclulated using the GCG GAP program with a gap creation penalty of 12 and a gap extension penalty of 4. The sequence alignment results are also presented in the figures referred to in Table 2.

Table 2 – Sequence Identities

S. cerevisiae					C. albicans	Human	Sequence identities (%)			FIG.
Nominated targets										
half-life	gene name	orf name	genbank DNA	genbank protein	source	genbank #	ca v sc	sc v hs	ca v hs	
0.11	RPC34	YNR003C	Z71618	CAA96279.1	stan-4-1929	U93869	50.4	28.3	27.3	1
0.34	POP3	YNL282W	Z71558	CAA96194.1	gtc5417	n/a	26.1	-	-	2
0.35	TFA2	YKR062W	Z28287	CAA82141.1	stan-4-2738 / gtc	NP_002086	40.8	23.2	19.4	3
0.36	NAB2	YGL122C	Z72644	CAA96830.1	stan-4-2144	AAD42873	32.2	22.5	22.8	4
0.37	MPT1	YMR005W	Z48613	CAA88520.1	stan-4-2743 / gtc	CAA72189	36.7	23.3	19.2	5
0.39	MTR2	YKL186C	Z28186	CAA82029.1	stan-4-3102	n/a	28.7	-	-	6
0.44	BOS1	YLR078C	X57792	CAA97636.1	stan-4-2841 / gtc	NP_003560	37.9	16.8	18.1	7
0.49	POL30	YBR088C	Z35957	CAA85038.1	gtc2521	P12004	54.5	35.7	41.3	8
0.54	RSA2	YMR131C	NC_001145	CAA88556.1	stan-4-2117	NP_005601	63	24	26.1	9
0.68	SQT1	YIR012W	U75717	AAB69630.1	stan-4-3094	NP_001078	44.5	22.9	25.1	10
0.81	MTW1	YAL034W-A	AB027473	BAA77792.1	stan-4-2532 / gtc	n/a	31.8	-	-	11

0.83	TFB1	YDR311W	M95750	AAB64747.1	stan-4-2961	W19128	32.4	23.3	23	12
0.84	SPC98	YNL126W	Z71402	CAA96007.1	stan-4-2821	AAC39727	30	21.5	19.9	13
0.85	BFR2	YDR299W	D84656	AAB64735.1	stan-4-3108	NM_000055	42.1	20.7	22.5	14
1.05	RNA1	YMR235C	Z49939	CAA90206.1	stan-4-2003 / gtc	CAA57714	51.5	32.1	33.7	15
1.06	GCD7	YLR291C	L07116	AAB67337.1	stan-4-2913	AAC42002	52.2	34.5	35.6	16
1.27	SKI6	YGR195W	L36940	CAA97221.1	stan-4-3104	BAA91279	62.5	34.8	39.1	17
1.28	NIP1	YMR309C	L02899	A46417	stan-4-2825	AAD03462	42.7	30	26.7	18
1.32	LCP5	YER127W	U18916	AAC03225.1	stan-4-2982	AL050003	34.7	18.6	18	19
1.63	NCE103	YNL036W	Z71312	CAA95901.1	stan-4-2981	n/a	34.7	-	-	20
1.67	ECO1	YFR027W	D50617	BAA09266.1	stan-4-2722 / gtc	n/a	34.8	-	-	21
1.86	ORC2	YBR060C	Z35929	CAA85003.1	stan-4-3102 / gtc	Q13416	26.7	21	22	22
1.93	CNS1	YBR155W	Z36024	CAA85114.1	stan-4-3053 / gtc	NP_004614	51.8	26.8	25.6	23
1.96	YPD1	YDL235C	Z74283	CAA98815.1	stan-4-2907	n/a	33.3	-	-	24
0.88*	TIM10	YHR005C-A	Z80875	AAB68435.1	stan-4-3104	NP_036588	68.1	36.6	36.6	25
1.30*	SRB4	YER022W	L12026	AAB64555.1	stan-4-3098	BAA88763	28.4	18	18	26
* half-life determined using temperature-sensitive strain										

Production and Isolation of Target Proteins

The invention is also based on the generation of fungal target protein to be used in analysis as an antifungal target. Such generation requires the use of vectors comprising sequences encoding for *S cerevisiae*, *C. albicans* and/or human target proteins, in particular those listed in Table 1, cells comprising the vectors, and methods for producing the *S cerevisiae*, *C. albicans* and/or human target protein homologs that involve culturing the cells.

A large number of vectors, including plasmid and fungal vectors, have been described for expression in a variety of eukaryotic and prokaryotic hosts. Such vectors will often include one or more replication systems for cloning or expression, one or more markers for selection in the host, *e.g.* antibiotic resistance, and one or more expression cassettes. The inserted target protein encoding sequences may be synthesized, isolated from natural sources, prepared as hybrids, etc. Ligation of the coding sequences to the transcriptional regulatory sequences may be achieved by known methods. Suitable host cells may be transformed/transfected/infected by any suitable method including electroporation, $CaCl_2$ mediated DNA uptake, fungal infection, microinjection, microprojectile, or other established methods.

A wide variety of host/expression vector combinations may be employed in expressing DNA sequences encoding the target proteins, in particular those listed in Table 1. Useful expression vectors, for example, may consist of segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable vectors include derivatives of

SV40 and known bacterial plasmids, *e.g.*, *E. coli* plasmids col El, pCR1, pBR322, pMal-C2, pET, pGEX (Smith *et al.*, Gene 67:31-40, 1988), pMB9 and their derivatives, plasmids such as RP4; phage DNAS, *e.g.*, the numerous derivatives of phage l, *e.g.*, NM989, and other phage DNA, *e.g.*, M13 and filamentous single stranded phage DNA; yeast plasmids such as the 2 micron plasmid or derivatives thereof; vectors useful in eukaryotic cells, such as vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and phage DNAs, such as plasmids that have been modified to employ phage DNA or other expression control sequences; and the like.

Appropriate host cells for expressing protein include bacteria, Archaebacteria, fungi, especially yeast, and plant and animal cells, especially mammalian cells. Of particular interest are *E. coli, B. subtilis, S. cerevisiae*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, and CHO cells, COS cells, HeLa cells, and immortalized mammalian myeloid and lymphoid cell lines. Preferred replication systems include M13, ColE1, SV40, baculovirus, lambda, adenovirus, and the like. A large number of transcription initiation and termination regulatory regions have been isolated and shown to be effective in the transcription and translation of heterologous proteins in the various hosts. Examples of these regions, methods of isolation, manner of manipulation, etc. are known in the art. Under the appropriate expression conditions, host cells can be used as a source of recombinantly produced target proteins. Advantageously, vectors may also include a promoter sequence operably linked to the *S. cerevisiae*, *C. albicans*, and/or human target protein encoding portion. The encoded *S. cerevisiae*, *C. albicans*, and/or human target protein may be expressed by using any suitable vectors and host cells, using methods disclosed or cited herein or otherwise known to those skilled in the relevant art. The particular choice of vector/host is not altogether critical to the invention.

For the purposes of this invention, the promoter sequence in the vector is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined for example, by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase.

Expression of *S. cerevisiae*, *C. albicans*, and/or human target protein may be controlled by any promoter/enhancer element known in the art, but these regulatory elements must be functional in the host selected for expression. Promoters which may be used to control *S. cerevisiae*, *C. albicans*, and/or human target protein gene expression include, but are not limited to, Cytomegalovirus immediate early promoter (CMV promoter; US Patent Nos. 5,385,839 and 5,168,062) the SV40 early promoter region (Benoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, Nature 296:39-42); prokaryotic expression vectors such as the β-lactamase promoter (Villa-Kamaroff, *et al.*, 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the *tac* promoter (DeBoer, *et al.*, 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter; and the animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift *et al.*, 1984, Cell 38:639-646; Ornitz *et al.*, 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl *et al.*, 1984, Cell 38:647-658; Adames *et al.*, 1985, Nature 318:533-538; Alexander *et al.*, 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder *et al.*, 1986, Cell 45:485-495), albumin gene control region which is active in liver (Pinkert *et al.*, 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf *et al.*, 1985, Mol. Cell. Biol. 5:1639-1648; Hammer *et al.*, 1987, Science 235:53-58), alpha 1-antitrypsin gene control region which is active in the liver (Kelsey *et al.*, 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogram *et al.*, 1985, Nature 315:338-340; Kollias *et al.*, 1986, Cell 46:89-94), myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead *et al.*, 1987,

Cell 48:703-712), myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason *et al.*, 1986, Science 234:1372-1378).

Nucleic acids encoding wild-type or variant *S. cerevisiae*, *C. albicans*, and/or human target proteins/polypeptides may also be introduced into cells by recombination events. For example, such a sequence can be introduced into a cell, and thereby effect homologous recombination at the site of an endogenous gene or a sequence with substantial identity to the gene. Other recombination-based methods, such as non-homologous recombinations or deletion of endogenous genes by homologous recombination, may also be used.

The invention is also based on the generation of isolated and purified *S. cerevisiae*, *C. albicans*, and/or human target proteins/polypeptides, including, *e.g.*, a polypeptide having any of the amino acid sequences depicted in Table 1, as identified by their SEQ ID NOS, as well as function-conservative variants of these polypeptides, including fragments that retain transcriptional and/or other growth regulatory activity as described above.

S. cerevisiae, *C. albicans*, and/or human-derived target proteins/polypeptides according to the present invention, including function-conservative variants, may be isolated from wild-type or mutant *S. cerevisiae* and/or *C. albicans* cells, respectively, or from heterologous organisms or cells (including, but not limited to, bacteria, fungi, insect, plant, and mammalian cells) into which a *S. cerevisiae*, *C. albicans*, and/or human-derived target protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins. Alternatively, polypeptides may be chemically synthesized by commercially available automated procedures, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis.

"Purification" of a *S. cerevisiae*, *C. albicans*, and/or human target protein/polypeptide refers to the isolation of the polypeptide in a form that allows its transcription and/or growth regulatory activity to be measured without interference by other components of the cell in which the polypeptide is expressed. Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion

exchange and partition chromatography, and countercurrent distribution. For some purposes, it is preferable to produce the polypeptide in a recombinant system in which the protein contains an additional sequence tag that facilitates purification, such as, but not limited to, a polyhistidine sequence. The polypeptide can then be purified from a crude lysate of the host cell by chromatography on an appropriate solid-phase matrix. Alternatively, antibodies produced against *S. cerevisiae*, *C. albicans*, and/or human target protein or against peptides derived therefrom can be used as purification reagents. Other purification methods are possible.

The polypeptides of the present invention obtained by expression of the polynucleotides of the present invention can be purified from transformed cell cultures by methods known to those of ordinary skill in the art, such as precipitation with ammonium sulphate or ethanol, extraction under acid conditions, anion or cation exchange chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and high performance liquid chromatography (HPLC). Techniques well-known to those of ordinary skill in the art can be used to regenerate the protein if it is denatured during its isolation or purification.

The isolated polypeptides may be modified by, for example, phosphorylation, sulfation, acylation, or other protein modifications. They may also be modified with a label capable of providing a detectable signal, *i.e.*, a reporter molecule, either directly or indirectly, including, but not limited to, radioisotopes and fluorescent compounds.

Antibodies Directed To Target Proteins

The present invention also encompasses antibodies that bind with high affinity to the *C. albicans* target proteins or fragments identified as described above. As used herein, antibodies with high affinity include without limitation antibodies that bind to any *C. albicans* target protein identified herein in its native or denatured, *i.e.*, folded or unfolded, conformation, particularly preferred antibodies are those which recognize either unfolded or folded target protein to be used in assays as described below. Thus, in one embodiment, the antibodies of the invention are those that are antibody preparations with high affinity for the target protein in its native conformation but not in its denatured, unfolded form, or *vice versa*.

Antibodies which specifically recognize a *C. albicans* target protein in either its native or non-native conformation, may advantageously be used in screens for potential antifungal compounds which bind or otherwise inhibit the biological activity of, the *C. albicans* target protein. In such a screen, antibodies specific for the *C. albicans* target protein in its native conformation may be used to test whether potential antifungal compounds prevent denaturation of the target protein, thus indicating a strong interaction with the target.

Following the binding of the potential antifungal compound to the *C. albicans* target protein, the *C. albicans* target protein is subjected to denaturing conditions, such as, for example, high temperature, pH, denaturing solvents, and denaturants such as, *e.g.*, urea. Following the application of these denaturation conditions, the sample containing the *C. albicans* target protein and a potential antifungal compound is reacted with an antibody specific for the *C. albicans* target protein in either its native or non-native conformation. Binding of this antibody type indicates that the binding of the potential antifungal compounds in the screen protected the target protein from denaturation. Thus, the antibodies of the invention which are specific for either the native or the non-native target protein are useful in the screening of antifungal compounds with any *C. albicans* target protein.

Examples of such types of screens can be found in U.S. Patent No. 5,585,277, issued December 17, 1996, and U.S. Patent No. 5,679,582, issued October 21, 1997, each of which are incorporated herein by reference. The antibodies of the invention may be polyclonal or monoclonal, but most preferably monoclonal. The antibodies may be elicited in an animal host by immunization with a *C. albicans* target protein, or fragments derived therefrom which carry epitopes of the *C. albicans* target protein, or may be formed by *in vitro* immunization of immune cells. The immunogens used to elicit the antibodies may be isolated from *C. albicans* cells or produced in recombinant systems. The antibodies may also be produced in recombinant systems programmed with appropriate antibody-encoding DNA. Alternatively, the antibodies may be constructed by biochemical reconstitution of purified heavy and light chains. The antibodies include hybrid antibodies (*i.e.*, containing two sets of heavy chain/light chain combinations, each of which recognizes a different antigen), chimeric antibodies (*i.e.*, in which either the heavy chains, light chains, or both, are fusion proteins), and univalent antibodies (*i.e.*, comprised of a heavy chain/light

chain complex bound to the constant region of a second heavy chain). Also included are Fab fragments, including Fab' and $F(ab)_2$ fragments of antibodies.

Methods for the production of all of the above types of antibodies and derivatives are well-known in the art and are discussed in more detail below. For example, techniques for producing and processing polyclonal antisera are disclosed in Mayer and Walker, 1987, Immunochemical Methods in Cell and Molecular Biology, Academic Press, London. Such antibodies are conveniently made using the methods and compositions disclosed in Harlow and Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, as well as immunological and hybridoma technologies known to those of ordinary skill in the art. Where natural or synthetic peptides derived from any *C. albicans* target protein are used to induce an specific immune response directed against the *C. albicans* target protein, the peptides may be conveniently coupled to a suitable carrier such as KLH and administered in a suitable adjuvant such as Freunds. Preferably, selected peptides are coupled to a lysine core carrier substantially according to the methods of Tam (Proc. Natl. Acad. Sci. USA 1988; 85:5409).

In one embodiment, a purified recombinant *C. albicans* target protein is used to immunize mice, after which their spleens are removed, and splenocytes used to form cell hybrids with myeloma cells and obtain clones of antibody-secreted cells according to techniques that are standard in the art. The resulting monoclonal antibodies are screened using *in vitro* assays such as those described herein for binding to the *C. albicans* target protein or inhibiting its biological activity. The antibodies are tested for specificity of binding to the *C. albicans* target protein in its native conformation by screening the antibodies for target protein binding before and after subjecting the *C. albicans* target protein to denaturing conditions.

Antibodies specific to a target protein in an unfolded conformation are also useful in screening methods as described below.

In addition to their use in the antifungal compound screens described above, the anti-target protein antibodies of the invention, may be used to quantify a selected undenatured *C. albicans* target protein, using immunoassays such as, but not limited to, ELISA. The antibodies may also be used to block the native function of the chosen *C. albicans* target protein by inhibiting its biological activity, immunodepleting cell extracts, or interfering with other reactions related to the function of the target protein. In addition,

these antibodies can be used to identify, isolate, and purify *C. albicans* target proteins from different sources, and to perform subcellular and histochemical localization studies as well as diagnostic analyses to determine the presence of an antigenic *C. albicans* target protein protein in a tissue, blood or serum sample.

Methods for Determining the Essential Nature of a Putative Essential Gene

Various methods can be used to determine whether the product of a gene is essential to the survival of a mycete or essential to the establishment or maintenance of an infection. The identification of the essential character of a gene provides additional information regarding its function and allows selection of genes for which the product constitutes a target of interest for an antifungal substance. Examples of these methods are summarized briefly below. These methods are described in the following works, each of which are hereby incorporated by reference herein: Guthrie C. and Fink G.R. (eds.), Methods in Enzymology, Vol. 194, 1991, 'Guide to Yeast Genetics and Molecular Biology', Academic Press Inc.; Rose A.H., A.E. Wheals and J.S. Harrison (eds.), The Yeasts, Vol. 6, 1995, 'Yeast Genetics', Academic Press Inc.; Ausubel F. *et al.* (eds.), Short Protocols in Molecular Biology, 1995, Wiley; and Brown A.J.P. and Tuite M.F. (eds.), Methods in Microbiology, Vol. 26, 1998, 'Yeast Gene Analysis' Academic Press Inc.

Depending on the circumstances, one of the methods described will be used, depending on the desired result. In particular, it is possible to proceed by a method of either direct inactivation of the gene or transitory inactivation of the gene. Below, we exemplify assays useful for determining the essentiality of *S. cerevisiae* and *C. albicans* genes.

S. cerevisiae Inactivation Analysis

In the yeast *S. cerevisiae*, the method used most generally comprises inactivation of the gene of interest at its site within the chromosome of the yeast. The wild type allele is inactivated by insertion of a genetic marker (for example a gene for auxotrophy or a resistance marker). This insertion is in general obtained by the method of gene conversion with the aid of linear deletion cassettes prepared by known methods, as described in Guthrie C. and Fink G.R. (eds.), Methods in Enzymology, or in Gultner *et al. Nucleic Acid Research*, 1996, 24: 2519-2524.

Preferred methods, yeast cells and vectors for determining if an *S. cerevisiae*

gene and/or protein is essential for growth and viability are described in U.S. Provisional Patent Application 60/056,719, filed August 22, 1997, U.S. Patent Application No. 09/138,024, filed August 21, 1998, now allowed and awaiting issue, and U.S. Patent Application No. 09/573,322, filed May 18, 2000, each of which are incorporated herein by reference.

Briefly, an *S. cerevisiae* strain in which expression of a particular gene can be tightly regulated is generated. To do this the wild-type allele of the gene of interest is replaced with an allele that can be regulated by exogenous metal. The replacement is generally carried out utilizing a double-crossover strategy with a linear piece of DNA prepared by known methods as described in U.S. Patent and Application Nos. cited above.

The recombinant cells comprise, for example:

(i) a first gene encoding a transcriptional repressor protein, the expression of which has been placed under the control of a metal ion-responsive element, wherein expression of the repressor protein is stimulated by the addition of a metal ion to the growth medium of the cells;

(ii) a second gene encoding a selected target protein, wherein expression of the target protein is controlled by a promoter, the activity of which is inhibited by the repressor protein; and

(iii) a third gene encoding a biomineralization protein, wherein the third gene is inactivated and wherein inactivation of the third gene enhances the transcriptional response of the metal-responsive element to added metal ions.

In a preferred embodiment, the first gene is ROX1; the second gene is a gene encoding for a target protein described herein, controlled by an ANB1 promoter; and the third gene is SLF1.

In a particularly preferred embodiment, the recombinant cells comprise an additional gene such that the cells comprise:

(i) a first gene encoding a transcriptional repressor protein, the expression of which has been placed under the control of a metal ion-responsive element, wherein expression of the repressor protein is stimulated by the addition of a metal ion to the growth medium of the cells;

(ii) a second gene encoding a target protein, wherein expression of the target protein is controlled by a promoter, the activity of which is inhibited by the repressor protein;

(iii) a third gene encoding a protein that targets ubiquitin-containing polypeptides for degradation, the expression of which has been placed under the control of a metal ion-responsive element, wherein expression of the ubiquitin targeting protein is stimulated by the addition of a metal ion to the growth medium of the cells, wherein the stability of the target protein is controlled by the ubiquitin targeting protein; and

(iv) a fourth gene encoding a biomineralization protein, wherein the fourth gene is inactivated and wherein inactivation of the fourth gene ènhances the transcriptional response of the metal-responsive element to added metal ions.

Thus, in a particularly preferred embodiment, the first gene is ROX1; the second gene, encoding for a target protein according to the invention, is controlled by an ANB1 promoter; the third gene is UBR1; and the fourth gene is SLF1.

Utilizing this preferred system, expression of the target protein gene is carried out in the absence of added metal ion. When it is desired to decrease or eliminate expression of the target protein gene, metal ions are added to the medium, which stimulate expression of the repressor and ubiquitin tarteting protein to a degree that is dependent upon the concentration of added metal ions and represses transcription of the target protein gene and reduces the stability of the protein. In the preferred system, expression of Rox1 and Ubr1 protein is induced by the addition of copper to the growth media, and thus, expression of the target protein is shut off. If the engineered *S. cerevisiae* strain containing the target protein gene under control of this repressible system stops growing and loses viability in the presence of copper, the target protein is shown to be essential and a cidal target.

S. cerevisiae inactivation analyses of the target proteins described in Table 1 were conducted as described herein and in Example 1, and the results are presented in FIGS. 27-52.

Once the *S. cerevisiae* target protein has been shown to be both essential for growth and viability, and a cidal target in *S. cerevisiae*, the homologous *C. albicans* gene and or protein must then be analyzed to determine if either are essential for growth and can act as a potential cidal target in *C. albicans*. The *C. albicans* gene is identified by comparative sequence analysis. When a DNA fragment is required for some type of analysis

(gene inactivation or protein expression) it is preferably obtained by PCR cloning using methods well known in the art (*See* for example, Eds. C.W. Dieffenbach and E.F. Dvekfler, PCR Primer:A Laboratory Manual Cold Spring Harbor Laboratory Press, Plainview, New York, 1995.)

C. albicans Deletion Analysis

Determining if a particular gene or protein is essential for growth is carried out by determining if, when the gene or protein is inactivated in *C. albicans*, the cells will survive. Because *C. albicans* is a diploid fungus which, largely due to the absence of a sexual phase in its life cycle, is resistant to a considerable number of genetic techniques that are applicable to *S. cerevisiae*, DNA constructs are used to inactivate, or delete all, or a portion, of the gene of interest in *C. albicans*. Such constructs provide for the inactivation or deletion of the wild type allele by insertion of a genetic selection marker (for example a gene for auxotrophy or a resistance marker). This insertion is in general obtained by the method of gene conversion with the aid of linear deletion cassettes prepared by known methods of DNA manipulation as described above.

In one embodiment, in order to assess whether the target protein gene is essential for growth in *C. albicans*, plasmids can be used to construct a double disruptant strain according to the methods outlined in Figures 53-78. If a double disruptant strain can be produces, then the gene is determined to be non-essential. Methods used in these constructions employ common techniques employed in the genetic manipulation and screening of *C. albicans*.

One commonly used approach utilizes *C. albicans* strain CAI4 (Fonzi and Irwin, 1993) to generate a uridine auxotrophic strain of *C. albicans* transformed with linearized DNA fragments containing the *CaURA3* gene (able to confer uridine prototrophy upon transformants) flanked by identical *HisG* sequences. This *HisG-CaURA3-HisG* cassette is flanked by sequences upstream of the gene of interest on one side and downstream of it on the other side.

Prototrophic transformants have undergone replacement of one copy of the gene of interest with the *HisG-CaURA3-HisG* cassette. Auxotrophic, uridine requiring derivatives can be isolated by selecting for 5' fluoro-orotic acid (FOA) resistance in the presence of uridine. The *URA3* gene product converts FOA into fluorouracil which is toxic.

FOA selection therefore allows one to select cells that have lost the *URA3* gene upon *cis*-recombination of the two identical *hisG* flanking regions.

To determine if the gene of interest is essential for growth, a second disruption plasmid is used in order to attempt to inactivate the second copy of the gene. The *CaURA3* gene, as described above, is able to confer uridine prototrophy upon transformants, and is flanked by identical *HisG* sequences. This *HisG-CaURA3-HisG* cassette is flanked by sequences upstream of the gene of interest on one side and downstream of the gene of interest on the other side. Generation of prototrophic transformants can occur by integration of the cassette into the non-disrupted allele of the gene of interest, by replacement of the hisG cassette with the CaURA3 cassette, or by non-homologous recombination events. Transformants that disrupt the second copy of the gene is proof that the gene of interest is not essential. In order to establish that a gene in *C. albicans* is essential for growth, at least 20 second round transformants should be analyzed. If analysis of 20 transformants demonstrates that the second copy of the gene is still present, this indicates that the gene is essential. All transformants are analyzed by Southern blotting. *Candida albicans* transformations are performed as described (Elble R., *Biotechniques* 1992;13:18-20).

A second commonly used approach utilizes *C. albicans* strain CAI8 (Fonzi and Irwin, 1993). CAI8 is a uridine and adenine auxotrohic strain that can be converted to uridine and adenine prototophy by transformation with C. albicans URA3 (CaURA3) and C. albicans ADE2 (CaADE2), respectively.

Deletion of the first allele of the gene of interest is accomplished by transformation of CAI8 to adenine prototophy with a linearized DNA fragment containing the CaADE2 gene flanked by sequences upstream of the gene of interest on one site and downstream of it on the other site.

To determine if the gene of interest is essential for growth, a second disruption plasmid is used in order to attempt to inactivate the second copy of the gene. The *CaURA3* is flanked by sequences upstream of the gene of interest on one site and downstream of it on the other site. Generation of adenine/uridine prototrophic transformants can occur by integration of the cassette into the non-disrupted allele of the gene of interest, or by non-homologous recombination events.. Transformants that disrupt the second copy of the gene is proof that the gene of interest is not essential. In order to establish that a gene in *C. albicans* is essential for growth at least 20 second round transformants should be

analyzed. If analysis of 20 transformants shows that the second copy of the gene is still present and could not be deleted, which indicates that the gene is essential. All transformants are analyzed by Southern blotting. *Candida albicans* transformations are performed as previously described (Elble, 1992).

URA3 can be used for either of the selectable markers as described above with the CAI8 strain.

These types of analytical procedures can also be carried out by transitory inactivation of the gene of interest with adjustable promoters other than that described above with the Rox1 repressor protein. To achieve this, the native promoter of the gene is replaced by an adjustable promoter directly on the chromosome or on an extra chromosomal plasmid. One example of another adjustable promoter for use in this method is the CAL promoter or its derivatives, or the tetO promoter (Mumberg *et al.* 1994, *Nucleic Acid Research*, 22: 5767-5768; Belli *et al.* 1998, *Yeast*, 14: 1127-1138). The essential character of the gene studied can thus be observed, while the promoter used is repressed, either in the haploid strains in the yeast *S. cerevisiae*, or after inactivation of the second allele in the diploid microorganism (for example *C. albicans*).

C. albicans deletion analyses were carried out for each of the target genes identified in Table 1, as described in this section and in Example 2. The results are presented in FIGS. 53-78, each figure representing a single target gene.

Methods for Identifying Homologous Genes

From a known essential gene in a species, genes which are homologous or have the same function in another species of mycete can be identified. The methods known to those of ordinary skill in the art can be used to identify a homolog to a gene studied in another species of mycete (so-called "orthologous" genes) or genes having the same function as the gene studied. Examples of methods which can be used are given below. These methods are described in the following works which are hereby incorporated by reference herein: Sambrook *et al.* 1989, Molecular Cloning, Cold Spring Harbor Laboratory Press; Ausubel F. *et al.* eds. Short Protocols in Molecular Biology, 1995, Wiley; and Guthrie C. and Fink G.R. eds. Methods in Enzymology, Vol. 194, 1991, 'Guide to Yeast Genetics and Molecular Biology', Academic Press Inc.

Such methods include screening for homology or gene complementation to

genomic or cDNA libraries of pathogenic mycetes, or PCR amplification of such library DNA using specific primers selected by virtue of their homology to the nucleotide sequence of interest.

The homologous DNA sequences of other mycetes as defined above can be isolated, in particular, by the PCR amplification methods known to those of ordinary skill in the art. A non-limiting of such PCR technique is carried out using degenerate nucleotide primers to amplify these homologous DNAs from genomic or cDNA libraries of the corresponding mycetes. The cDNAs can also be prepared from mRNAs isolated from mycetes of various species studied in the context of the present invention, directed to *Saccharomyces cerevisiae* and *Candida albicans*, namely *Candida stellatoidea*, *Candida tropicalis*, *Candida parapsilosis*, *Candida krusei*, *Candida pseudotropicalis*, *Candida quillermondii*, *Candida glabrata*, *Candida lusianiae* or *Candida rugosa*, or also mycetes of the type *Aspergillus* or *Cryptococcus*, and in particular, for example, *Aspergillus fumigatus*, *Coccidioides immitis*, *Cryptococcus neoformans*, *Histoplasma capsulatum*, *Blastomyces dermatitidis*, *Paracoccidioides brasiliens* and *Sporothrix schenckil* , or also mycetes of the classes of *Phycomycetes* or *Eumycetes*, in particular the sub-classes of *Basidiomycetes, Ascomycetes, Mehiascomycetales* (yeast) and *Plectascales, Gymnascales* (fungus of the skin and hair) or of the class of *Hyphomycetes*, in particular the sub-classes *Conidiosporales* and *Thallosporales*, and among these the following species: *Mucor, Rhizopus, Coccidioides, Paracoccidioides (Blastomyces, brasiliensis), Endomyces (Blastomyces), Aspergillus, Menicilium. (Scopulariopsis), Trichophyton (Ctenomyces), Epidermophton, Microsporon, Piedraia, Hormodendron, Phialophora, Sporotrichon, Cryptococcus, Candida, Geotrichum, Trichosporon* or also *Toropsulosis*.

Homologous polynucleotides can thus be obtained using the usual methods of cloning and screening, such as those of cloning and sequencing from fragments of chromosomal DNA extracted from cells. For example, to obtain such homologous polynucleotides, it is possible to start from a library of chromosomal DNA fragments. A probe corresponding to a radiolabeled oligonucleotide, preferably made up of 17 nucleotides or more and derived from a partial sequence, can be prepared. The clones containing a DNA identical to that of the probe can thus be identified under stringent conditions. By sequencing individual clones identified in this way using sequencing primers resulting from the original sequence, it is then possible to prolong the sequence in both directions to determine the

sequence of the complete gene. Such sequencing can usually be carried out effectively using a double-stranded denatured DNA prepared from a plasmid. Such techniques are described by Maniatis, T., Frisch, E.F., and Sambrook as indicated above. (Laboratory Manual, Cold Spring Harbor, New York (1989), in particular in 1.90 and 13.70 in the chapters on screening by hybridization and sequencing from double-stranded denatured DNA).

The genomic DNA or cDNA libraries can be prepared by known methods and the polynucleotide fragments obtained are integrated into an expression vector, for example a vector such as pRS423 or its derivatives, which can be used both in the bacterium *E. coli* and in S. cerevisiae. Screening of the library will be carried out by conventional methods of *in situ* hybridization on a replica of bacterial colonies. The hybridization conditions will be adapted to the stringency required for the reaction so that fragments more or less homologous with the gene studied are identified. The genes of other species of mycetes can also be identified by known so-called "gene complementation" methods. For example, a strain of *S. cerevisiae* in which an identified essential gene has been placed under the control of an adjustable promoter can be transformed by a representative sample of a DNA or cDNA library corresponding to the mycete studied. When yeasts are cultured under conditions such that the promoter is repressed, the only yeasts that can survive are the ones that carry a recombinant vector containing a sequence of the mycete studied which is functionally equivalent to the initial essential gene. The gene sequence in the mycete studied is then identified by isolating the recombinant vector and sequencing it by known methods. In the same way, the so called "plasmid shuffle" method allows selection of yeasts which have lost expression of the initial essential gene and contain a functionally equivalent sequence originating from another mycete.

This type of study can be performed on various species: the genes which are functionally equivalent or homologous in sequence to an essential gene can be isolated in other mycetes, and in particular in the various mycetes which are pathogenic to humans. For this, it is possible to use, in particular, mycetes belonging to the classes *Zygomycetes, Basidiomycetes, Ascomycetes* and *Deuteromycetes*. More particularly, the mycetes will belong to the sub-classes *Candida* spp., in particular *Candida albicans, Candida glabrata, Candida tropicalis, Candida parapsilosis* and *Candida krusei*. The mycetes will also belong to the sub-classes *Aspergillus fumigatus, Coccidioides immitis, Cryptococcus neoformans, Histoplasma capsulatum, Blastomyces dermatidis, Paracoccidioidesbrasiliensis* and

Sprorothrix schenckii.

Inhibition of Fungal Growth

The present invention provides for a number of strategies to inhibit fungal growth by inhibiting the biological activity of the target proteins provided herein. As described above, these fungal target proteins are involved in a wide range of activities related to growth and viability, such as, but not limited to, DNA transcription, mRNA translation, mRNA and protein processing and trasport, cell division, growth regulation, cell cycle regulation, and other processes. Although the exact function of some target proteins is not yet known, the target proteins provided by the invention all have the common feature of being involved in fungal growth. In the section below, transcription is exemplified as one potential mechanism through which growth can be affected, but it is to be understood that other mechanisms not specifically described below can be used for studying and/or implementing growth inhibition using the methods described herein.

Transcription

The present invention provides methods of modifying gene transcription by contacting a *S. cerevisiae* and/or *C. albicans* target protein with substances that bind to, or interact with, such a protein or the DNA/RNA encoding such a protein. These substances may modify the influence of the *S. cerevisiae* and/or *C. albicans* target protein on transcription, chromatin remodeling or other processes essential to gene transcription. Substances that bind to, or interact with, the *S. cerevisiae* and/or *C. albicans* target protein or the DNA/RNA encoding such a protein can prevent or enhance its biological activity, which may directly or indirectly inhibit fungal growth.

For example, anti-sense or non-sense nucleotide sequences that hybridize with the *S. cerevisiae* and/or *C. albicans* target protein DNA or RNA and either completely inhibit or decrease their translation or transcription can prevent and inhibit the transcription of other fungal genes. Alternatively, compounds that can bind to or interact with the *S. cerevisiae* and/or *C. albicans* target protein can prevent or enhance the function of the protein in the transcription process. These substances include antibodies that are reactive with and bind to either or both of the *S. cerevisiae* and/or *C. albicans* target proteins.

Candidate Inhibitors

Once it has been determined that the target protein is a cidal target in *Saccharomyces cerevisiae* and essential for growth *Candida albicans*, the protein may be used as a cidal target in order to isolate candidate inhibitors of fungal growth and/or infection.

As noted above, a "candidate inhibitor," as used herein, is any compound with a potential to inhibit, in *Candida albicans* or other fungal species, the biological activity of a target protein. Candidate inhibitor compounds are first identified in a primary screen against the *C. albicans* target protein. This primary screen may be affinity based, mechanistic (*e.g.*, *in vitro* transcription assay), or cell-based (*e.g.*, reporter assay). Such assays are described further below. A candidate inhibitor is tested in a concentration range that depends upon the molecular weight of the molecule and the type of assay. For example, for inhibition of protein/protein or protein/DNA complex formation or transcription elongation small molecules (as defined below) may be tested in a concentration range of 1pg - 100 ug/mL, preferably at about 100 pg - 20 ug/mL; large molecules, *e.g.*, peptides, may be tested in the range of 10 ng - 100 ug/mL, preferably 100 ng - 10 ug/mL.

Inhibitors of *Candida albicans* growth or viability may target the *C. albicans* target proteins described herein, or it may target a protein or nucleic acid that interacts with the *C. albicans* target protein to prevent the natural biological interaction that occurs *in vivo*. An inhibitor identified as described herein must possess the property that at some concentration it will inhibit *Candida albicans* growth or viability, most preferably at the same concentration it will not significantly affect the growth of mammalian, particularly human, cells.

Candidate inhibitors include peptide and polypeptide inhibitors having an amino acid sequence based upon the *C. albicans* target protein sequences described herein. For example, a fragment of the *C. albicans* target protein may act to prevent the growth of wild type *Candida albicans* cells because it acts as a competitive inhibitor with respect to the *C. albicans* target protein binding to other proteins involved in *Candida* growth, *e.g.*, chromatin binding, cell division, transcription, or another essential activity.

Inhibitory compounds to be tested are screened from large libraries of synthetic or natural compounds. Numerous means are currently used for random and directed synthesis of saccharide, peptide, and nucleic acid based compounds. Synthetic compound libraries are commercially available from Maybridge Chemical Co. (Trevillet,

Cornwall, UK), Comgenex (Princeton, NJ), Brandon Associates (Merrimack, NH), and Microsource (New Milford, CT). A rare chemical library is available from Aldrich (Milwaukee, WI). Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available from *e.g.* Pan Laboratories (Bothell, WA) or MycoSearch (NC), or are readily producible. Additionally, natural and synthetically produced libraries and compounds are readily modified through conventional chemical, physical, and biochemical means.

Compounds useful as inhibitors may be found within numerous chemical classes, though typically they are organic compounds, and preferably small organic compounds. Small organic compounds have a molecular weight of more than 50 yet less than about 2,500 daltons, preferably less than about 750, more preferably less than about 350 daltons. Exemplary classes include heterocycles, peptides, saccharides, steroids, and the like. The compounds may be modified to enhance efficacy, stability, pharmaceutical compatibility, and the like. Structural identification of an agent may be used to identify, generate, or screen additional agents. For example, where peptide agents are identified, they may be modified in a variety of ways to enhance their stability, such as using an unnatural amino acid, such as a D-amino acid, particularly D-alanine, by functionalizing the amino or carboxylic terminus, *e.g.* for the amino group, acylation or alkylation, and for the carboxyl group, esterification or amidification, or the like. Other methods of stabilization may include encapsulation, for example, in liposomes, etc.

Primary Inhibitor Screening

High-Throughput Methods For Screening Inhibitors

In a preferred embodiment, a high-throughput screening protocol, also referred to as ATLAS, is used to survey a large number of test compounds for their ability to bind or otherwise interact with a *C. albicans* target protein. High-throughput screening methods are described in U.S. Patent Nos. 5,585,277 and 5,679,582, in U.S.S.N. 08/547,889, and in the published PCT application PCT/US96/19698, and may be used for identifying a ligand that binds the target proteins described herein. According to these methods, a ligand, or a plurality of ligands for a *C. albicans* target protein is identified by its ability to influence the extent of folding or the rate of folding or unfolding of the target protein. Experimental conditions are chosen so that the target protein unfolds to a

measurable extent, whether reversible or irreversible. If the test ligand binds to the target protein under these conditions, the relative amount of folded:unfolded target protein or the rate of folding or unfolding of the target protein in the presence of the test ligand will be different, *i.e.* higher or lower, than that observed in the absence of the test ligand. Thus, the method encompasses incubating the *C. albicans* target protein in the presence and absence of a plurality of test ligands under conditions in which (in the absence of ligand) the target protein would partially or totally unfold. This is followed by analysis of the absolute or relative amounts of folded vs. unfolded target protein or of the rate of folding or unfolding of the target protein.

An important feature of this method is that it will detect any compound that binds to any sequence or domain of the *C. albicans* target protein, and not only to sequences or domains that are intimately involved in a biological activity or function. The binding sequence, region, or domain may be present on the surface of the target protein when it is in its folded state, or may be buried in the interior of the protein. Some binding sites may only become accessible to ligand binding when the protein is partially or totally unfolded.

Briefly, to carry out this method, the test ligand or ligands are combined with the *C. albicans* target protein, and the mixture is maintained under appropriate conditions and for a sufficient time to allow binding of the test ligand. Experimental conditions are determined empirically. When testing test ligands, incubation conditions are chosen so that most ligand:target protein interactions would be expected to proceed to completion. The test ligand is present in molar excess relative to the target protein. The target protein can be in a soluble form, or, alternatively, can be bound to a solid phase matrix. The matrix may comprise without limitation beads, membrane filters, plastic surfaces, or other suitable solid supports.

In a preferred embodiment, binding of test ligand or ligands to the target protein is detected through the use of proteolysis. This assay is based on the increased susceptibility of unfolded, denatured polypeptides to protease digestion relative to that of folded proteins. In this case, the test ligand-target protein combination, and a control combination lacking the test ligand, are treated with one or more proteases that act preferentially upon unfolded target protein. After an appropriate period of incubation, the level of intact *i.e.* unproteolysed target protein is assessed using one of the methods described below *e.g.* gel electrophoresis and/or immunoassay.

There are two possible outcomes that indicate that the test ligand has bound the target protein. Either 1) a significantly higher, or 2) a significantly lower absolute amount of intact or degraded protein may be observed in the presence of ligand than in its absence.

Proteases useful in practicing the present invention include without limitation trypsin, chymotrypsin, V8 protease, elastase, carboxypeptidase, proteinase K, thermolysin, papain and subtilisin (all of which can be obtained from Sigma Chemical Co., St. Louis, MO). The most important criterion in selecting a protease or proteases for use in practicing the present invention is that the protease(s) must be capable of digesting the target protein under the chosen incubation conditions, and that this activity be preferentially directed towards the unfolded form of the protein. To avoid "false positive" results caused by test ligands that directly inhibit the protease, more than one protease, particularly proteases with different enzymatic mechanisms of action, can be used simultaneously or in parallel assays. In addition, co-factors that are required for the activity of the protease(s) are provided in excess, to avoid false positive results due to test ligands that may sequester these factors.

In a typical embodiment of this method, purified target protein is first taken up to a final concentration of about 1-100 g/mL in a buffer containing 50 mM Tris-HCl, pH 7.5, 10% DMSO, 50 mM NaCl, 10% glycerol, and 1.0 mM DTT. Proteases, such as, for example, proteinase K or thermolysin (proteases with distinct mechanisms of action), are then added individually to a final concentration of 0.2-10.0 g/mL. Parallel incubations are performed for different time periods ranging from 5 minutes to one hour, preferably 30 minutes, at 4°C, 15°C, 25°C, and 35°C. Reactions are terminated by addition of an appropriate protease inhibitor, such as, for example, phenylmethylsulfonyl chloride (PMSF) to a final concentration of 1mM (for serine proteases), ethylenediaminotetraacetic acid (EDTA) to a final concentration of 20 mM (for metalloproteases), or iodoacetamide (for cysteine proteases). The amount of intact protein remaining in the reaction mixture at the end of the incubation period may then be assessed by any method, including without limitation polyacrylamide gel electrophoresis, ELISA, or binding to nitrocellulose filters. It will be understood that additional experiments employing a narrower range of temperatures can be performed to establish appropriate conditions. This protocol allows the selection of appropriate conditions (*e.g.*, protease concentration and digestion temperature) that result in

digestion of approximately 70% of the target protein within a 30 minute incubation period, indicating that a significant degree of unfolding has occurred.

In another embodiment, the relative amount of folded and unfolded target protein in the presence and absence of test ligand is assessed by measuring the relative amount of the protein that binds to an appropriate surface. This method takes advantage of the increased propensity of unfolded proteins to adhere to surfaces, which is due to the increased surface area, and decrease in masking of hydrophobic residues, that results from unfolding. If a test ligand binds the *C. albicans* target protein (*i.e.*, is a ligand), it may stabilize the folded form of the target protein and decrease its binding to a solid surface. Alternatively, a ligand may stabilize the unfolded form of the protein and increase its binding to a solid surface.

Surfaces suitable for this purpose include without limitation microtiter plates constructed from a variety of treated or untreated plastics, plates treated for tissue culture or for high protein binding, nitrocellulose filters and PVDF filters.

In another embodiment, the extent to which folded and unfolded target protein are present in the test combination is assessed through the use of antibodies specific for either the unfolded state or the folded state of the protein *i.e.* denatured-specific ("DS"), or native-specific ("NS") antibodies, respectively. (Breyer, *J. Biol. Chem.* 1989; 264(5):13348-13354). Polyclonal or monoclonal antibodies are prepared as described above. The resulting antibodies are screened for preferential binding to the *C. albicans* target protein in its denatured state. These antibodies are used to screen for inhibitors of these interactions.

In another embodiment, molecular chaperones are used to assess the relative levels of folded and unfolded protein in a test combination. Chaperones encompass known proteins that bind unfolded proteins as part of their normal physiological function. In this embodiment, a test combination containing the test ligand and the *C. albicans* target protein is exposed to a solid support *e.g.* microtiter plate or other suitable surface coated with a molecular chaperone, under conditions appropriate for binding the target protein with its ligand and binding of the molecular chaperone to unfolded target protein. The unfolded target protein in the solution will have a greater tendency to bind to the molecular chaperone-covered surface relative to the ligand-stabilized folded target protein. Thus, the ability of the test ligand to bind target protein can be determined by determining the amount

of target protein remaining unbound, or the amount bound to the chaperone-coated surface. Alternatively, a competition assay for binding to molecular chaperones can be utilized.

Once conditions are established for high-throughput screening as described above, the protocol is repeated simultaneously with a large number of test ligands at concentrations ranging from, *e.g.*, 20 to 200 M. Observation of at least a two-fold increase or decrease in the extent of digestion of the target protein signifies a "hit" compound, *i.e.*, a ligand that binds the target protein. Preferred conditions are those in which between 0.1% and 1% of test ligands are identified as "hit" compounds using this procedure.

In yet another embodiment, the test and control combinations described above can be contacted with a conformation-sensitive probe containing a reporter molecule such as, *e.g.*, a fluorescent molecule or radionucleotide, *i.e.*, a probe that binds preferentially to the folded, unfolded, or molten globule state of the *C. albicans* target protein or whose reporter-mediated properties are in any way affected by the folding status of the *C. albicans* target protein.

Phage Display Technology Screening

In addition to the high-throughput screening techniques described above, technologies for molecular identification can be employed in the identification of inhibitor molecules. One of these technologies is phage display technology (U.S. Patent No. 5,403,484. Viruses Expressing Chimeric Binding Proteins). Phage display permits identification of a binding protein against a chosen target. Phage display is a protocol of molecular screening which utilizes recombinant bacteriophage. The technology involves transforming bacteriophage with a gene that encodes an appropriate ligand (in this case, a candidate inhibitor) capable of binding to the target molecule of interest. For the purposes of this disclosure, the target molecule may be a *C. albicans* target protein. The transformed bacteriophage (which preferably is tethered to a solid support) express the candidate inhibitor and display it on their phage coat. The cells or viruses bearing the candidate inhibitor which recognize the target molecule are isolated and amplified. The successful inhibitors are then characterized.

Phage display technology has advantages over standard affinity ligand screening technologies. The phage surface displays the microprotein ligand in a three dimensional conformation, more closely resembling its naturally occurring conformation. This allows for more specific and higher affinity binding for screening purposes.

Biospecific Interaction Analysis Screening

Another relatively new screening technology which may be applied to the inhibitor screening assays of this invention is biospecific interaction analysis (BIAcore, Pharmacia Biosensor AB, Uppsala, Sweden). This technology is described in detail by Jonsson *et al.* (Biotechniques 11:5, 620-627 (1991)). Biospecific interaction analysis utilizes surface plasmon resonance (SPR) to monitor the adsorption of biomolecular complexes on a sensor chip. SPR measures the changes in refractive index of a polarized light directed at the surface of the sensor chip.

Specific ligands (*i.e.*, candidate inhibitors) capable of binding to the target molecule of interest (*i.e.*, a *C. albicans* target protein or a protein-protein or protein-DNA complex containing the *C. albicans* target protein) are immobilized to the sensor chip. In the presence of the target molecule, specific binding to the immobilized ligand occurs. The nascent immobilized ligand-target molecule complex causes a change in the refractive index of the polarized light and is detected on a diode array. Biospecific interaction analysis provides the advantages of; 1) allowing for label-free studies of molecular complex formation; 2) studying molecular interactions in real time as the assay is passed over the sensor chip; 3) detecting surface concentrations down to 10 pg/mm^2; detecting interactions between two or more molecules; and 4) being fully automated (Biotechniques 11:5, 620-627 (1991)).

Screening Through Use Of A Transcription Assay

In cases where the target protein has been identified as being required for transcription *per se* and/or elongation, the present invention encompasses the identification of agents useful in modulating fungal gene transcription, particularly the transcription of genes by RNA polymerase II in a target protein-dependent manner. Thus, if the target protein has been identified as being essential for transcription and/or elongation, inhibitors of *Candida albicans* growth and viability may also be screened either by measuring inhibition of any of the activities described above, or by assaying formation of a protein/DNA complex or inhibition of sporulation when cells are contacted with *Candida albicans* inhibitors.

In Vitro Transcription Assay

If an essential target protein has been identified as being required for transcription, and it has been identified according to any of the screening methods described above, its activity and effect on transcription can be confirmed by adding it to an *in vitro* transcription reaction, and measuring its effect on the target protein-mediated activated transcription, using an *in vitro* transcription assay. For example, DNA of interest (*i.e.*, DNA to be transcribed) can be admixed with (i) purified RNA polymerase II, (ii) the SRB proteins, (iii) transcription factors b, e, g or a, (iv) the *C. albicans* target protein and (v) the substance (ligand) to be tested. The mixture is maintained under conditions sufficient for transcription to occur. The resulting combination is referred to as a test mixture. DNA transcription can be assessed by determining the quantity of mRNA produced. Transcription is determined in the presence of the substance being tested and compared to DNA transcription in the absence of the test substance taking place under identical conditions (*e.g.*, a control mixture). If transcription occurs to a lesser extent in the test mixture, (*i.e.*, in the presence of the substance being evaluated) than in the control mixture, the substance may have interacted with one or more SRB proteins , or with the *C. albicans* target protein, preferably in such a manner as to inhibit transcription. If transcription occurs to a greater extent in the test mixture than in the control mixture, the substance has interacted in such a manner as to stimulate transcription.

Transcription of DNA sequences, or translation of mRNA sequences encoding the *C. albicans* target protein can also be inhibited or decreased by inhibitor compounds, resulting in decreased production of, or the complete absence of the *C. albicans* target protein. Gene transcription can be modified by introducing an effective amount of a substance into a cell that inhibits transcription of the gene encoding the *C. albicans* target protein, or that inhibits translation of mRNA encoding the *C. albicans* target protein. For example, antisense nucleotide sequences can be introduced into the cell that will hybridize with the gene encoding the target protein and inhibit transcription of the gene. (*See*, *Current Protocols in Molecular Biology*, Eds. Ausubel *et al.* Greene Publ. Assoc., Wiley-Interscience, NY, NY, 1997). Alternatively, an antisense sequence can be introduced into the cell that will interfere with translation of the mRNA encoding the *C. albicans* target protein.

Secondary Screens - Measurement of Inhibition of Candida albicans Growth in Culture

Once a putative inhibitor has been identified in the primary screen or screens, it may be desirable to determine the effect of the inhibitor on the growth and/or viability of *Candida albicans* in culture. Methods for performing tests on fungal growth inhibition in culture are well-known in the art.

Non-limiting examples of such procedures test the candidate inhibitor compounds for antifungal activity against a panel of three strains: *C. albicans*, *S. cerevisiae*, and *A. nidulans*. One such procedure is based on the NCCLS M27A method (The National Committee for Clinical Laboratory Standards, Reference Method for Broth Microdilution Antifungal Susceptibility Testing of Yeasts; approved standard, 1997) to measure minimum inhibitory concentrations (MICs) and minimum fungicidal concentrations (MFCs). An overview of this of this protocol follows.

Media

1. *Sabouraud dextrose agar* (SDA): 10 g Bacto Neopeptone; 40 g Bacto Dextrose; 15 g Bacto Agar. Suspend contents in 1 liter of water and boil while stirring to dissolve completely. Autoclave for 15 minutes. SDA is conveniently sold as a powdered mix by DIFCO (Cat #0109-17-1).

2. *Potato dextrose agar* (PDA): 4 g Potato extract; 20 g Bacto Dextrose; 15 g Bacto Agar. Suspend contents in 1 liter of water and boil while stirring to dissolve completely. Autoclave for 15 minutes. PDA is conveniently sold as a powdered mix by DIFCO (Cat #0013-17-6).

3. *RPMI-1640*: 10.4 g powdered media (Sigma R-6504, w/ glutamine & w/o bicarbonate); 2.0 g $NaHCO_3$ (Sigma S-6297); 34.53 g MOPS buffer (Sigma M-6270). Dissolve powdered media and $NaHCO_3$ in 900 ml distilled water. Add MOPS and stir until dissolved. Adjust pH to 7.0 using 1N NaOH. Bring final volume to 1 liter, filter sterilize, and store at 4°C.

4. *RPMI-1640 with 12.5 % mouse serum*: 10.4 g powdered media (Sigma R-6504, w/ glutamine & w/o bicarbonate); 2.0 g $NaHCO_3$ (Sigma S-6297); 34.53 g MOPS buffer (Sigma M-6270); 50 ml mouse serum (Sigma S-7273). Dissolve powdered media and $NaHCO_3$ in 750 ml distilled water. Add MOPS and stir until dissolved. Adjust pH to 7.0 using 1N NaOH and bring volume to 875 ml. Remove 350 ml and add to it 50 ml

of mouse serum. Bring remaining volume of media (525 ml) to 600 ml with the addition of 75 ml of distilled water. Filter sterilize each solution and store at 4°C.

Inoculum Preparation

1. *Yeasts:* Yeasts (*Saccharomyces cerevisiae* and *Candida albicans*) are cultured on Sabouraud dextrose agar (SDA) plates in a 35°C incubator. Strains on SDA plates are stored at 4°C and used as working stock cultures. Working stock plates are prepared once a month from frozen stocks of cells. Inoculum for susceptibility testing is prepared from fresh 24 hour cultures. 5-10 colonies are scraped from the plate and suspended in three milliliters of sterile 0.85% saline (8.5 g/liter NaCl). The cell density of the solution is determined by measuring the absorbance in a spectrophotometer (Shimadzu UV-1201S UV-VIS Spectrophotometer) set at 600 nm. An absorbance value between 0.1 and 0.4 is required for an accurate reading.

For *C. albicans*, *e.g.*, strain ATCC 10231, 1.0 OD_{600} unit is approximately 10^7 cells per ml while for *Saccharomyces cerevisiae* strain CTY552 1.0 OD_{600} unit is slightly less than 10^7 cells per ml. Dilute the cell suspension with the appropriate medium (typically RPMI-1640) to OD_{600}=0.0003 for *Candida* and OD600=0.0004 for *Saccharomyces*. The diluted suspension should contain approximately 3 X 10^3 cells per ml (this is a 2X concentration inoculum). Two 100 ul aliquots of this dilution should be spread on SDA plates and incubated at 35°C for 1-2 days to determine the precise number of colony forming units. An acceptable range for the inoculum (2X) is 1-5 X 10^3 cfu/ml (100-500 for 100 ul). Following two-fold dilution of the inoculum with compound, the final concentration of cells will be 0.5-2.5 X 10^3 per ml. The inoculum should be kept at 4°C and used within a few hours.

2. *Filamentous fungi*: Filamentous fungi (*Aspergillus* spp.) should be cultured on Potato dextrose agar (PDA) plates in a 35°C incubator. A fresh plate should be started from frozen cell stocks once a month. Inoculum of *Aspergillus* for susceptibility testing is prepared from plates incubated at 35°C for 5 days. Colonies are covered with five ml of sterile 0.85% saline (8.5 g/liter NaCl) and gently rocked for 10-15 minutes. To dislodge the conidia, use an automatic pipettor to gently wash over the colonies. The saline solution is removed from the plate and the heavy particles allowed to settle for 3-5 minutes. The upper suspension is removed and vortexed for 15 sec. The turbidity of the solution is determined by measuring the absorbance in a spectrophotometer (Shimadzu UV-1201S UV-

VIS Spectrophotometer) set at 600 nm. An absorbance value between 0.1 and 0.4 is required for an accurate reading.

Dilute the cell suspension with the appropriate medium (typically RPMI-1640) to OD_{600}=0.0004. The final suspension should contain approximately 3 X 10^3 cfu per ml (this is a 2X concentration inoculum). Two 100 ul aliquots of this dilution should be spread on SDA plates and incubated at 35°C for 1-2 days to determine the precise number of colony forming units. An acceptable range for the inoculum (2X) is 1-5 X 10^3 cfu/ml (100-500 for 100 ul). Following two-fold dilution of the inoculum with compound, the final concentration of cells will be 0.5-2.5 X 10^3 per ml. The inoculum should be kept at 4°C and used within a few hours.

Compound Preparation

Stock solutions and concentrations tested will vary from compound to compound. In general, though, stock solutions of 12.8 mg/ml in DMSO (Sigma D-8779) should be prepared. This will allow for a 128 ug/ml starting test concentration containing 1% DMSO. Stock solutions should be stored at -20°C and dilutions for antifungal testing should be freshly prepared before each assay.

For compounds of unknown activity or ones with MIC values of >4 ug/ml, a range of concentrations from 128 ug/ml to 0.125 ug/ml should be used. More active compounds, such as Amphotericin B (Sigma A2411) and Itraconazole (Research Diagnostics Inc. cat# 30.211.44), require a lower range of concentrations (16 ug/ml to 0.016 ug/ml). Stock solutions of Amphotericin B and Itraconazole should be prepared at 1.6 mg/ml in DMSO. Amphotericin B is sold as a powder that is approximately 80% Amphotericin B. Stock solutions should be made accordingly (2.0 mg of powder for a 1 ml solution of 1.6 mg/ml Amphotericin B).

Stock solutions of control compounds (1.6 mg/ml, Amphotericin B or Itraconazole) are initially diluted in medium to a concentration of 32 ug/ml while stock solutions of test compounds (typically 12.8 mg/ml) are diluted to 256 ug/ml. Both of these (control and test compounds) represent 1:50 dilutions. For an assay with three fungal strains, 40 microliters of a stock solution should be diluted to 2.0 ml with room temperature medium. If a stock solution of a test compound is not at 12.8 mg/ml, the appropriate

dilution must be calculated. Serial dilutions will be produced (see below) using these initial dilutions. Addition of cells to compound will produce an additional two-fold dilution.

Natural product extracts are tested at concentrations ranging from 200 to 204,800 fold dilution of the extract based upon the initial culture volume. The extract should first be diluted 100 fold then serial dilutions produced as directed below.

Assay Setup

Antifungal susceptibility tests should be setup in polystyrene, 96-well, flat bottom plates (Costar 9017). To every well in columns 2-12 is added 100 microliters of media. An electronic multichannel (12) pipettor with no tip on channel one makes this job simple. To every well in column one is added 200 microliters of diluted compound (32 ug/ml for Amphotericin B and Itraconazole controls, 256 ug/ml for test compounds, 100-fold dilution for natural product extracts). A manual multichannel (8) pipettor is then used to set up a series of 2-fold dilutions. 100 microliters is removed from each well of column one and mixed with 100 microliters in column 2. This is done successively (column two to column three etc.) to produce a set of 11 serial dilutions (column 12 is a drug free control).

To every well in two rows, 100 ul of inoculum (2X) of a single strain is added. To the final two rows on the plate (G & H), only media is added. Addition of inoculum is best accomplished using an electronic multichannel (12) pipettor. This setup (see below) creates a starting cell density of 500-2500 per ml (100-500 per well) and drug concentration ranging from 16 ug/ml to 0.016 ug/ml for controls (Amphotericin B and Itraconazole), 128 ug/ml to 0.125 ug/ml for pure test compounds, and 200 to 204,800-fold dilutions for natural product extracts.

It is important to determine the number of colony forming units (CFUs) present in each strain inoculum (2X). Two 100 ul aliquots of each inoculum (2X) should be spread on SDA plates and incubated at 35°C for 1-2 days to determine the precise number of colony forming units. An acceptable range for the inoculum (2X) is 1-5 X 10^3 cfu/ml (100-500 for 100 ul). Following two-fold dilution of the inoculum with compound, the final concentration of cells will be 0.5-2.5 X 10^3 per ml. The plates should then be placed in a dark, 35°C incubator for 48 hours.

Modified Assay Setup for Low Solubility Compounds

Some compounds are not very soluble in aqueous media even at low

concentrations and dilution artifacts can result from precipitation of the compounds. To avoid such problems a series of two fold dilutions at 100 times the final concentration is prepared from the stock solution in the same solvent (typically DMSO). Each intermediate solution is then diluted to final strength with 1X inoculum.

This type of assay setup involves making a series of 11, 2-fold dilutions in DMSO ranging from 12,800 ug/ml to 12.5 ug/ml for test compounds and 1600 ug/ml to 1.6 ug/ml for control compounds (Amphotericin B and itraconazole). Two microliters of diluted compound are placed into each well of the appropriate column (12,800 ug/ml in column 1, down to 12.5 ug/ml in column 11, and DMSO to column 12). To every well in two rows, 200 ul of inoculum (1X) of a single strain is added. To the final two rows on the plate (G & H), only media (200 ul) is added. Addition of inoculum is best accomplished using an electronic multichannel (12) pipettor. Final concentrations of cells and compounds are the same as described above for the standard assay setup. Please note that the inoculum in this assay is at 1X concentration, while the inoculum for the assay described above is a 2X concentrate. The 1X inoculum is made by adding an equal volume of media to the 2X inoculum.

NCCLS recommends using this type of assay setup for insoluble compounds, including Amphotericin B and Itraconazole. While we are able to obtain reasonably consistent results for Amphotericin B and Itraconazole using the standard assay setup, some test compounds may benefit from doing the serial dilutions in DMSO. Compounds that form heavy precipitates upon dilution to media should be considered for this assay, particularly if the compound seems to be a promising candidate or inconsistent results are obtained in the standard assay.

Reading the Results

Minimum Inhibitory Concentration (MIC): The MIC is the lowest concentration of an antifungal agent that inhibits growth of the organism. For Amphotericin B, the lowest drug concentration which gives no visible growth is the MIC. For Itraconazole (and other azoles), the lowest drug concentration which reduces growth to $\leq$ 20% of the growth control (column 12) is the MIC.

For test compounds that give a sharp endpoint (like Amphotericin B), the lowest drug concentration which gives no visible growth is the MIC. For test compounds that give a trailing effect on inhibition of cell growth (like the azoles), the lowest drug

concentration which reduces growth to $\leq$ 20% of the growth control (as determined by measurement of turbidity) is the MIC.

The turbidity of each well is determined by measuring the absorbance at 415 nm on a plate reader (BIO-RAD Model 3550-UV). The rows containing no cells (G & H) serve as a control for absorbance. Column 12, containing no compound, serves as the growth control.

Minimum Fungicidal Concentration (MFC): The MFC is the lowest concentration of an antifungal agent that results in an inviable culture. Two slightly different standards and assays are applied, depending on the circumstances. For each of the two methods, though, culture viability should be determined beginning with the drug dilution immediately below the MIC and continuing through to the highest drug concentration.

The first and more rigorous standard considers a culture to be inviable if it contains $\leq$ 1% of the colony forming units of the starting culture. This is determined by completely removing the cells from a well of the microtiter plate and placing them in a microfuge tube containing 1.3 ml of RPMI media. The cells are spun for 2 minutes, supernatant poured off, cells resuspended in the remaining media, and spread on an SDA plate. The plate is incubated at 35°C for 1-2 days, and the colonies counted. These numbers are compared to the original cfu count from day 1 of the assay.

A second, simpler method is more practical for processing a large number of samples and is the method that we routinely use. Following resuspension of the cells by pipetting, 15 microliters is spotted directly to an SDA plate and incubated for 2 days at 35°C. A culture is considered inviable if no colonies form on the plate. While this method is much simpler than the one above, it is less quantitative and no efforts are made to wash the compound away from the cells before plating. One may observe inhibition of growth on the agar plate if a compound is still present at high enough concentrations

The control compound Amphotericin B is a cidal drug and the MIC is typically equal to the MFC. Itraconazole, in contrast, is a static drug and viable cells should be recovered from wells containing compound at concentrations well above the MIC.

Quality Control

Cell density of the inoculum (2X) must be between 1 and 5 X 10^3 cfu/ml (100-500 cfu per 100 microliters). Starting cell concentration in the assay will be 0.5 to 2.5

X 10^3 cfu/ml.

Acceptable MIC range values (ug/ml):

	Am B	Itraconazole
Candida albicans, *e.g.*, ATCC 10231	0.25-1.0	0.25-1.0
Saccharomyces cerevisiae, *e.g.*, CTY552	0.25-1.0	0.25-1.0
Aspergillus nidulans, *e.g.*, NRRL 194 (ATCC 38163)	0.5-2.0	0.25-1.0

If the starting cell density or MIC values do not fall within the acceptable range, all results in the assay for the particular strain in question are considered invalid and the assay should be repeated.

Secondary Screens - Mechanistic Assays

The preferred inhibitor compounds of the invention are those which possess antifungal activity, although compounds with significant activity in an *in vitro* mechanism-based assay may be considered for further development. Such secondary assays are performed to determine the mechanism of action of these compounds. Such secondary mechanistic assays include *in vitro* experiments, as well as and *in vivo* experiments in fungi, to determine the mechanistic inhibitory activity of these compounds. The precise nature of these assays will depend on the target.

Compounds that prevent cell growth through inhibition of the target protein are considered for further development.

Counterscreening in Other Species

In parallel to secondary screen assays, counterscreens are performed to determine if the compounds inhibit the activity of any human homolog. The precise nature of the counterscreen(s) will depend on the nature of the target protein. These counterscreens may include an affinity assay to determine if the compound binds the human homolog or an *in vitro* or cell-based mechanistic assay to determine if the compound inhibits the activity of the human protein.

Cytotoxicity studies on mammalian cells are also performed to determine if the compound is toxic to mammalian cells in culture. Compounds that do not bind to and/or inhibit the activity of the human homolog will be considered for further development.

Transcription Inhibition Counterscreen Using Human Homolog

When the essential target protein has been identified as being required for growth and as an inhibitor of *Candida albicans* according to one or more of the assays described herein, it may be tested further in order to determine its effect on the host organism. In the development of useful antifungal compounds for human therapeutics, it is desirable that such compounds act as effective agents in inhibiting the viability of the fungal pathogen while not significantly inhibiting human cell systems. Specifically, inhibitors of *Candida albicans* identified in any one of the above described assays may be counterscreened for inhibition of a human homolog of the target protein.

If available, the human gene encoding for the target protein can be expressed and purified utilizing published methods and its homology to the yeast target protein homolog(s). The human homolog can be contacted with candidate inhibitor in assays such as those described above using a human cell culture system. The effectiveness of a *C. albicans* inhibitor as a human therapeutic is determined as one which exhibits a low level of inhibition against its human homolog relative to the level of inhibition with respect to the *C. albicans* target protein. For example, it is preferred that the amount of inhibition by a given inhibitor of the human homolog in a human system be no more than 20% with respect to the amount of inhibition of the *C. albicans* target protein.

Such inhibitors are "selective inhibitors" of the *C. albicans* target protein which "selectively inhibit" *C. albicans* biological activity. The lack of effect of a test compound on mammalian transcription or other growth-related mechanisms is tested by replacing yeast components with an analogous human *in vitro* transcription system as in *e.g.* Manley *et al. Proc.Natl.Acad.Sci.USA* 77:3855, 1980.

An example of one such mammalian cytotoxicity screening method is described in Example 3.

Chemical Analoging

It is important to note that some compounds may prove to be cytotoxic, but not inhibitory of the activity of the human homolog. Compounds that exhibit such non-target based cytotoxicity are still considered for further development. Chemical analoging efforts may be used to separate the target-based antifungal activity from the non-target-based cytotoxicity activity.

Chemical analoging is also used to identify compounds with improved antifungal activity and reduced cytotoxicity. The secondary assays and counterscreens described above are used in parallel with antifungal assays to ensure that compounds remain active against the appropriate target, *i.e.*, remain inhibitory with the same mechanism of action.

Antifungal testing against a broad spectrum of fungal species and a large number of isolates is also performed at this point. The broad spectrum of fungal species will include those resistant to existing therapeutics, *e.g.*, Amphotericin B and various azoles such as, for example, intraconzole and fluconazole. Compounds which inhibit growth of fungi, particularly *Candida* and *Aspergillus* species, at a concentration of 4 ug/ml or less, exhibit minimal cytotoxicity, and have a confirmed mechanism of action are considered for further development..

Preclinical Development of Candidate Drugs

Subsequent preclinical development of compounds includes, but is not limited to: formulation, toxicology, pharmacokinetics, animal efficacy studies, and medicinal chemistry. Compounds with the desired characteristics are selected for clinical trials in human subjects.

Dosage and Pharmaceutical Formulations

For therapeutic uses, inhibitors identified as described herein may be administered in a pharmaceutically acceptable/biologically compatible formulation. The compositions of the present invention can be administered in dosages and by techniques well known to those skilled in the medical, veterinary, and agricultural arts taking into consideration such factors as the age, sex, weight, species and condition of the particular patient, and the route of administration. The compositions of the present invention can be administered alone or in combination, or can be co-administered or sequentially administered with additional antifungal agents, such as, *e.g.*, nystatin, amphotericin B, flucytosine and the various antifungal azoles.

Such pharmaceutical compositions can be used in particular for treatment of topical and systemic fungal infections and can be administered bucally, rectally, parenterally or locally by topical application to the skin and the mucous membranes, or by intravenous or

intramuscular injection. These compositions can be solid or liquid and can be in any of the pharmaceutical forms generally used in human medicine, such as, for example, simple or coated tablets, capsules, granules, suppositories, injectable preparations, ointments, creams, gels and aerosol preparations. The pharmaceutical compositions of the invention are prepared by the usual methods known to those of ordinary skill in the art. The active principle can be incorporated in them with excipients usually employed in pharmaceutical compositions, such as talc, gum arabic, lactose, starch, magnesium stearate, cacao butter, aqueous or non-aqueous vehicles, fatty substances of animal or plant origin, paraffin derivatives, glycols, various wetting, dispersing or emulsifying agents and preservatives.

Liquid preparations are useful for 1) mucosal administration, *e.g.*, oral, nasal, anal, vaginal, peroral, intragastric administration and the like, in the form of solutions, suspensions, syrups, elixirs; and 2) topical administration *e.g.*, in the form of a cream, ointment, lotion or spray. Further, liquid pharmaceutical formulations comprising the inhibitors to be used for parenteral, subcutaneous, intradermal, intramuscular, intravenous administrations, and the like, such as sterile solutions, suspensions or emulsions, e.g, for administration by injection, can be formulated without undue experimentation.

In order for a composition to be administered to an animal or human, and for any particular method of administration, it is preferred to determine the toxicity, such as by determining the lethal dose (LD) and LD_{50} in a suitable animal model, *e.g.*, mouse; the dosage of the composition(s), and the concentration of components in the composition; and the timing of administration in order to maximize the antiviral and/or antimicrobial response. Such factors can be determined without undue experimentation by such methods as titrations and analysis of sera for antibodies or antigens, *e.g.*, by ELISA and/or EFFIT analysis. Such determinations do not require undue experimentation from the knowledge of the skilled artisan, the present disclosure and the documents cited herein.

The formulations can be administered in a pharmaceutically effective amount and/or an antifungal effective amount, taking into account such factors as the relative activity and toxicity for the target indication, *e.g.*, antifungal activity, as well as the route of administration, and the age, sex, weight, species and condition of the particular patient.

As discussed above, the pharmaceutical compositions of the present invention can be solutions, suspensions, emulsions, syrups, elixirs, capsules, tablets, creams, lotions and the like. The compositions may contain a suitable carrier, diluent, or excipient, such as

sterile water, physiological saline, glucose, or the like. Moreover, the compositions can also be lyophilized, and/or may contain auxiliary substances, such as wetting or emulsifying agents, pH buffering agents, adjuvants, gelling or viscosity enhancing additives, preservatives, flavoring agents, colors, and the like, depending upon the route of administration and the preparation desired. Standard texts, such as "Remington's Pharmaceutical Science", 17th Ed., 1985, incorporated herein by reference, may be consulted to prepare suitable preparations, without undue experimentation.

The amount of inhibitor administered will be determined according to the degree of pathogenic infection and whether the infection is systemic or localized, and will typically be in the range of about 1ug - 100 mg/kg body weight. Where the inhibitor is a peptide or polypeptide, it will be administered in the range of about 100 - 500 ug/mL per dose. A single dose of inhibitor or multiple doses, daily, weekly, or intermittently, is contemplated according to the invention.

The route of administration will be chosen by the physician, and may be topical, oral, transdermal, nasal, rectal, intravenous, intramuscular, or subcutaneous.

The following examples are intended as non-limiting illustration of the present invention.

EXAMPLE 1: <u>*S. cerevisiae* **Inactivation Analysis**</u>

Yeast genomic DNA preparation

This protocol can be used to prepare genomic DNA from Candida albicans cultures as well as Saccharomyces cerevisiae. Streak a yeast stock culture from a glycerol stock to a YPD (Bio101 Cat# 4001-242) plate and incubated for 48 hours at 30°C. Pick a single, distinct colony into 5 ml of YPD media (Bio101 Cat# 4001-042), and incubate overnight at 30°C in a roller drum. Cells from 1 ml of this culture are pelleted with a 5 second spin in a microcentrifuge. The cells are washed one time with 1 ml TE (10 mM Tris-Cl, pH 8.0, 1 mM EDTA) and respun. Resuspend the pellet in 0.2 ml Extraction Buffer (2% TritonX100, 1% SDS, 100mM NaCl, 10mM Tris pH 7.5 and 1mM EDTA) and add 0.2 ml phenol/chloroform/isoamyl (25:24:1, v:v:v). Add 0.3 g acid washed 400 micron glass beads. Vortex for 5 minutes. Add 0.2 ml TE; spin in a microcentrifuge for 10 minutes at 10-13 krpm. Remove the aqueous phase to a fresh tube. Precipitate with 2.5

volumes absolute ethanol. Spin and resuspend the pellet in 400 ul TE plus 3 ul of a 10 mg/ml RNase A stock. Incubate at 37°C for 5 minutes. Add 10 ul 4 M ammonium acetate and 1 ml absolute ethanol. Mix by inversion and centrifuge for 8 minutes in a microcentrifuge. Air dry the pellet and resuspend in 50 ul TE. Store at 4°C. The solution may appear somewhat cloudy. Before diluting this stock for use in PCR reactions or Southern blotting, vortex the stock sample briefly.

Alternately, the YeaStar Genomic DNA Kit is available from Zymo Research (Cat. # D2002). It has the advantage of avoiding the use of glass beads and phenol:choloroform mixtures, and produces very clean genomic DNA, although in some cases it has proven to be a somewhat less reproducible method than that detailed above.

Transformation of S. cerevisiae

Streak strain to a rich media plate (such as YPD) and incubate at 30°C for 48 hours. Pick a single distinct colony to 2-5 ml YPD media and incubate overnight on a roller drum. Dilute to A600 = 0.2 in 200 ml YPD and incubate at 30°C until A_{600} = 0.8 (about 4 hours growth under normal circumstances). Divide the culture into 4 sterile 50 ml tubes. Centrifuge at medium low speed, for instance in a Beckman JT-6 at 3000 rpm for 5 minutes. Resuspend and combine the pellets in 20 ml H_2O. Re-centrifuge. Resuspend the pellet in 10 ml TEL (10mM Tris pH 7.5, 1 mM EDTA, 0.1 M lithium acetate). Recentrifuge again and resuspend in 2 ml TEL. Competent cells are stable at room temperature for up to four hours. If you wish to make frozen stocks, you may add sterile glycerol (from a 50% stock) to a final concentration of 15%, then freeze by placing in a -80°C freezer (do not quick freeze in liquid nitrogen or dry ice/ethanol bath). The frozen competent cells can be expected to be 3-5 fold less competent than freshly made competent cells.

Add 100 μg well sheared single stranded carrier DNA and the 30 μl digested plasmid DNA to a clean eppendorf tube. Add 100 ml competent cells and mix. Add 0.8 ml PLATE (40% PEG-3350 10mMTris pH7.5, 1 mM EDTA, 0.1 M lithium acetate) and mix well. Incubate 30 minutes at 30°C. Heat shock 20 minutes at 42°C. Centrifuge for 5 seconds in a microcentrifuge and remove the supernatant. Wash the pellet with 1 ml TE, spin again and plate the pellet in a minimal volume (<50 μl) onto selective media such as (-)HIS plates.

TEL and PLATE solutions are available commercially (SIGMA Cat. T-0809 and P-8966), and seem to be stable at room temperature. We have found that for TEL and

PLATE made in the laboratory, the solutions work best if made fresh the day of the transformation from stock solutions of Tris-Cl , EDTA , PEG-3350 and lithium acetate.

After 48 to 72 hours incubation at 30°C, depending on the growth rate of the specific strain, individual colonies are coordinately struck with a sterile toothpick to two identically arrayed plates, one of which is (-)HIS and one of which is (-)HIS (+)Cu. Pick at least 12 colonies in this manner and incubate the resultant plates for 48-72 hours (again, depending on the strain growth rate) at 30°C. Be sure to pick a colony or two of CUY106 as a positive control for growth on the (-) HIS (+) Cu plate. After incubation, the plates are scored for growth. In the case of true copper sensitive strains, there will be a clear lack of growth on the (-) HIS (+) Cu plates, and clear growth on the (-)HIS plates.

Copper titration

Single colonies from a selective plate (see above) are picked to CSM media (Bio101 Cat. # 4500-022) and grown overnight at 30°C in a roller drum. The use of Bio101 CSM appears to be critical to the reproducibility of the titrations. Cultures are diluted to A600 = 0.2 and are 2 ml portions are aliquoted to sterile capped culture tubes. From a 500 mM stock, copper sulfate is added to each tube to final concentrations of 0 uM ((-) copper control), 10 uM, 20 uM, 50 uM, 100 uM, 200 uM, 500 uM 1.0 mM, 1.5 mM and 2.0 mM. The ten tubes are incubated at 30°C on a roller drum for 16-20 hours. The A600 of each aliquot is measured, and the results are graphed on a semi-log plot: Y axis = A600 of sample normalized to the A600 of the (-)copper control (linear scale). X axis = concentration of $CuSO_4$ (log scale).

Copper time course

Single colonies from a selective plate (see above) are picked to CSM media (Bio101 Cat. # 4500-022) and grown overnight at 30°C in a roller drum. As is the case for the copper titrations, the use of Bio101 CSM appears to be critical to the reproducibility of the copper time courses. Cultures are diluted in 25 ml of CSM to A600 = 0.02 - 0.1. the cultures are split evenly between two sterile 50 ml tubes and allowed to grow in a shaker/incubator for 1 hour at 30°C. Addition of 1 mM copper sulfate (from a 500 mM sterile stock) to one of the cultures defines the 0 time point. At each time point, a 1.2 ml aliquot is taken from each culture for analysis, and the cultures are quickly returned to incubation at 30°C with shaking. The exception to this is the 0 time point, at which time only the culture which does not receive added copper is assayed as the data point for both

the cultures. Part of each aliquot is used to measure the A600, while the rest is used to perform a serial 10-fold dilution series: 100 ul of the aliquot is diluted serially with 900 ul aliquots of sterile water. Fresh pipette tips are used for each step of the dilution series, representing 101, 102, 103, 104 and 105 fold dilutions of the original culture. Appropriate dilutions are plated to YPD plates, and the plates are marked with a strain identifier, time point, whether or not they contain copper, and which dilution has been plated. Plates are placed at 30°C and checked both 48 and 72 hours after they have been plated; visible colonies are counted and normalized to colonies per ml of original culture, based on the dilution factor, and the plating factor (since only 100 ul and not 1 ml was plated).

Appropriate dilutions to plate to YPD:

For CUY106, and other copper insensitive strains:

At 0 time point:	10^3, 10^4, 10^5
At time points less than 10 hours:	10^3, 10^4, 10^5
At time points greater than 10 hours:	10^4, 10^5, 10^6

For genes of unknown cidality:

At 0 time point:	10^3, 10^4, 10^5
At time points less than 10 hours:	10^1, 10^3, 10^5
At time points greater than 10 hours:	10^0, 10^2, 10^4, 10^6

The 100 dilution o refers to a plating of 100 μl of undiluted culture. It is recommended for cultures containing copper sulfate that the undiluted samples be spun in a microcentrifuge for 5 seconds and the pellets resuspended in sterile water before plating to YPD in order to avoid contamination by copper sulfate. For all other samples in the dilution series, this extra step has proven unnecessary. In cases of extreme cell non-survival, a second time course is recommended, to confirm the results of the first. In this case, the appropriate dilutions to plate will depend on the results of the original experiment: static effects may be more carefully assayed by biasing towards greater dilutions, while large fungicidal effects can be captured with lesser dilutions at the later time points. In some cases, we have found that concentration of the culture is necessary (for instance, concentration of 1 ml to a volume of 100 μl or even 10 ml to 100 μl to obtain a measurable number of live cells following exposure to copper (the latter case requires adjustments to the volumes used in the experiment to accommodate the large volumes needed).

Results from *S. cerevisiae* inactivation analyses for the target genes described in Table 1 are shown in FIGS. 27-53.

EXAMPLE 2: **_C. albicans_ Transformation**

From a single colony on a plate, grow up a 1 ml overnight culture of Candida albicans in YPD supplemented with 20 μg/ml uridine. at 30°C with agitation. Dilute the culture into 50 ml uridine-supplemented YPD and grow at 30°C with agitation. When the A_{540} of the culture reaches 2, cool the cells on ice for 10 minutes, then Centrifuge at 5000 rpm for 10 minutes at 4°C. Wash the pellet two times with 10 ml TE and recentrifuge each time. Resuspend the pellet in 1 ml TELD (10 mM Tris-Cl, 1 mM EDTA, pH 7.5, 0.01 M lithium acetate, 0.01 M DTT). It is important to make TELD fresh from 10X stocks of each of the components (10X DTT should be stored frozen). Spin briefly in a microcentrifuge. Resuspend the pellet in 200 ul TELD. This is sufficient competent yeast for 4 transformations. To a fresh tube add: 50 μl competent yeast preparation, 5 μl 10 mg/ml carrier DNA (Clontech), 1-2 μl of digested and gel purified plasmid fragment (at 1-2 μg/ml), 300 μl of PEG Solution TELD (10 mM Tris-Cl, 1 mM EDTA, pH 7.5, 0.01 M lithium acetate, 0.01 M DTT, 40% PEG4000 (VWR Cat. # 9727-2)). Mix by inversion. Incubate 30 min at 30°C, then heat shock 20 minutes at 42°C. Spin 15 seconds in a microcentrifuge. Resuspend the pellet in 200 μl TE and spread on (-)URA plates.

EXAMPLE 3: **Mammalian Cell Cytotoxicity Screen**

Reagents

From ATCC: CV-1 fibroblast cell line originated from a male African monkey kidney. Cat. No.: CCL-70

From Gibco BRL:

Dulbecco's modifed Eagle's Medium ("DMEM") 1X liquid.	Cat. No.: 11965-065
Dulbecco's modifed Eagle's Medium without Phenol red.	Cat. No.:11054-020
Fetal bovine serum	Cat. No.: 26140-079
Gentamicin reagent solution	Cat. No.:15710-015
Trypsin-EDTA	Cat. No.: 25300-54

From Sigma:

In vitro toxicology assay kit, XTT based.	Cat. No.:TOX-21.

(XTT is 2,3-bis(2-Methoxy-4-nitro-5-sulfophenoyl)-2H-tetrazolium-5-carboxyanilideinn salt)

Procedure

1. Split CV-1 cell at 1:20 using DMEM medium supplemented with 10% FBS and 10 g/ml gentamycin.

2. Three days after the splitting, CV-1 cell should reach about 80-90% confluency.

3. Aspirate the medium out and add 5 ml of PBS.

4. Add 3 ml of trypsin and let stand for 3 minutes. Add 2 ml of DMEM to inactivate the trypsin.

5. Take 0.5 ml of cell and diluted with 10 ml of DMEM. This should make the cell concentration in the range 0.5-1.5 x 10^5 cells / ml.

6. Add 100 μl cell suspension to row 2-8 of 96 well plates. Add medium only to row 1.

7. Incubate cells for 24 hours.

8. Make1:50 dilution of the compound to be tested with concentration of 12.8 mg/ml.

9. Add 300 ul to column 1 from row 4 to row 8.

10. Row 1 and row 2 of column 1 should be filled with 300 μl medium only. Row 3 of column 1 should be filled with 300 μl medium with 2 %DMSO so that final concentration of DMSO will start with 1%.

11. Fill columns 2 ,3, 4, 5 and 6 with 200 μl DMEM medium.

12. Make a 1 to 3 serial dilution from column 1 to column 6.

13. Take out 100 μl of each different conc of compound into the cell plate from column 1 to 6 and duplicate with 7- 12.

14. Incubate the cells for another 24 hours.

15. Dissolve 5 mg of XTT into 25 ml of DMEM medium without phenol red.

16. Take out the compound solution by aspiration.

17. Wash the 96 well plate with 300 μl PBS and sit for 3 minutes.

18. Add 100 μl XTT solution to column 1-6 and add DMEM medium (without phenol red) to column 7-12.

19. Measure $O.D.^{450}$ and subtract $O.D.^{650}$ at the plate reader. Also, take

time points at 1 hr intervals for 4 hours.

20. Split the CV-1 cells 1:20 using DMEM medium supplemented with 10% FBS and 10% genamycin.

XTT is a measure of mitochondrial activity and, therefore, is considered a reasonable measure of cell growth and viability. After subtracting the OD690 from OD 450, each compound-treated datapoint shall be compared with that of no-compound treatment and this determines the percentage of growth. The percentage of inhibition is defined as one minus the percentage of growth. Percentage of inhibition is plotted vs compound concentration. TC_{50} is defined as the compound concentration that inhibits cell growth by 50%. The data from the cytotoxicity assay together with the results of the antifungal assays can be used to calculate a therapeutic ratio (TC_{50}/MIC). The higher this ratio, the more attractive the compound. Analoging and medicinal chemistry can be used to improve this ratio.

* * *

All of the references identified hereinabove, are hereby expressly incorporated herein by reference to the extent that they describe, set forth, provide a basis for or enable compositions and/or methods which may be important to the practice of one or more embodiments of the present inventions.

WE CLAIM:

1. A method of screening or testing a candidate anti-fungal compound for interaction with an essential protein, comprising;

a) providing an essential protein selected from the group consisting of RPC34, POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;

b) providing one or more test compounds;

c) contacting said essential protein with said one or more test compounds; and

d) determining the interaction of the test compound with said essential protein.

2. The method of claim 1, wherein said essential protein comprises a fragment, a function-conservative variant, a fragment or an active fragment of the essential protein. [

3. A method of screening or testing a candidate anti-fungal compound for modulation of activity of an essential protein, comprising;

a) providing an essential protein selected from the group consisting of RPC34, POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;

b) providing one or more test compounds;

c) contacting said essential protein with said one or more test compounds;and

d) determining the modulation of activity of said essential protein in the presence of said test compound.

4. The method of claim 3, wherein said essential protein comprises a fragment, a function-conservative variant, a fragment or an active fragment of the essential protein.

5. A method of screening or testing a candidate anti-fungal compound for interaction with an essential protein in a culture of cells, comprising;

a) providing an essential protein within a culture of cells that express said

essential protein is selected from the group consisting of RPC34, POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;

b) providing one or more test compounds;

c) contacting said culture of cells with said one or more test compounds;and

d) determining the interaction said test compound with said essential protein.

6. The method of claim 5, wherein said culture of cells comprises bacterial cells, fungal cells, yeast cells or mammalian cells.

7. The method of claim 5, wherein said culture of cells comprises recombinant cells.

8. The method of claim 5, wherein when expression or function of said essential protein is reduced or blocked, growth rate of a fungus expressing said essential protein is inhibited.

9. The method of claim 5, wherein when expression or function of said essential protein is reduced or blocked, viability of a fungus expressing said essential protein becomes reduced.

10. The method of claim 5, wherein said essential protein comprises a fragment, a function-conservative variant, a fragment or an active fragment of the essential protein.

11. A method of screening or testing a candidate anti-fungal compound for effects on growth or viability of a culture of cells, comprising;

a) providing an essential protein within a culture of cells that express an essential protein selected from the group consisting of RPC34, POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;

b) providing one or more test compounds;

c) contacting said culture of cells with said one or more test compounds;and

d) determining the effects on the growth or viability of said culture of cells.

12. The method of claim 11, wherein said culture of cells comprises fungal cells or yeast cells.

13. The method of claim 11, wherein said culture of cells comprises recombinant cells.

14. The method of claim 11, wherein when expression or function of said essential protein is reduced or blocked,the growth rate of a fungus expressing said essential protein is inhibited.

15. The method of claim 11, wherein when expression or function of said essential protein is reduced or blocked, viability of a fungus expressing said essential protein is reduced.

16. The method of claim 11, wherein said essential protein comprises a fragment, a function-conservative variant, a fragment or an active fragment of said essential protein.

17. A method of screening or testing a candidate anti-fungal compound for interaction with an essential protein in a non-human animal, comprising;

a) providing a non-human animal with a cell or group of cells expressing an essential protein selected from the group consisting of RPC34, POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;

b) providing one or more test compounds;

c) contacting said non-human animal with said one or more test compounds;and

d) determining the interaction of said test compound with said essential protein.

18. The method of claim 17, wherein when the interaction of said test compound with said essential protein reduces or blocks expression or function of said essential growth rate of a fungus expressing said essential protein is inhibited.

19. The method of claim 17, wherein when the interaction of said test compound with said essential protein reduces or blocks expression or function of said essential, viability of a fungus expressing said essential protein is reduced.

20. The method of claim 17, wherein said essential protein comprises a fragment, a function-conservative variant, a fragment or an active fragment of the essential protein.

21. A method of screening or testing the effects of a candidate anti-fungal compound on growth or viability of a cell or group of cells expressing an essential protein in a non-human animal, comprising;

a) providing the non-human animal with the cell or group of cells expressing an essential protein selected from the group consisting of RPC34, POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;

b) providing one or more test compounds;

c) contacting said test animal with said one or more test compounds;and

d) determining the effects on the growth or viability of said cell or group of cells.

22. The method of claim 21, wherein when expression or function of said essential protein is reduced or blocked growth rate of a fungus expressing said essential protein is inhibited.

23. The method of claim 21, wherein when expression or function of said essential protein is reduced or blocked, viability of a fungus expressing said essential protein becomes reduced.

24. The method of claim 21, wherein said essential protein comprises a fragment, a function-conservative variant, a fragment or an active fragment of said essential protein.

25. The method of claim 3, wherein the modulation of activity comprises modulation of fungal gene transcription.

26. The method of claim 5, wherein the interaction is assessed by binding of said test compound with said essential protein or activity of said essential protein in the presence of said test compound.

27. The method of claim 17, wherein the interaction is assessed by binding of said test compound with said essential protein or activity of said essential protein in the presence of said test compound.

28. A method of screening or testing a candidate anti-fungal compound for binding with an essential protein, comprising;

a) providing an essential protein selected from the group consisting of RPC34, POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;

b) providing one or more test compounds;

c) contacting said essential protein with said one or more test compounds;and

d) determining the binding of the test compound with said essential protein.

29. A method of screening or testing a candidate anti-fungal compound for modulation transcription of a gene encoding an essential protein, comprising;

a) providing a gene encoding an essential protein selected from the group consisting of RPC34, POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;

b) providing one or more test compounds;

c) contacting said gene with said one or more test compounds; and

d) determining the modulation of transcription of said gene of said essential protein in the presence of said test compound

Rpc34p (YNR003C)

Comparison	% Identity
Sac-Can	50.4%
Sac-Hum	28.3%
Can-Hum	27.3%

```
CARPC34    1 -----MSEMLVSDKARHLYTKMREYPTSKLEDQ----DELQTLFDIKKGSELMEYLQELV
SCRPC34    1 MSGMIENGLQLSDNAKTLHSQMMSKGIGALFTQ----QELQKQMGIGSLTDLMSIVQELL
HSRPC39    1 -MGEVKVKVQPPD-ADPVEIENRIIELCHQFPHGITDQVIQNEMPHIEAQQRAVAINRLL

CARPC34   52 NGKYVKISKMGDQLKFQTVAEEEAKKVSSMSDDEAMIYSYIEASGREGIWIKTIKAKTNL
SCRPC34   57 DKNLIKLVKQNDELKFQGVLESEAQKKATMSAEEALVYSYIEASGREGIWSKTIKARTNL
HSRPC39   59 SMGQLDLLRSNTGLLYRIKDSQNAGKMKGSDNQEKLVYQIIEDAGNKGIWSRDIRYKSNL

CARPC34  112 HQHIVQKCLKNLENNRYIKSIKSVKHPTRKIYMLYNLQPSIDVTGGPWFTDSELDIEFIE
SCRPC34  117 HQHMVLKCLKSLESQRYVKSVKSVKFPTRKIYMLYSLQPSVDITGGPWFTDGELDIEFIN
HSRPC39  119 PLTEENKILKNLESKKLIKAVKSVAASKKKVYMLYNLQPDRSVTGGAWYSDQDFESEFVE

CARPC34  172 TLLEVCWRFIVGKTMYIKDEEADNEDINPLQTTYHNHHPG--VNLDQLVEFINNSNIISV
SCRPC34  177 SLLTIVWRFISENTFPNGFKNFEN---GPKKNVFYAPNVKNYSTTQEILEFITAAQVANV
HSRPC39  179 VLNQQCEKFLQSKAETAR----ES-----KQNPMIQRNSS-FASSHEVWKYICELGISKV

CARPC34  230 ELGINDIRSLCDVLIYDDRIEEVGGNQENSGEEKATWQSITDKGNTILQNNYQDLKNVVS
SCRPC34  234 ELIPSNIRSLCEVLVYDDKLEKVT-HD--C--YRVTLESILQMN------------QGEGE
HSRPC39  229 ELSMEDIETILNTLIYDGKVEMTIIAAKEGTVGSVDGHMKLYRA------------VNPII

CARPC34  290 EDCENYLQQNQSDFSVFSYKSTIQDIQDESDIVYIDSWMNE
SCRPC34  278 PEAGNKALEDEEEFSIFNYFKMFPASKHDKEVVYFDEWTI-
HSRPC39  278 PPTG-LVRAPCGLCPVFDDCHEGGEIS-PSNCIYMTEWIEF
```

Figure 1

Pop3p (YNL282w)

Comparison	Identity
Sac-Can	26.1%

```
CAPOP3     1  MNKSNKVKKPSVAKVSTKAASSSLKSQEAKRQVERPILDNSFT-QSNQWPFIEPTIANDI
SCPOP3     1  MSGSLKSLDKKIAK---------------RQVYKPVLDNPFTNEAHMWPRVHDQPLIWQ

CAPOP3    60  VDLLEVLLKMQDSTFKYRGFNPTVSALEKQAAANRGIHKNACVQIKYVFVCKYD-ISPAT
SCPOP3    46  LLQSSIINKLIHIQSKENYPWELYTDFNEIVQYLSGAHGNS--DPVCLFVCNKDPDVPLV

CAPOP3   119  LTNVFPTLCFTASKSAEDRVKLIQLPRGSLERLSKALGVDRVGIFGLTKDTEGAQPLFDL
SCPOP3   104  LLQQIPLLCYMAPMT----VKLVQLPKSAMDTFKS---VSKYGMLLLRCDDRVDKKFVSQ

CAPOP3   179  INENVKDIEAPWLDCIFREEMVFNQPNTKHVASTVGRKKNKK
SCPOP3   157  IQKNVDLLQFPWLNAIKYRPTSVK--LLKTTVPIVSKKRQK-
```

Figure 2

Tfa2p (YKR062W)

Comparison	Identity
Sac-Can	40.8%
Sac-Hum	23.2%
Can-Hum	19.4%

```
YKR062w_SAC          1 MSKNRDP-LLANLNAFKSKVKSAP-VIAPAKVGQKKTNDTVITIDGNTRKRTASERAQEN
YKR062w_CAN          1 ----MSD-LSAQLSAFKNKIKSGPSVIVPKKATFTQS-------P-------SSPLSSST
gi|4504195_HUMAN     1 ----MDPSLLRERELFKKRALSTP--VVEKRSASSES---------------SSSSSKKK

YKR062w_SAC         59 TLNSAKNPVLVDIKKEAGSNSSNAISLDDDDDDEDFGSSPSKKVRPGSIAAAALQANQTD
YKR062w_CAN         42 TTTTSKN--DANVKKRSTTDSVTRVLKK-------------QK------------ANMGE
gi|4504195_HUMAN    40 KTKVEHG--GSSGSKQNSDHSNGSFNLKALS------------------------GSSGY

YKR062w_SAC        119 TSKSHDSSKLLWATEYIQKKGKPVLVNELLDYLS-MKKDDK---VIELLKKIDRIEEDPK
YKR062w_CAN         75 MTGSHLSIQLHLAVEYIKEHDQPLSVEKLQNYLS-FDISHT---LLPLLNEIDRVKYDES
gi|4504195_HUMAN    74 KFGVLAKIVNYMKTRHQRGDTHPIALDEILDETQHIDIGLKQKQWLMTEALVNNPKIEVI

YKR062w_SAC        175 KGTEKYISTYDVHSPSELLKLLRS--QVTFKGISCKDLKDGWPQCDETINQLEEDSKILV
YKR062w_CAN        131 KGTLEYVSLHNIRSSDDVLEFLRR--QTTFKGTSVKELKDGWAGCVAAIDELESQGKILV
gi|4504195_HUMAN   134 DGKYAFKPKYNVRDKKALLRLLDQHDQRGLGGILLEDIEEALPNSQKAVKALG-DQILFV

YKR062w_SAC        233 LRTKKDKTPRYVWYNSGGNLKCIDEEFVKMWENVQLPQFA--ELPRKLQDLGLKPAS-VD
YKR062w_CAN        189 LRNKKENAPRIVWANNGGELGYIDTEFKDMWDQVKLPEPD--VLYQKLLDQGLKPTG-AD
gi|4504195_HUMAN   193 NRPDKK---KIEEENDKSCQFSVDEEFQKEWRSVTVDSMDEEKIEEYLKRQGISSMQESG

YKR062w_SAC        290 PATIKRQTKRVEVKKKRQRKGKITNTHMTGILLKDYSHRV---
YKR062w_CAN        246 PNLIKKQPQQKEKKQKKARRGKITNTHMKGILLKDYSQLV---
gi|4504195_HUMAN   250 PKKVAPIQRRKKPASQKKRRFKTHNEHLAGVLKDYSDITSSK
```

Figure 3

Nab2p (YGL122C)

Comparison	Identity
Sac-Can	32.2%
Sac-Hum	22.8%
Can-Hum	22.5%

```
CANAB2     1 MQFAPDNQIGKELQQNLIQEIQRRFNKPAEDAVDIADYIIYLIVAKKSEQEIVAEVKDID
SCNAB2     1 ----MSQEQYTENLKVLVAEKLAGIPNFNEDIKYVAEYIVLLIVNGGTVESVVDELASLF
HS_PART    1 ------------------------------------------------------------

CANAB2    61 ISIDVGFLG-------------------DVYLEIRKLEVKYN-QPPAAVEEASQPQQEQ
SCNAB2    57 DSVSRDTLANVVQTAFFALEALQQGESAENIVSKIRMVNAQSLGQSDIAQQQQQQQQQQ
HS_PART    1 ------------------------------------------------------------

CANAB2   100 --------QQQSQASVVAPQIPIGPKKQLTEEEKIALRSQRFGTT--------------T
SCNAB2   117 PDIAQQQPQQQPQLQPLQPQLGTQNAMQTDAPATPSPISAFSGVVNAAAPPQFAPVDNSQ
HS_PART    1 ------------------------------------------------------------

CANAB2   138 RLSGRGGRGGITKTRTDFRNGHN---NKNFLDPKKLDQIISGANNGAIKEVPLPPKGRCP
SCNAB2   177 RFTQRGG-GAVGKNRRGGRGGNRGGRNNNSTRFNPLAKALGMAGESNMNFTPTKKEGRCR
HS_PART    1 ----------PQQLHLLSRQLED---PNGSFS-NAEMSELSVAQK------PEKLLERCK

CANAB2   195 DFPYCKN-QNCEKAHPTKNCFNYPICPNPPGTCNFLHPDQDQELIAKLETSKKEFEEKKK
SCNAB2   236 LFPHCPLGRSCPHAHPTKVCNEYPNCPKPPGTCEFLHPNEDEELMKEMERTREEFQKRKA
HS_PART   41 YAPACKNGDECAYHHPISPCKAEPNC-KFAEKCLFVHPN---------------------

CANAB2   254 NQLMVKQG--------SCKYGLKCAKENCPFAHPTPANPESGKIETLEWCPQGKNCQDRNC
SCNAB2   296 DLLAAKRKPVQTGIVLCKEGALCSNPSCPFSHPTPAN-EDAKVIDLMWCDKNLTCDNPEC
HS_PART   79 ----------------CKYDAKCIKPDCPFTHVSRRI----------QLCRYFPACKKMEC

CANAB2   307 TKSHP--------PPPTANSEKLLSAAQLALEQCKFGSQCTNLKCPRRHATSAVPCRAGAE
SCNAB2   355 RKAHSSLSKIKEVKPISQKKAAPPPVEKSLEQCKFGTHCTNKRCKYRHARSHIMCREGAN
HS_PART  114 PFYHP-------------------------KHCRFNTQCTRPDCTEYHPTINVPPRHALK

CANAB2   360 CRRVDCIFSHPLKEPCRFGTKCTNKVCMYQHPEGRTLASHTWTRDGSGNNNSTSN-RSFA
SCNAB2   415 CTRIDCLFGHPINEDCRFGVNCKNIYCLFRHPPGRVLP---EKKGAAPNSNVPTNERPFA
HS_PART  149 WIRPQTSE----------------------------------------------------

CANAB2   419 VSEDQIMEQVAQA-------------
SCNAB2   472 LPENAIIENAPPQTSFTHQEDTEMN
HS_PART      --------------------------
```

Figure 4

Mpt1p (YMR005W)

Comparison	Identity
Sac-Can	36.7%
Sac-Hum	23.3%
Can-Hum	19.2%

```
CAMPT1      1 ------------------------------------------------------MSHKSM
SCMPT1      1 ---------------------------------MANSPKKPSDGTGVSASDTPKYQHLVP
HSTFIID   661 ALRQLTPDSAAFIQQSQQQPPPPTSQATTALTAVVLSSSVQRTAGKTAATVTSALQPPVL

CAMPT1      7 TSTPQESSNLKRQLE-NSEDSSSPN--KRSKTETTTENQSSWESDFNSLP-----VELLQ
SCMPT1     28 ETKPAFNLSPGKASE-LSHSLPSPSQIKSTAHVSSTHNDAAGNTDDSVLPKNVSPTTNLR
HSTFIID   721 SLTQPTQVGVGKQGQPTPLVIQQPPKPGALIRPPQVTLTQRPMVALRQPHNRIMLTTPQQ

CAMPT1     59 TEDNG------ISPAPAPATPID--TINASSTKE--RD--------Q------DTSKLND
SCMPT1     87 VESNGDTNNMFSSPAGLALPKKDDKKKNKGTSKADSKDGKASNSSGQNAQQQSDPNKMQD
HSTFIID   781 IQLNPLQPVPVVKPAVLPGTKALSAVSAQAAAAQKNKLKEPGGGSFR------DDDDIND

CAMPT1     95 AIAAAGVDIQQEEEILLQQQLNRKSAEGMASNLKSVIRSSKLPPFLHNYHLAAFIDKVAK
SCMPT1    147 VLFSAGIDVR-EEEALLNSSINASKSQVQTNNVKIPN----HLPFLHPEQVSNYMRKVGK
HSTFIID   835 VASMAGVNLS--EESARILATNSELVGTLTRSCKDET-------FLLQAPLQRRILEIGK
CAMPT1    155 QNGIQQNFLMDGEMLELISAACETWLSNLATKTIIISRHRRRGIPVIN-KKSGSSSVERS
SCMPT1    202 EQNFNLTPTKNPEILDMMSSACENYMRDILTNAIVISRHRRKAVKIN----SGR---RS
HSTFIID   886 KHGITELHP---DVVSYVSHATQQRLQNLVEKISETAQQKNFSYKDDDRYEQASDVRAQL

CAMPT1    214 EISKELRSLALKQKEMEEKRVNKRVMLGLEKSTKDASKNDENGESKAGAEETLHRAANAT
SCMPT1    254 EVSAALRAIALIQKKEEERRVKKRIALGLEK---------EDYENKIDSEETLHRASNVT
HSTFIID   943 KFFEQLDQIEKQRKDEQEREILMRAAKSRSRQ--------EDPEQLRLKQKAKEMQQQEL

CAMPT1    274 AAMMTMNPGRKKYSWMTSSATAGGGSDFGKSSGGSSKDSGKHQSPIISVRGDNGLRFREI
SCMPT1    305 AGIRAGS--KKQYGWITSSVNKP-TSLGAKSSGKVASD--------ITARGESGLKFREA
HSTFIID   995 AQMRQRDANLTALAAIGPRKKRK-VDCPGPGSGAEGSGPG---SVVPGSSGVGTPRQFTR

CAMPT1    334 RSGNSIEMKDLLGAIEDEKMGIRNAVIKGYAKLKD
SCMPT1    354 REEPGIVMRDLLFALENRRNSVQTIISKGYAKLRD
HSTFIID  1051 QRITRVNLRDLIFCLENERE-TSHSLLLYKAFLK-
```

Figure 5

Mtr2p (YKL186c)

Comparison	Identity
Sac-Can	28.7%

```
CAMTR    1 --MNQDPTQQLEPFLKRFLASLDLLYTQPTSQPFPNVESYATQLGSNLKRSSAIIVNGQP
SCMTR    1 MNTNSNTMVMNDANQAQITATFTKKILAHLDDPDSNKLAQFVQLFN--PNNCRIIFNATP

CAMTR   59 IIPSPQEDCKLQFQKKWLQTPLSSHQLTSYDGHLIPGTGTFVVHFSAKVRFDQSGRNRLG
SCMTR   59 FAQAT------VFLQMWQNQVVQTQHALTGVDYHAIPGSGTLICNVNCKVRFDESGRDKMG

CAMTR  119 ESADLFQE-NNS-IVSKTN----QRPIWGSWFGVDVNLVVDENVMQDGE--IINSMDYRF
SCMTR  114 QDATVPIQPNNIGNRNRPNDMNKPRPLWGPYFGISLQLIIDDRIFRNDFNGVISGFNYNM

CAMTR  171 TYVPNDSIIKV
SCMTR  174 VYKPEDSLIKI
```

Figure 6

Bos1p (YLR078C)

Comparison	% Identity
Sac-Can	37.9%
Sac-Hum	16.8%
Can-Hum	18.1%

```
CABOS1    1 ----------MNSIYNHGIKQTQTITKDLTQFEKNL-STSPISLQGAITTSLTAFRKTIK
SCBOS1    1 ----------MNALYNHAVKQKNQIQQELARFEKNS-VTAPISLQGSISATLVSLEKTVK
HSSTX7    1 MSYTPGVGGDPTQLAQRISSNIQKITQCSVEIQRTLNQLGTPQDSPELRQQLQQKQQYTN

CABOS1   50 EYSDLLEKNVNDT----SYTKHENRLNKFNQD--LNEFTLKFDTLKKQRDIQVQEAN-KQ
SCBOS1   50 QYAEHLNRYKEDTNAEEIDPKFANRLATETQD--LHDFTAKEKDLKQS----YNENNSRT
HSSTX7   61 QLAKETDKYIKEFG-SLPTTPSEQRQRKIQKDRLVAEFTTSLTNFQKVQR---QAAEREK

CABOS1  103 ELLGRRHISTTATAALGSTSSDNPYESSSNPSQQQQQQTQDEQNTMSYREGLYHEKNSLE
SCBOS1  104 QLFGSGASHVMDSDNPFSTSETIMNKRNVGGASANGKEGSSNGGGLPLYQGLQKEQSVFE
HSSTX7  117 EFVARVRASSRVSGSFPEDSSKERNLVSWESQIQPQVQVQDEEITEDDLRLIHERESSIR

CABOS1  163 RGSEQLDRILEMGQQAFEDIVEQNEILRKVQTKFEESLITLGVSQGTIRSVERRAKQDKW
SCBOS1  164 RGNAQLDYILEMGQQSFENIVEQNKILSKVQDRMSNGLRTLGVSEQTIISINKRVFKDKL
HSSTX7  177 QLEADIMDINEIFKDLGMMIHEQGDVIDSIEANVENAEVHVQQANQQLSRAADYQRKSRK

CABOS1  223 IFWFCVVVMLVVFYYIVKLFR----
SCBOS1  224 VFWIALIILIICIYYVIKWIR----
HSSTX7  237 TLCIIILILVIGVAIISLIIWGLNH
```

Figure 7

Pol30p (YBR088c)

Comparison	Identity
Sac-Can	54.5%
Sac-Hum	35.7%
Can-Hum	41.3%

```
GTCCAPOL30    1 MLEGKFEEAALLKKVVEAIKDCVKKCNFNCSEHGITVQAVDDSRVLLVSLLIGQTSFSE-
SCPOL30       1 MLEAKFEEASLFKRIIDGFKDCVQLVNFQCKEDGIIAQAVDDSRVLLVSLEIGVEAFQEY
HS_PCNA       1 MFEARLVQGSILKKVLEALKDLINEACWDISSSGVNLQSMDSSHVSLVQLTLRSEGFDTY

GTCCAPOL30   60 RCDRDVTLGIDLESFSKILKSANNEDFLTLIAEDSPDQIMAILEEKQKEKISEYSLKLMD
SCPOL30      61 RCDHPVTLGMDLTSLSKILRCGNNTDTLTLIADNTPDSIILLFEDTKKDRIAEYSLKLMD
HS_PCNA      61 RCDRNLAMGVNLTSMSKILKCAGNEDIITLRAEDNADTLALVFEAPNQEKVSDYEMKLMD

GTCCAPOL30  120 IDSEFLQIDDMEYDAVVNMPSSDFAKIVRDLKNLSESLRVVVTKDSVKFTSEGDSGSGSV
SCPOL30     121 IDADFLKIEELQYDSTLSLPSSEFSKIVRDLSQLSDSINIMITKETIKFVADGDIGSGSV
HS_PCNA     121 LDVEQLGIPEQEYSCVVKMPSGEFARICRDLSHIGDAVVISCAKDGVKFSASGELGNGNI

GTCCAPOL30  180 ILKPYTNLKNERESVTISLDDPVDLTFGLKYLNDIVKAATLSDVITIKLADKTPALFEFK
SCPOL30     181 IIKPFVDMEHPETSIKLEMDQPVDLTFGAKYLLDIIKGSSLSDRVGIRLSSEAPALFQFD
HS_PCNA     181 KLSQTSNVDKEEEAVTIEMNEPVQLTFALRYLNFFTKATPLSSTVTLSMSADVPLVVEYK

GTCCAPOL30  240 MQSGGYLRFYLAPKFDDDEY-
SCPOL30     241 LKSG-FLQFFLAPKFNDEE--
HS_PCNA     241 IADMGHLKYYLAPKIEDEEGS
```

Figure 8

Ymr131cp (YMR131C)

Comparison	Identity
Sac-Can	63.0%
Sac-Hum	24.0%
Can-Hum	26.1%

```
CAYMR131C    1 MSKRSAEDDLSGNGSTSHTAVKTNKDSTPTTTNGKEEEPENMDIGEFEEPYGDEFESI-E
SCYMR131C    1 MSKRSIEVNEEQD---RVVSAKTESHSVPAIPAS--EEQE-APKNDLEEQLSDEFESIGF
HSRBBP4      1 ------------------------------------------------------------

CAYMR131C   60 IIELEDNNDEEDDEMIDENSTQAKIEELEAKEQEQ---EQQSSIYLPHKSKPLGPDEVLE
SCYMR131C   55 IIEDE-GDDEIND-EDDLRKKCEEAETLVQKDQSEGNKEKIQEEYLPHMSEPLGPDEVLF
HSRBBP4      1 ---------------------------MADKEAAFDDAVEERVINEEYKIWKKN----

CAYMR131C  117 ADPTVYEMLHNINLPWPCLTVDILPDSLGNERRSYPATVYIATATQAAKAKDNELIANKA
SCYMR131C  113 ADPTVYEMLHNVNMPWPCLTLDVIPDILGSERRNYPQSILITTATQSSRKKENELHVLAL
HSRBBP4     28 -TPFIYDLVMTHALEWPSLTAQWLPDVTRPEGKDESIHRLVLGTHTS---DEQNHLVIAS

CAYMR131C  177 SSLAKTLVKDENE-EDEEDEDDIDDVDSDPILLSES-IPLRHTTNRIRVSPHAQQTGEYI
SCYMR131C  173 SNLAKTLLKDDNEGEDDE-EDDED--DVDPVIENEN-IPLRDTTNRLKVSPFAISNQEVI
HSRBBP4     84 VQLPNDDAQFDASHYDSEKGEFGGFGSVSGKIEIEIKINHEGEVNPARYMPQNP----CI

CAYMR131C  235 TASMSENGEVYIFDLLAQYKAFETPGYMIPKSSKRPIHTIRAHGNVEGYGLDWSPLVNTG
SCYMR131C  229 TATMSENGDVYIYNLAPQSKAFSTPGYQIPKSAKRPIHTVKNHGNVEGYGLDWSPLIKTG
HSRBBP4    140 IATKTPSSDVLVFDYTKHP---SKP---DPSGECNPDLRLRGHQ-KEGYGLSWNPNLS-G

CAYMR131C  295 ALLSGDMSGRIYLTNRDTS---SWTTDKTPFEASQS-SIEDIQWSTGEHTVFATGGCDGY
SCYMR131C  289 ALLSGDCSGQIYFTQRHTS---RWVTDKQPFTVSNNKSIEDIQWSRTESTVFATAGCDGY
HSRBBP4    192 HLLSASDDHTICLWDISAVPKEGKVVDAKTIFTGHTAVVEDVSWHLLHESLFGSVADDQK

CAYMR131C  351 ICIWDTRSK-KHKPAISVIASKSDVNVISWSSKINHLLASGHDDGSWGVWDLRNFTNNTT
SCYMR131C  346 IRIWDTRSK-KHKPAISVKASNTDVNVISWSDKIGYLLASGDDNGTWGVWDLRQFTPSNA
HSRBBP4    252 LMIWDTRSNNTSKPSHSVDAHTAEVNCLSFNPYSEFILATGSADKTVALWDLRNLKLKLH

CAYMR131C  410 SNPSPVANYDFHKSPITSISFNPLDESILEAVSSEDNTVTLWDLAVEADDEEISQQRKEAQ
SCYMR131C  405 DAVQPVAQYDFHKGAITSIAFNPLDESIVAVGSEDNTVTLWDLSVEADDEEIKQQAAETK
HSRBBP4    312 S--------FESHKDEIFQVQWSPHNETILASSGTDRRLNVWDLSKIG--EEQS-----PE

CAYMR131C  470 EIHDIPPQLLFVHWQR--DVKDVRWHPQIPGCLVSTGGD-GLNIWKTISVE---------
SCYMR131C  465 EIQEIPPQLLFVHWQK--EVKDVKWHKQIPGCLVSTGTD-GLNVWKTISV----------
HSRBBP4    358 DAEDGPPELLFIHGGHTAKISDFSWNPNEPWVICSVSEDNIMQVWQMAENIYNDEDPEGS

CAYMR131C      ---------
SCYMR131C      ---------
HSRBBP4    418 VDPEGQGS
```

Figure 9

Sqt1p (YIR012W)

Comparison	Identity
Sac-Can	44.5%
Sac-Hum	22.9%
Can-Hum	25.1%

```
CASQT1     1 ------------------MSHQQE--DVVDDTQEEYINVN---EVAEEVADDDQAPPDEE
SCSQT1     1 ------------------MEPQEEF-ITTEEVEQEIVPTV---EVEQDVPVDIEGENDDC
HSAAMP     1 MDSGRRLGPEKWIRRLRRMESESESGAAADTPPLETLSFHGDEEIIEVVELD-PGPPDPD

CASQT1    38 DEEMELLDEHETLELDMSNN---------------------SWTYFDKHTDSTFTIFSHP
SCSQT1    39 DE--MMNDDEEALEVDMSNN---------------------SLTYFDKHTDSVFAIGHHP
HSAAMP    60 DLAQEMEDVDFEEEEEEEGNEEGWVLEPQEGVVGSMEGPDDSEVTFALHSASVFCVSLDP

CASQT1    77 KLPMVLTEGG-DNTAYLWTTHHIQPPKFVGEITGHKESVISGGFTADGKFVVTADMNGLIQ
SCSQT1    76 NLPIVCTGGG-DNLAHLWTSHSQPPKFAGTLTGYGESVISCSFTSEGGFIVTADMSGKVL
HSAAMP   120 KTNTLAVTGGEDDKAFVWRLSD--GELLFECAGHKESVTCAGFSHDSTLVATGDMSGLLK

CASQT1   136 VFKATKGGEQWVKFGELDEVEEVLEVTVHPTIP-FFAFGATDGSIWMYQIDESSKLLVQI
SCSQT1   135 VHMGQKGGAQWKLASQMQEVEEIVWLKTHPTIARTFAFGATDGSVWCYQINEQDGSLEQL
HSAAMP   178 VWQVDTKEEVWS-----FEAGDLEWMEWHPRAP-VLLAGTADGNTWMWKVPNGD---CKT

CASQT1   195 MSGFSHTLKCNGAVFIDG-KDENDLTLVSISEDGTVVNWNCFTGQVNYKLQPHDDFKGVE
SCSQT1   195 MSGEVHQQDCSMGEFINTDKGENTLELVICSLDSTIVAWNCFTGQQLFKIT-QAEIKGLE
HSAAMP   229 FQGPNCPATC-GRVLPDG---K--RAVVGY-EDGTIRIWDLKQGSPIHVLK---GTEGHQ

CASQT1   254 SPWVTVKVH------GN--LVAIGGRDGQLSIVNNDTGKIVHTLKTLDNVD--------D
SCSQT1   254 APWISISLAPETLTKGNSGVVACGSNNGLLAVINCNNGAILHLSTVIEEKPE-----QD
HSAAMP   279 GPLTCVAANQD----GS--LILTGSVDCQAKLVSATTGKVVGVFRPETVASQPSLGEGEE

CASQT1   298 IAELSIEALSWCESKNINLLAVGLVSGDXLLEDTQQWRLRKNLKVDDAITKLQFVGETPI
SCSQT1   309 ELDASIESISWSS--KFSLMAIGLVCGEILLYDTSAWRVRHKFVLEDSVTKLMFDNDD--
HSAAMP   333 SESNSVESLGFCS--VMPLAAVGYLDGTLAIYDLATQTLRHQCQHQSGIVQLLWEAGTAV

CASQT1   358 LVGNSMDGKXYKWEPRTGEKXFAGVGTNMGSYGLCYFK------IEVKNWLLLVDERCFH
SCSQT1   365 LFASCINGKVYQFNARTGQEKFVCVGHNMGVLDFILLHPVANTGTEQKRKVITAGDEGVS
HSAAMP   391 VYTCSIDGIVRLWDARTGRLLTDYRGHTAEILDFALSK-------DASLVVTTSGDHKAK

CASQT1   412 WSLFMK---
SCSQT1   425 LVFEVPN--
HSAAMP   444 VFCVQRPDR
```

Figure 10

Mtw1p (YAL034w-A)

Comparison	Identity
Sac-Can	31.8%

```
CAMTW1     1 MSDKTIDERTTAILTEHLEFAPLTLIDDVINAVNEIMYKGTTAIETYLKEQKQLMKNGIT
SCMTW1     1 MSAPTM--RSTSILTEHLGYPPISLVDDIINAVNEIMYKCTAAMEKYLLS-KSKIGE---

CAMTW1    61 KVTEDEIEIGMCKLESLLESTIDKNFDKFELYCLRNIFNIPKDLIPYIQLSHQQGIEFKS
SCMTW1    55 EDYGEEIKSGVAKLESLLENSVDKNFDKLELYVLRNVLRIPEEYIDANVFRLEN---QKD

CAMTW1   121 DNVEQKREFDQQIKNLQLKIMQELQLRKILKEQLVKVQKEIKVLIAIDNDFKKIDFASGG
SCMTW1   112 LVIVDENELKKSEEKLREKVNDVELAFKKNEMLLKRVTKVKRILFTIRGFKQKINELLKC

CAMTW1   181 GGNEESIRIILKNLQPIDETLYFLISQIKNLINQIEQLSNKVNTNLKTQKFIPN-------
SCMTW1   172 KDDVQLQKILESLKPIDDTMTLLTDSLRKLYVDSESTSSTEEVEALLQRLKTNGKQNNKD

CAMTW1   234 LRDKEIDGRTFRVLQQTGIWKDLEKNDIKILVQGNDNNNNNNNNNNNTLTDIQNQDDIDM
SCMTW1   232 FRTRYIDIRTNNVLRKLGELGDKE-----------DEKQSAKPDARTQAGDIVS---IDI

CAMTW1   294 IIPEQDDIDVDAIKNINAQIF
SCMTW1   278 EEP-QLDLLDDVL--------
```

Figure 11

Tfb1p (YDR311w)

Comparison	Identity
Sac-Can	32.4%
Sac-Hum	23.0%
Can-Hum	23.3%

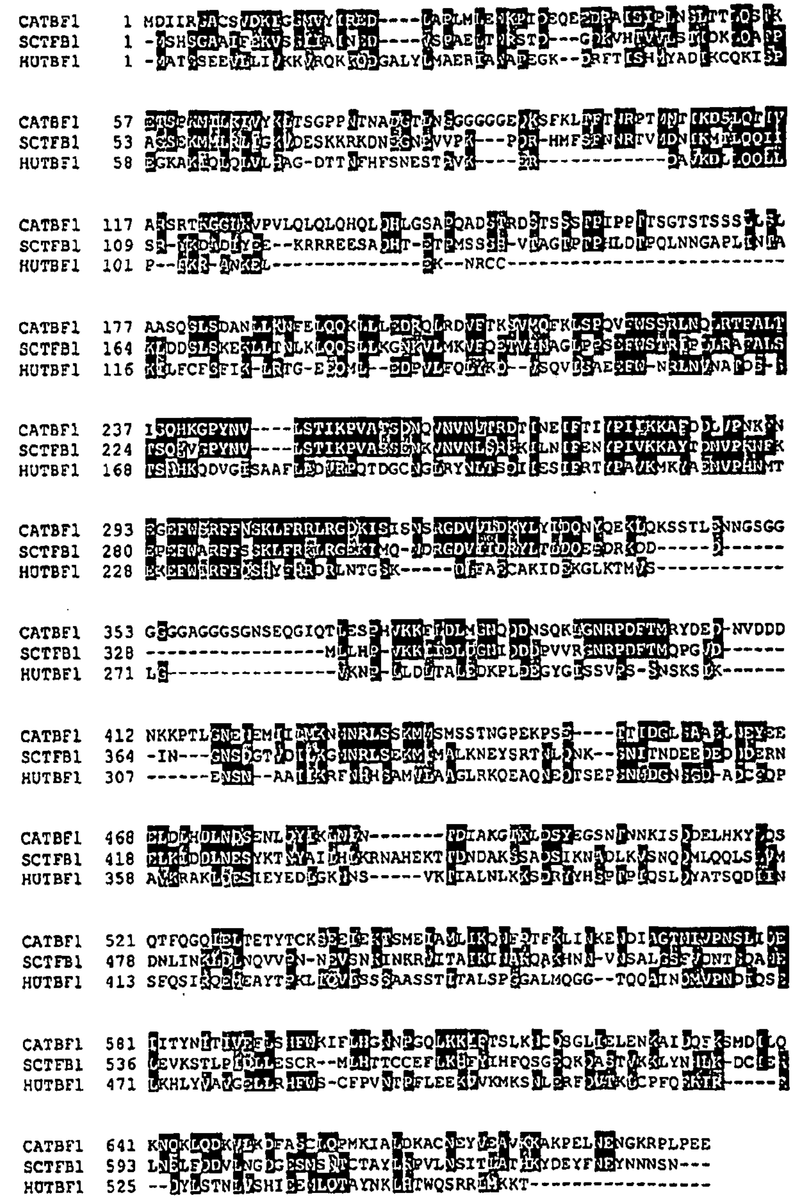
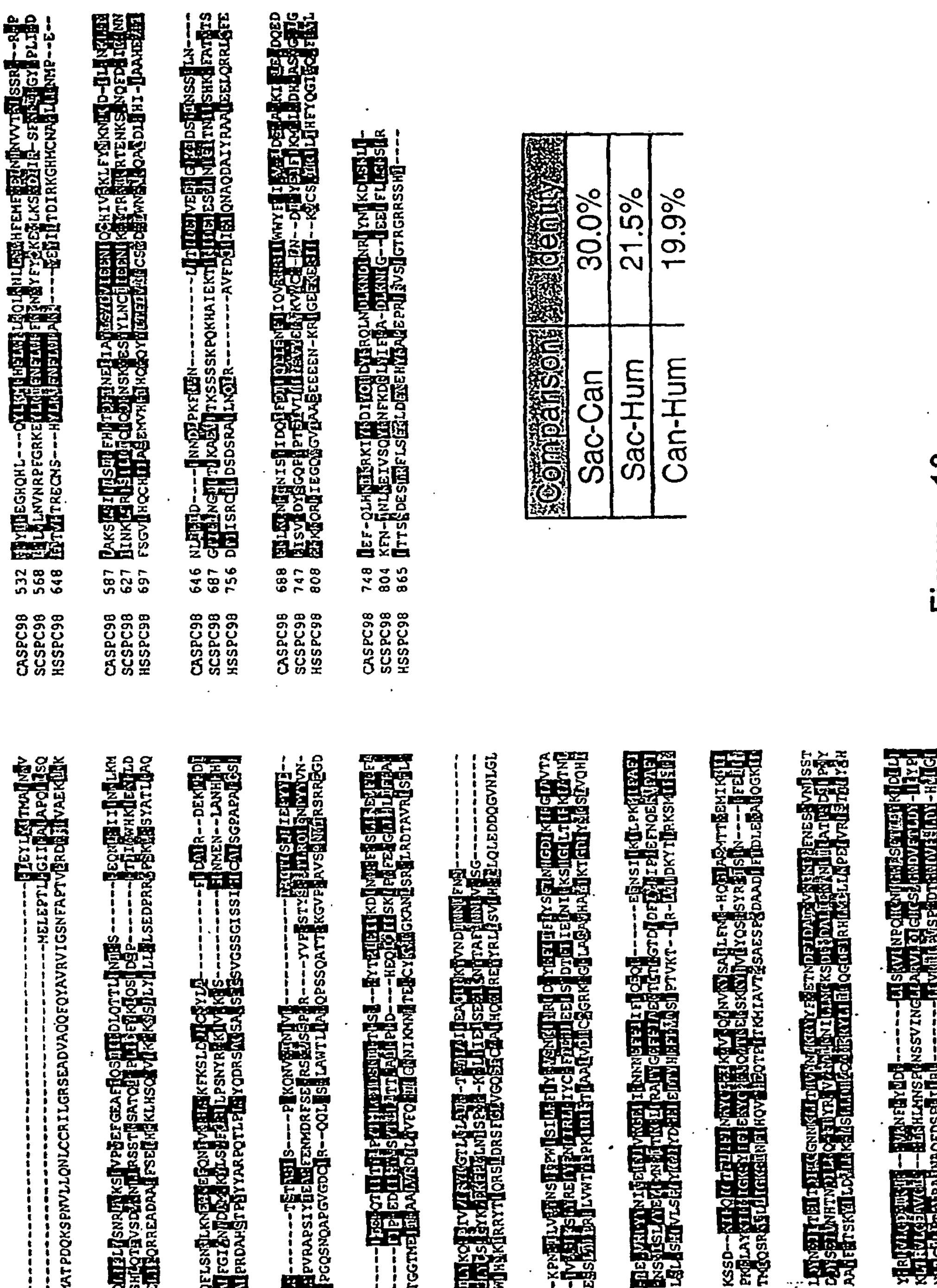


Figure 12

Spc98p (YNL126W)



Comparison	Identity
Sac-Can	30.0%
Sac-Hum	21.5%
Can-Hum	19.9%

Figure 13

Bfr2p (YDR299W)

Comparison	Identity
Sac-Can	42.1%
Sac-Hum	22.5%
Can-Hum	20.7%

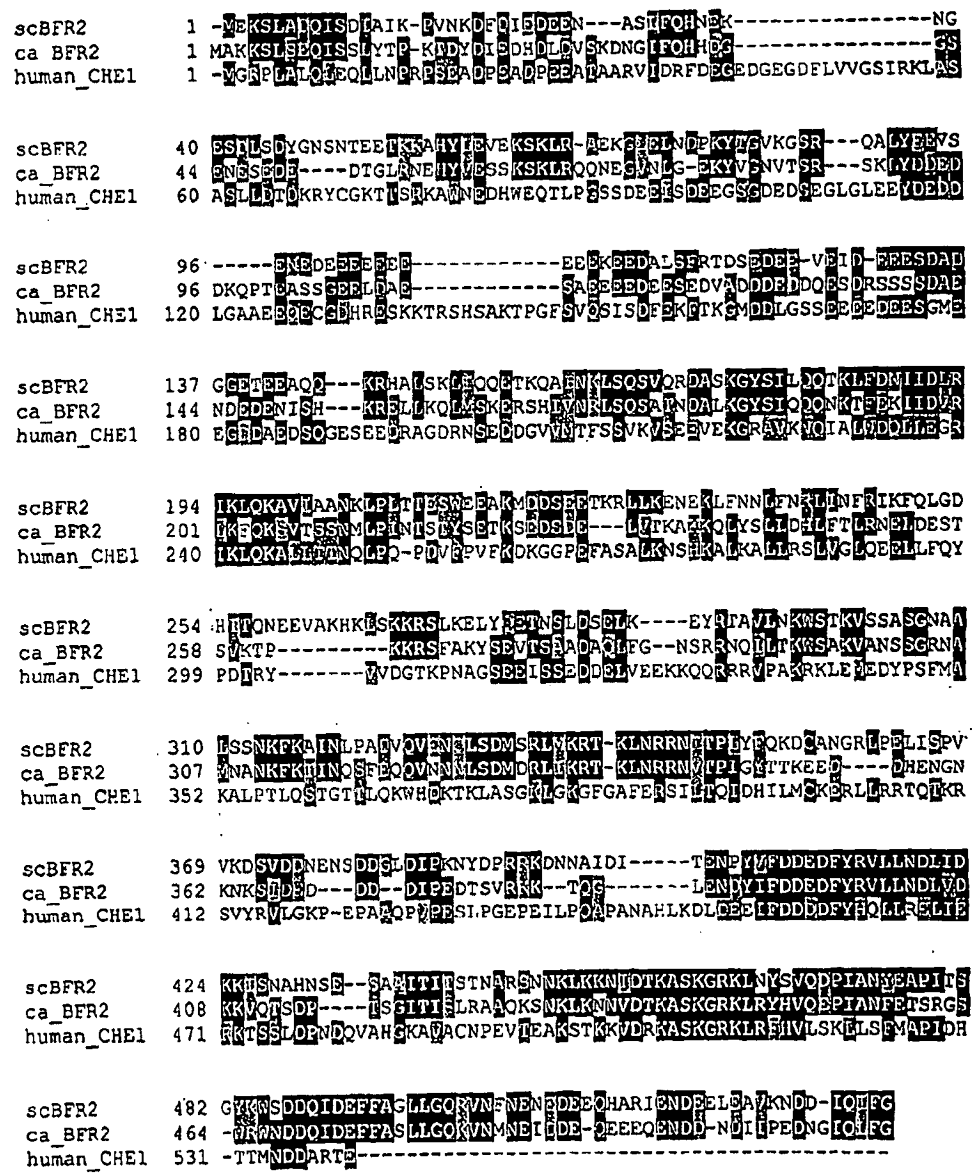


Figure 14

Rna1p (YMR235C)

Comparison	Identity
Sac-Can	51.5%
Sac-Hum	32.1%
Can-Hum	33.7%

```
CAYMR235C    1 MASVEVELGVTPETTYSISG--------KQLKEDSESDIAPYIKELTEKENVKKVDFSGNT
SCYMR235     1 MATLHEVPQHEEEQVYSISG--------KALKLTTSDDIKPYLEELAALKTCTKLDLSGNT
HS575269     1 MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNT

CAYMR235C   54 IGTEASKALSEALLKH---KDTIVETNFSDLYTGRLNTEIPQSLEYLLPALSKLP-TLKL
SCYMR235    54 IGTEASEALAKCIAENTQVREESLVEVNFADLYTSRLVDEEVDSLKFLLPVLIKCP-HLEI
HS575269    61 VGVEAARVIAKALEKK---SE-LKRCHWSDMFTGRLRTEIPPALISLGEGLITAGAQLVE

CAYMR235C  110 INLSDNAFGLQPIDPLEAYLAK--AVEIEHLILSNNGMGPFAGSRIGGSLFKLAKAKKAE
SCYMR235   113 VNLSDNAFGLRPIELLIEDYWAH--AVNIKHLILSNNGMGPFAGERIGKALFHLAQNKKAA
HS575269   117 LDLSDNAFGPDGVQGFEALLKSSACFTLQELKLNNCGMGIGGGKILAAALTECHRKSSAQ

CAYMR235C  168 GK-ESLKTFICGRNRLENGSVNYLSVGLRNHKE-LEVVRLYQNGIRPAGISKLVEQGLSN
SCYMR235   171 SK-PFLETFICGRNRLENGSAVYLAIGLKSHSEGLKVVKLYQNGIRPKGVATLIHYGLQY
HS575269   177 GKPLALKVFVAGRNRLENDGATALAEAFRVIGT-LEEVHMPQNGINHPGITALAQAFAVN

CAYMR235C  226 NKKLKVLDLQDNTITTRGAIHIAESLSNWP-LLVELNLNDSLLKNKGSIKLVEAFHAGDE
SCYMR235   230 LKNLEILDLQDNTFTKHASLILAKALPTWKDSLFELNLNDCLLKTAGSDEVFKVFTEVK-
HS575269   236 -PLLKVLNLNDNTFTEKGAVAMAEALKTLR-QVEVINFGDCLVRSKGAVAIADAIRGGL-

CAYMR235C  285 KPQLITLKLQYNELETDSLRVIADAIASK--LPQLKFLELNGNRFEED-SEHIDKINGIF
SCYMR235   289 FPNLHVLKFEYNEMAQETIEVSFLPAMEKGNLPELEKLEINGNRLDED-SEALDLLCSKF
HS575269   293 -PKLKELNLSGCEIKRDAALAVAEAMADK---AELEKLDLNGNTLGEEGCEQLQEVLEGF

CAYMR235C  342 EERGYGE--IDEIDELEEVDSEEEE-IDEIDEGEDTTLEEDLRLTQLEEELAGVSLEEKD
SCYMR235   348 DE--------LEVDDFEEVDSEIEEGEDEEDENEDEKLEE-IETERLEKELLEVQVDI--
HS575269   349 NMAKVLASLSDEEDEEEEEEGEEEEEEAEEEEEEDEEPEEEEEEEEEEPQQRGQGEKSA

CAYMR235C  399 G--------NVDEWAEELSKTHIKZ------------------------------------
SCYMR235   397 -------------IAERLAETEIK-------------------------------------
HS575269   409 TPSRKILDPNTGEPAPVLSSPPPADVSTFLAFPSPEKLLRLGPKSSVLIAQQTDTSDPEK

CAYMR235C      ------------------------------------------------------------
SCYMR235       ------------------------------------------------------------
HS575269   469 VVSAFLKVSSVFKDEATVRMAVQDAVDALMQKAENSSSFNSNTFLTRLLVHMGLLKSEDK

CAYMR235C      ------------------------------------------------------------
SCYMR235       ------------------------------------------------------------
HS575269   529 VKAIANLYGPLMALNHMVQQDYFPKALAPLLLAFVTKPNSALESCSFARHSLLQTLYKV
```

Figure 15

Gcd7p (YLR291C)

Comparison	Identity
Sac-Can	52.2%
Sac-Hum	34.5%
Can-Hum	35.6%

```
CAGCD7     1 ---------MSKLLTPEILALIDPVVSSLKRHQ-LVDDKEIALTIAQLLMKVISAARWSN
SCGCD7     1 MSSQAFTSVHPNAATSDVNVTIDTFVAKLKRRQ-VQGSYAIALETLQLLMRFISAARWNH
HSGCD7     1 -------MPGSAAKGSELSERIESFVETLKRGGGPRSSEEMARETLGLLRQIITDHRWSN

CAGCD7    51 TYDLIELIRQVGVIFTEAYPRKVIPGNIVRRVLAHIRDETETETETETEQTDNI--PMMS
SCGCD7    60 VNDLIEQIRDLGNSLEKAHPTAFSCGNVIRRILAVLRDEVEEDTMSTTVTSTSVAEPLIS
HSGCD7    54 AGELMELIRREGRRMTAAQPSETTVGNMVRRVLKIIREEYGRLHGRSDESDQQE------

CAGCD7   109 SMFSLLATHNK-NETIKEQTQLQLKKQTSDMRATIIQGIRDLVDEISNVNDGIETMAVDL
SCGCD7   120 SMFNLLQKPEQPHQNRKNSSGSSSMKTKTDYRQVAIQGIKDLIDEIKNIDEGIQQIAIDL
HSGCD7   108 SLHKLLTSGGL-NEDFSFHYAQLQ--SN------IIEAINELLVELEGTMENIAAQALEH

CAGCD7   168 IHDDEILLTPTPNSETVQHFLIKARLK--RKFTVVVTENYPNDIKAAHKFVKTLAEHNIE
SCGCD7   180 IHDHEILLTPTPDSKTVLKFLITARERSNRTFTVLVTEGEPNNTKNAHEFAKKLAQHNIE
HSGCD7   159 IHSNEVIMTIG-FSRTVEAFLKEAARK--RKFHVIVAECAP--FCQGHEMAVNLSKAGIE

CAGCD7   226 TLLIPDTTIYAVMSRVGKVIIGTNAVFANGGCLS-NSGVANVVECAKEHRTPVFAVAGLF
SCGCD7   240 TLVVPDSAVFALMSRVGKVIIGTKAVFVNGGTISSNSGVSSVCECAREFRTPVFAVAGLY
HSGCD7   214 TTVMTDAAIFAVMSRVNKVIIGTKTILANGALRA-VTGTHTLALAAKHHSTPLIVCAPMF

CAGCD7   285 KLSPLYPFTRNDLIEVGNSGKVLNYDDFELVQNVDVVTNPLEDYIPPQHIDIFMTNIGGF
SCGCD7   300 KLSPLYPFDVEKFVEFGGSQRILPRMD---PRKRLDTVNQITDYVPPENIDIYITNVGGF
HSGCD7   273 KLSPQFPNEEDSFHKFVAPEEVLPFTEG-DILEKVSVHCPVFDYVPPELITLFISNIGGN

CAGCD7   345 SPSFIYRIVLDNYKAEDNKLE----
SCGCD7   357 NPSFIYRIAWDNYKQIDVHLDKNKA
HSGCD7   332 APSYIYRLMSELYHPEDHVL-----
```

Figure 16

Ski6p (YGR195W)

Comparison	Identity
Sac-Can	62.5%
Sac-Hum	39.1%
Can-Hum	34.8%

```
CASKI6    1 ---MELYSPEGLRIDGRRWNELRRFECRINTHPNSSDGSSYVEQGNTKVMCTVQGPIEPA
SCSKI6    1 MSRLEIYSPEGLRLDGRRWNELRRFESSINTHPHAADGSSYMEQGNNKIITLVKGPKEPR
HSSKI6    1 MAGLELLSDQGYRVDGRRAGELRKIQARMGVFAQ-ADGSAYIEQGNTKALAVVYGPHEIR

CASKI6   58 LRSQQHSERANIEVNINIASFSTFERKKRSR-NERRLVELKTTLEKTFEESVMINLYPRT
SCSKI6   61 LKSQMDTSKALLNVSVNITKFSKFERSKSSHKNERRVIEIQTSLVRMFEKNVMLNIYPRT
HSSKI6   60 SRARALPDRALVNCQYSSATFSTGERKRRPH-GDRKSCEMGLQLRQTFEAAILTQLHPRS

CASKI6  117 NIVINVQVLCQDGGMLAAVINSITLALIDAGISMYDYVSGVSCGLYDQTPLLDVNNLEEH
SCSKI6  121 VIDIEIHVLEQDGGIMGSLINGITLALIDAGISMFDYISGISVGLYDTTPLLDTNSLEEN
HSSKI6  119 QIDIYVQVLQADGGTYAACVNAATLAVIDAGIPMRDFVCACSAGFVDGTALADLSHVEEA

CASKI6  177 DMS-CLTVGVIGKSEKLALMLLEDKMPLDRLESVLSIGIAGSHKIRELMDQEVRKHGIIR
SCSKI6  181 AMS-TVTLGVVGKSEKLSLLLVEDKIPLDRLENVLAIGIAGAHRVRDLMDEELRKHAQKR
HSSKI6  179 AGGPQLALALLPASGQIALLEMDARLHEDHLERVLEAAAQAARDVHTLLDRVVRQHVREA

CASKI6  236 ASKMQ--
SCSKI6  240 VSNASAR
HSSKI6  239 SILEGDG
```

Figure 17

Nip1p (YMR309C)

Comparison	Identity
Sac-Can	42.7%
Sac-Hum	30.0%
Can-Hum	26.7%

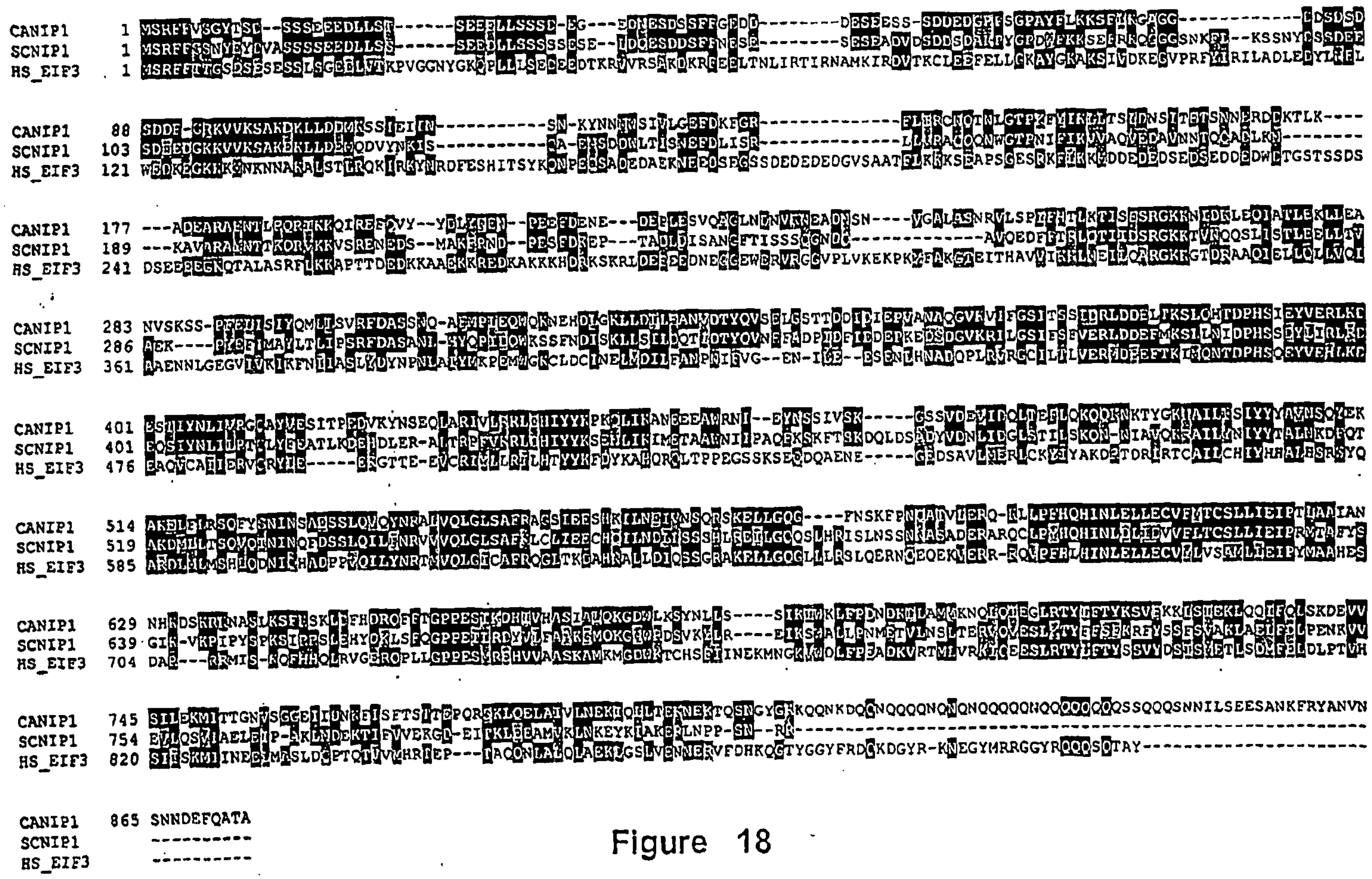


Figure 18

Lcp5p (YER127W)

Comparison	Identity
Sac-Can	34.7%
Sac-Hum	18.0%
Can-Hum	18.6%

```
CALCP5_SER     1 MSKVDTVLKEIISSTKSTEASVKELIIAFVKDSSSQHP----ELVRNLLAKSNSSLEGVSL
SCLCP5         1 MSELNALLKDINGSLTATSESIERLSGIYSNSATDEIPESNQLHEHLFYDAKKPAEKVSL
HS_CAB43232    1 MAALGVLESDLPSAVTLLKNLQEQVMAVTAQVKS--------LTQKVQAGAYPTEKGESF

CALCP5_SER    57 LGLKNESLVSYINNLVLVVLSHLERLESDSETGSSAVERSIIQRVTLEKGVKPLEKKLSY
SCLCP5        61 LSLKNGSMLGYINSLLMLIGNRLDDECKD-PSAMDARERSIQHRVVLERGVKPLEKKLAY
HS_CAB43232   53 LEVKDQLLLMYEMDLTHLILDKASGGSLQ---GHDAVLRLVEIRTVLEK-LRPLDQKLKY

CALCP5_SER   117 QLDKMIRAYGRMEQDEIKAEQKLNDRGSGENDENDENDSEEDSEEDSEDESEDDELAYRP
SCLCP5       120 QLDKLTRAYVKMEKEYKDAEKRALEKSTLVNHSG--ND---DSE-D--DESSEDELAYRP
HS_CAB43232  109 QIDKLIKTAVTGSLSENDPLRFKPHPSNMMSKLS--SE---DEE-E--DEAEDD----QS

CALCP5_SER   177 DASSFAKLTSAKTKSKPTSSAVSTSNEK---------YRPPKISAMAPPTAVKSHD-LDAN
SCLCP5       172 NTSGIINTNKKSSAYRVEETAKQENGEENDDNETGVYKPPKITAVLPPQQTHFEDRFDAR
HS_CAB43232  157 EASG------------K-KSVKGVSKK-----------YVPPRLVPVHYDETEAERE--KKR

CALCP5_SER   228 TTSSK-NR-KLQSMEEYLQEQSDMPMVEASVGSTIVEHGRGGVKTQHDRKKEREIQTYEE
SCLCP5       232 EHKDRSNKSRMQAMEEYIRESSDQPDWSASIGADIVNIHGRGGIKSLRDTEKERRVTSEEE
HS_CAB43232  193 LERAKRRALSSSVIRELKEQYSDAP---------EEIRDARHPHVTRQSQEDQHRIN-YEE

CALCP5_SER   286 DNFVRLPTSQTKK-SFKEKQRD---IRNQFAGEDVSMFNNNKDVTRQGTSR-KRKATTVW
SCLCP5       292 DNFTRLNITNKAE-KRKQKQRERNARMNVIGGEDEGIFSSKRKLEDSTSRRGAKKTRSAW
HS_CAB43232  244 SMMVRLSVSKREKGRRKRANVMSSQLHSLTHFSDISALTGGTVHLDEDQNP-IKKRKKIP

CALCP5_SER   341 DKVKKKKNT
SCLCP5       351 DRAQRRL--
HS_CAB43232  303 QKGRKKKGQ
```

Figure 19

Nce103p (YNL036w)

Comparison	Identity
Sac-Can	34.7%

```
CANCE103    1 MGRENILKYQLEHDHESDLVTEKDQSLLLDNNNNLNGMNNTIKTHPVRVSSGNHHNNFPFT
SCNCE103    1 -------------------------------------------------MSATESSSIFT

CANCE103   61 LSSESTLQDFLNNNKFEVDSIKHNHGNQIFDLNGQGQSPHTLWIGCSDSRAGDQCLATLP
SCNCE103   12 LSHNSNLQDILAANAKWASQMNNIQPTLFPDHNAKGQSPHTLEIGCSDSRYNENCLGVLP

CANCE103  121 GEIFVHRNIANIVNANDISSQGVIQFAIDVLKVKKIIVCGHTDCGGIWASLSKKKIGGVL
SCNCE103   72 GEVFTWKNVANICHSEDLTLKATLEFAIICLKVNKVIICGHTDCGGIKTCLINQREALPK

CANCE103  181 DLWLNPVRHIRAANLKLLEEYNQDPKLKAKK-----LAELNVISSVTAEKRHPSASVAEK
SCNCE103  132 VNCSHLYKYLDDIDTMYHEESQNLIHLKTQREKSHYLSHCNVKRQFNRIIENPIVQTAVQ

CANCE103  236 KNEIEVWGMLYDVATGYLSQVEIPQDEFEDLFHVHDEHDEEEYNPH
SCNCE103  192 NGELQVYGLLYNVEDGLLQTVSTYTKVTPK----------------
```

Figure 20

Eco1p (YFR027w)

Comparison	% Identity
Sac-Can	34.8%

```
CAECO1     1 MGSINSQ-----KAQKIQSILALPSNFKK---ITCSTCDMTYNPHISQDKLLHNKYHTNF
SCECO1     1 MKARKSQRKAGSKPNLIQSKLQVNNGSKSNKIVKCDKCEMSYSSSTSIEDRALHEKYHTLQ

CAECO1    53 INGIPWN----------YKTDNDVLIIENFTLVETPKLNSTGKSLKLTKTRQTFKGSIICI
SCECO1    61 LHGRKWSPNWGSIVYTERNHSRTVHLSRSTGTITPLNSSPLKKSSPSITHQEEKIVYVRP

CAECO1   104 NKSNKRHIQKVELLLNMVNQELNASQDS-GQWKKPEFDRSKAFVIIIDSKAIGLCTTDTI
SCECO1   121 DKSNG-EVRAMTEIMTIVNNELNAPHDENVIWNSTTEEKGKAFVYIRNDRAVGIIIIENL

CAECO1   163 QP------DQGRWMIHKTQSIVPNQINKNVVIGISRIWISRKWRQYGEGKKLLNVVLKNS
SCECO1   180 YGGNGKTSSRGRWMVYDSRRLVQN-VYPDFKIGISRIWVCRTARKLGIATKLIDVARENI

CAECO1   217 IYSVQLLKNQVAFSQPSFSGGMLAKSENGVKHKSGEMLLPVYIE
SCECO1   239 VYGEVIPRYQVAWSQPIDSGGKLASKYNGIMHKSGKILLPVYI-
```

Figure 21

ORC2p (YBR060C)

Comparison	Identity
Sac-Can	26.7%
Sac-Hum	22.0%
Can-Hum	21.0%

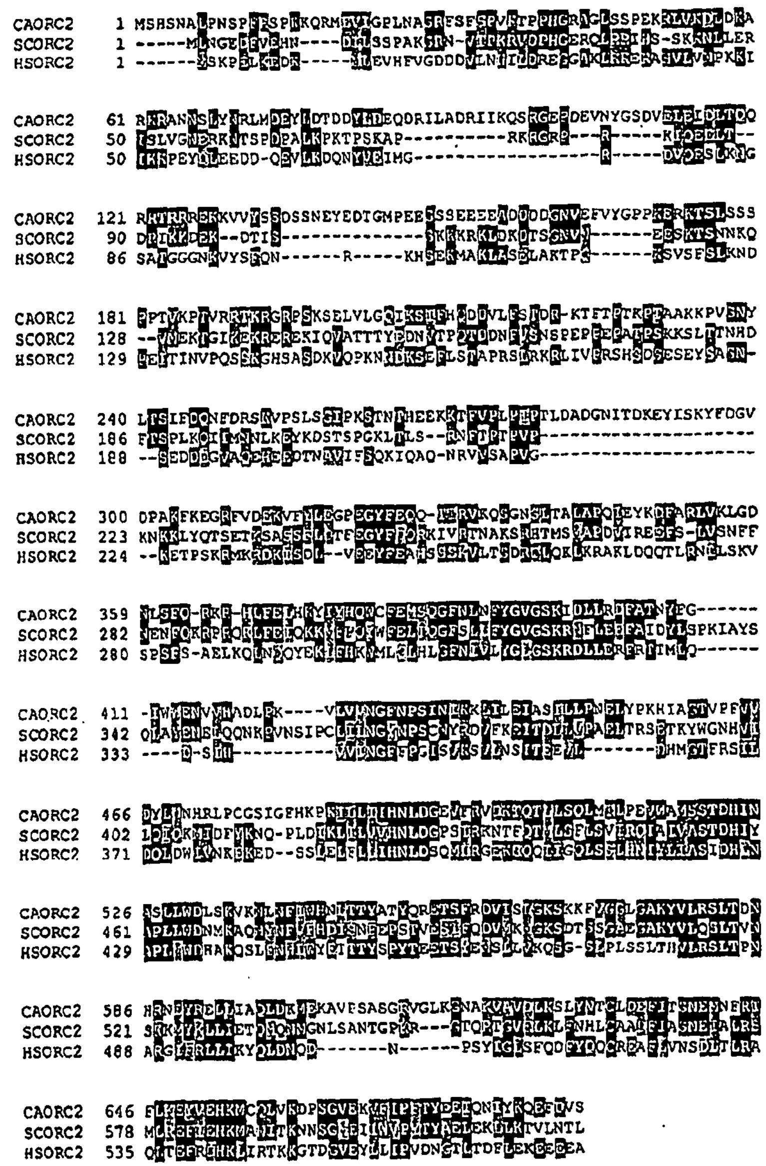


Figure 22

Cns1p
(YBR155W)

Comparison	Identity
Sac-Can	51.8%
Sac-Hum	25.6%
Can-Hum	26.8%

```
SCCNS1    1 MSSVNANGG----YTKPQ---KYVPGPGDPELPPQLSEFKDKTSDEILKEMNRMPFFMTK
CACNS1    1 MSKIEPVTEKEEEYVSEWDRRRYVPKAGEPELPPQLSEESNKTIDEVIEEINRIPFFMT-
HSTTC4    1 ---MEQPGQ---DPTSEDVMDSDIEKFQSQ---PYRGGEH---EDQWEKEFEKVFLFMS-

SCCNS1   54 LDETDGAGGENVELEALKALAYEGE--PHEIAENFKKQGNELYKAKREKDARELYSKGLA
CACNS1   60 LDETDGDGGENVNLEALKSLAYEGE--PEEIASNFKNQGNNCYKFKKYKDAIIEYTKGLE
HSTTC4   48 RAPSEIDPRENPDLACLQSIIFDEERSPEEQAKTYKDEGNDYFKEKDYKKAVISYTEGLK

SCCNS1  112 VECEDKSINESLYANRAACELELKNYRRCIEDCSKALTINPKNVKCYYRTSKAFFQLNKL
CACNS1  118 VNCDVDAINSALYLNRAACNLELKNYRRCIEDCKKVLMLDEKNIKACFRSGKAFFAIEKY
HSTTC4  108 KKCADPDINAVLYTNRAAAQYYLGNFRSALNDVTAARKLKPCHLKAIIRGALCHLELIHF

SCCNS1  172 EEAKSAATFANQRIDPENKSILNMLSVID-RKEQELKAKEEKQQREAQERENKKIMLESA
CACNS1  178 EEAIKVLEYG-LNIEPENKDLQKLLQQVQKRQETLAQIKAKKAQEEEQER-LKNIMLENS
HSTTC4  168 AEAVNWCDEG-LQIDAKEKKLLEMRAKADKLKRIEQRDVRKANLKEKKER-NQNEALLQA

SCCNS1  231 MTLRNITNIKIHSPVE--------ILNEGKIRLEDPM------DEESQLIYPALIMYPTQ
CACNS1  236 IKLRHIEIVKSSSPPE--------VLKTAKIRLEDPK------DYQSQLIEPAMILYPTT
HSTTC4  226 IKARNIRLSEAACEDEDSASEGLGELFLDGLSTENPHGARLSLDGQGRLSWPVLFLYPEY

SCCNS1  277 DEFDFVGEVSELTTVQELVDIVLEGPQERFKKEGKENFTPKKVLVFMETK--AGGLIKAG
CACNS1  282 DEFDFIAEHSELTTPIELLEMVLNRPREWEDDPKHKDENVKKLECFMETE--SGGLIKVG
HSTTC4  286 AQSDFISAFHEDSRFIDHLMVMFGETPSWDLEQKYCLIIWRSTLRMRTGQNYTGGLPRAP

SCCNS1  335 KKLTEHDILKKESPDVPLFDNALKIYIVPKVESEGWISKWDKQKALERRSV
CACNS1  340 KIISSK---------------------------------------------
HSTTC4  346 CYRFYSTRGTL----------------------------------------
```

Figure 23

Ypd1p (YDL235c)

Comparison	Identity
Sac-Can	33.3%

```
CAYPD1    1   NKTFIMSEDKLQKLQDSGLVDWAVFSEIVIMDEDEEGFSKSLVEVFVSQVEETFEEIDKY
SCYPD1    1   -----------MSTIPSELINWTILNEIISMDDDDSDFSKGLIIQFIDQAQTTFAQMQRQ

CAYPD1   61   LK-EKNLEKLSSSGHFLKGSAAALGLTKISNQCERIQNYGHKIN-FDNFQLEDIKTKGDS
SCYPD1   50   LDGEKNLTELDNLGHFLKGSSAALGLQRIAWVCERIQNLGRKMEHFFPNKTELVNTLSD-

CAYPD1  119   AVSAENVAVNDGETNPENGSNGNETSNNKTNTSNIPDESSDDFWIALIEDALAKARDGFD
SCYPD1  109   ------------KS-IINGINIDED--DEEIKIQVDDKDENSIYLILIAKALNQSRLEFK

CAYPD1  179   QSRRALDEYYE---
SCYPD1  154   LARIELSKYYNTNL
```

Figure 24

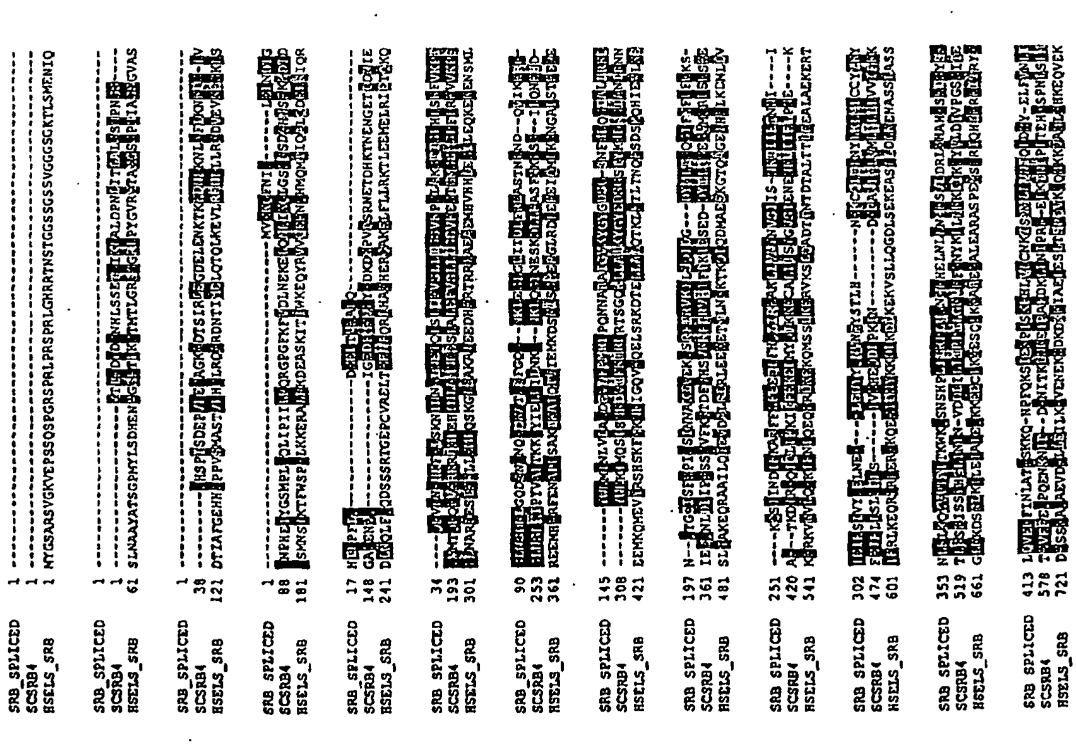
Tim10p (YHR005C-A)

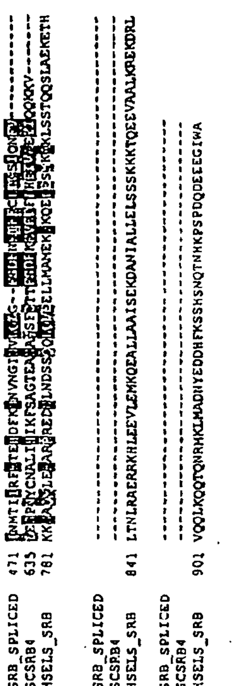
```
CATIM10     1 --MFGLGGTTPQISSQQKLQAAEAELDMVTGMFNALVSQCHTKCINKSYNEADISKQESL
SCTIM10     1 MSFLGFGGGQPQLSSQQKIQAAEAELDLVTDMFNKLVNNCYKKCINTSYSEGELNKNESF
HSTIM10     1 --------MDP-LRAQQ--LAAELEVEMMADMYNRMTSACHRKCVPPHYKEAELSKGESV

CATIM10    59 CLDRCVAKYFETNVQVGENMQKLGQSGQFMGRR---------
SCTIM10    61 CLDRCVAKYFETNVQVGENMQKMGQSFNAAGKF---------
HSTIM10    50 CLDRCVSKYLDIHERMGKKLTELSMQDEEIMKRVQQSSGPA
```

Comparison	Identity
Sac-Can	68.1%
Sac-Hum	36.6%
Can-Hum	36.6%

Figure 25

Srb4p (YER022W)





Comparison	Identity
Sac-Can	28.4%
Sac-Hum	18.0%
Can-Hum	18.0%

Figure 26

S. cerevisiae RPC34 (YNR003C) inactivation

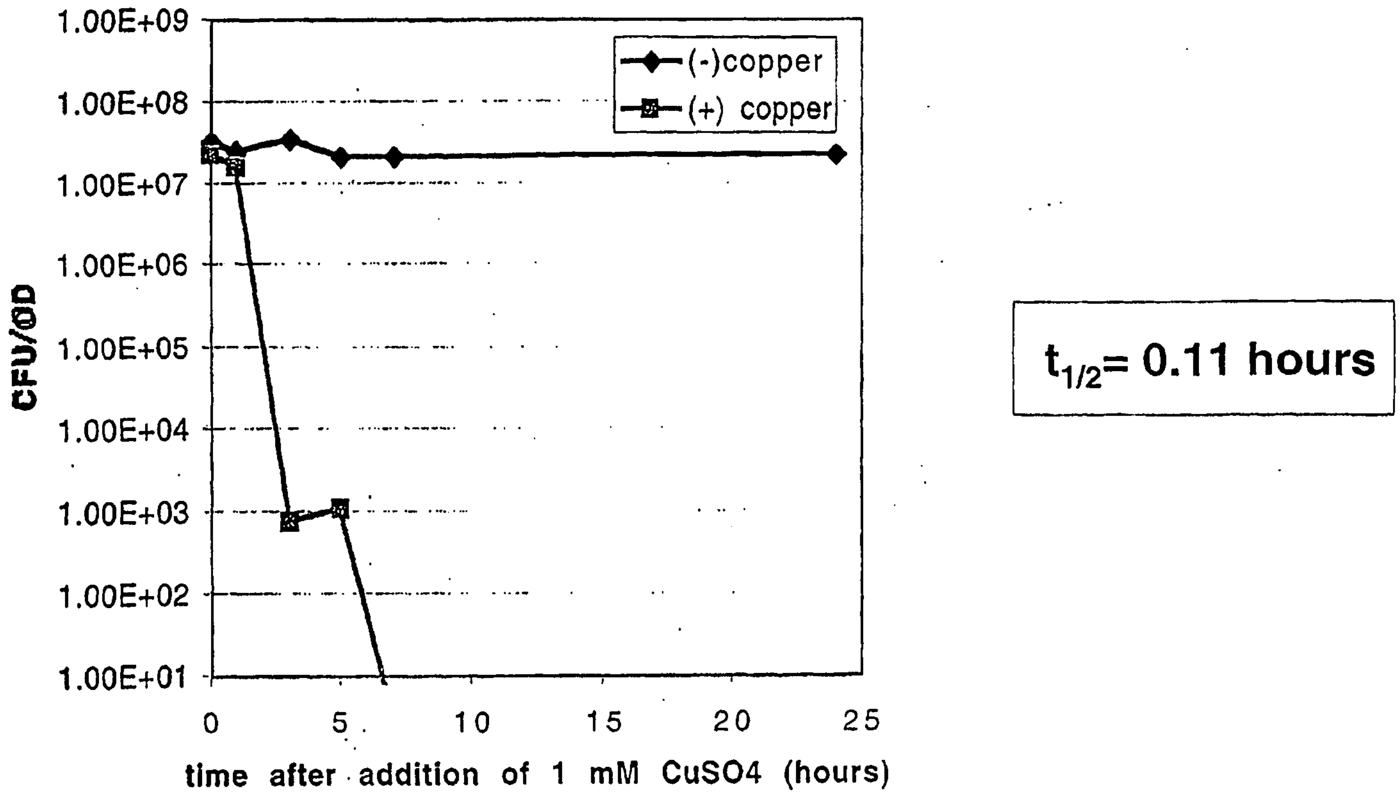
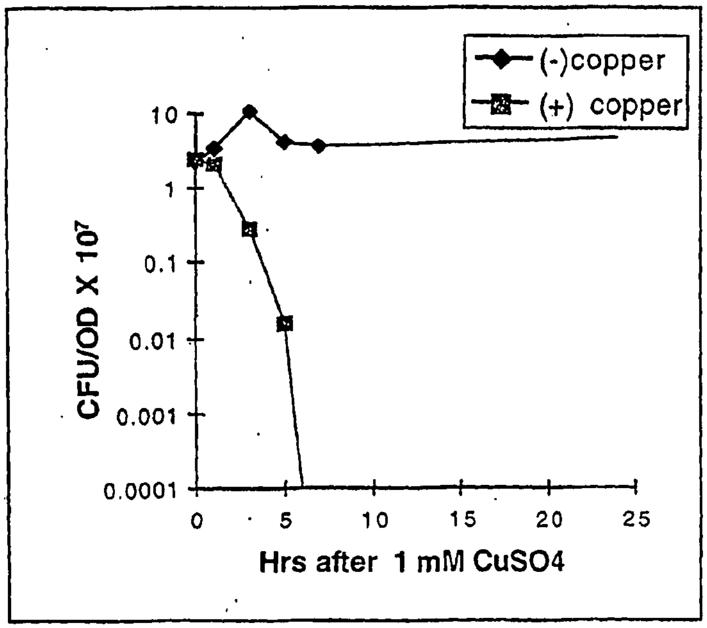


Figure 27

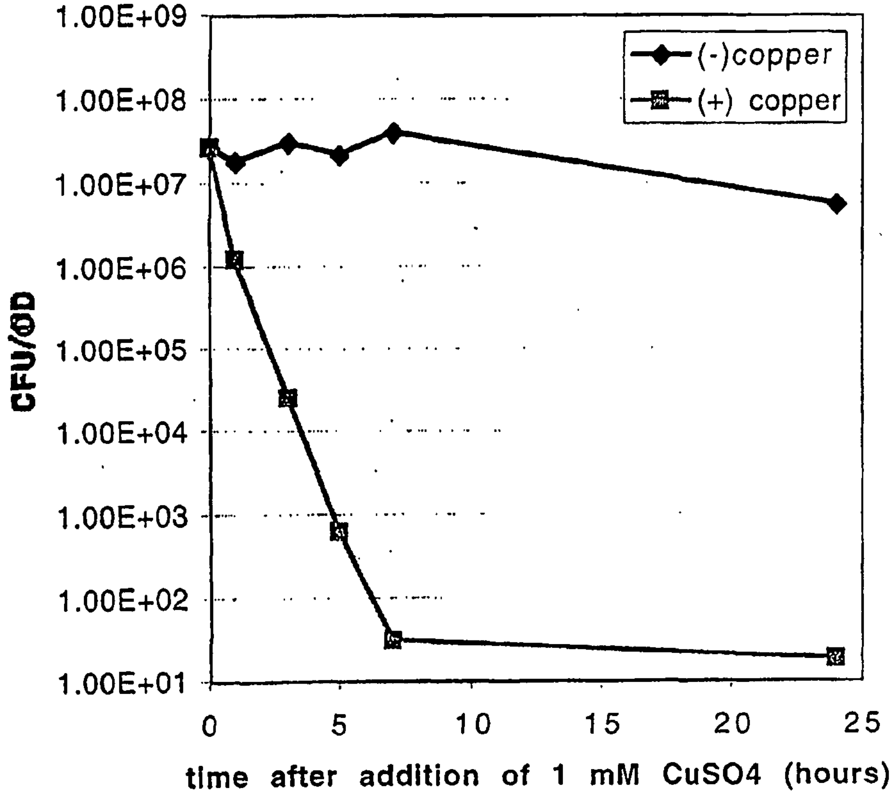
S. cerevisiae POP3 (YNL282W) inactivation



$t_{1/2}$= 0.34 hours

Figure 28

S. cerevisiae TFA2 (YKR062W) inactivation



$t_{1/2}$= 0.35 hours

Figure 29

S. cerevisiae NAB2 (YGL122C) inactivation

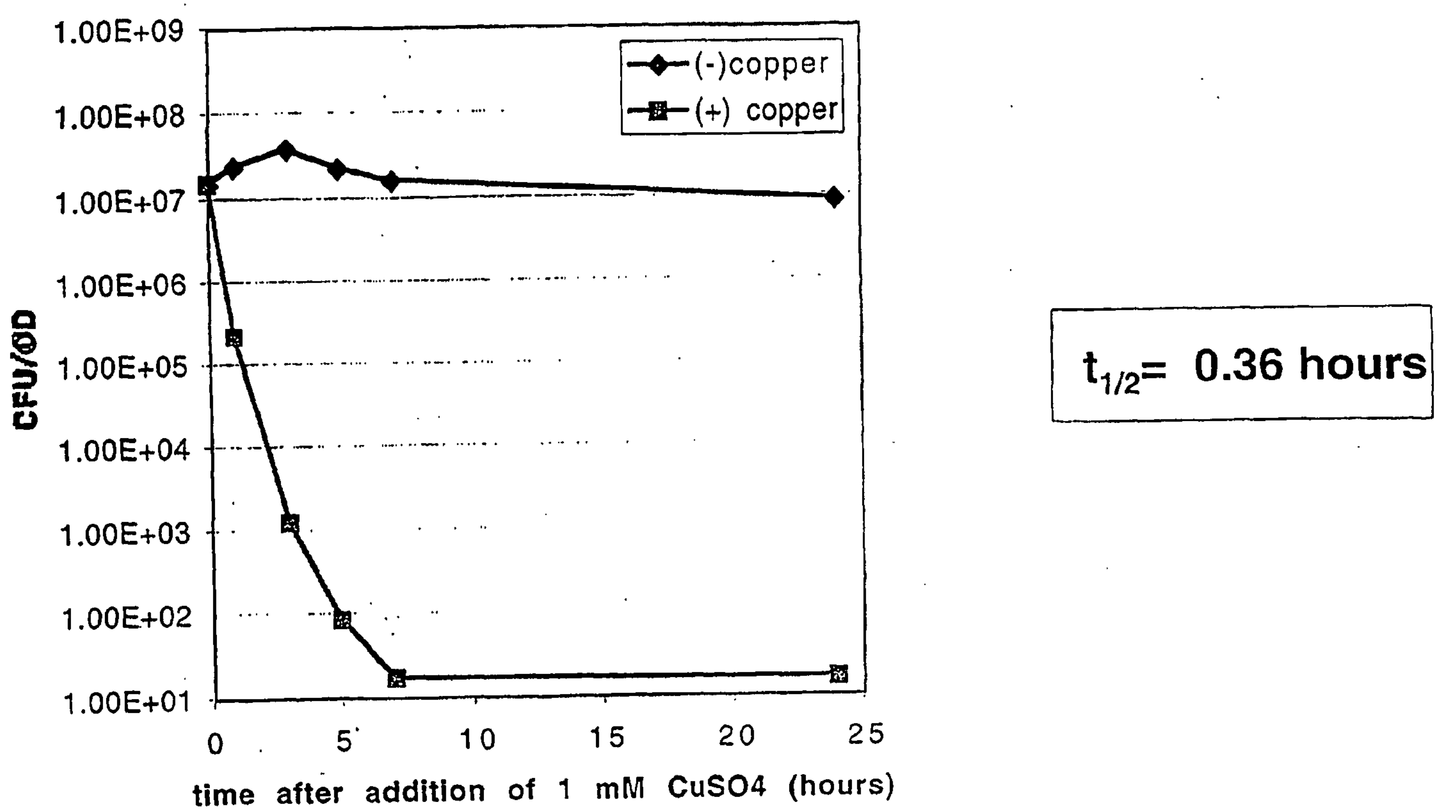


Figure 30

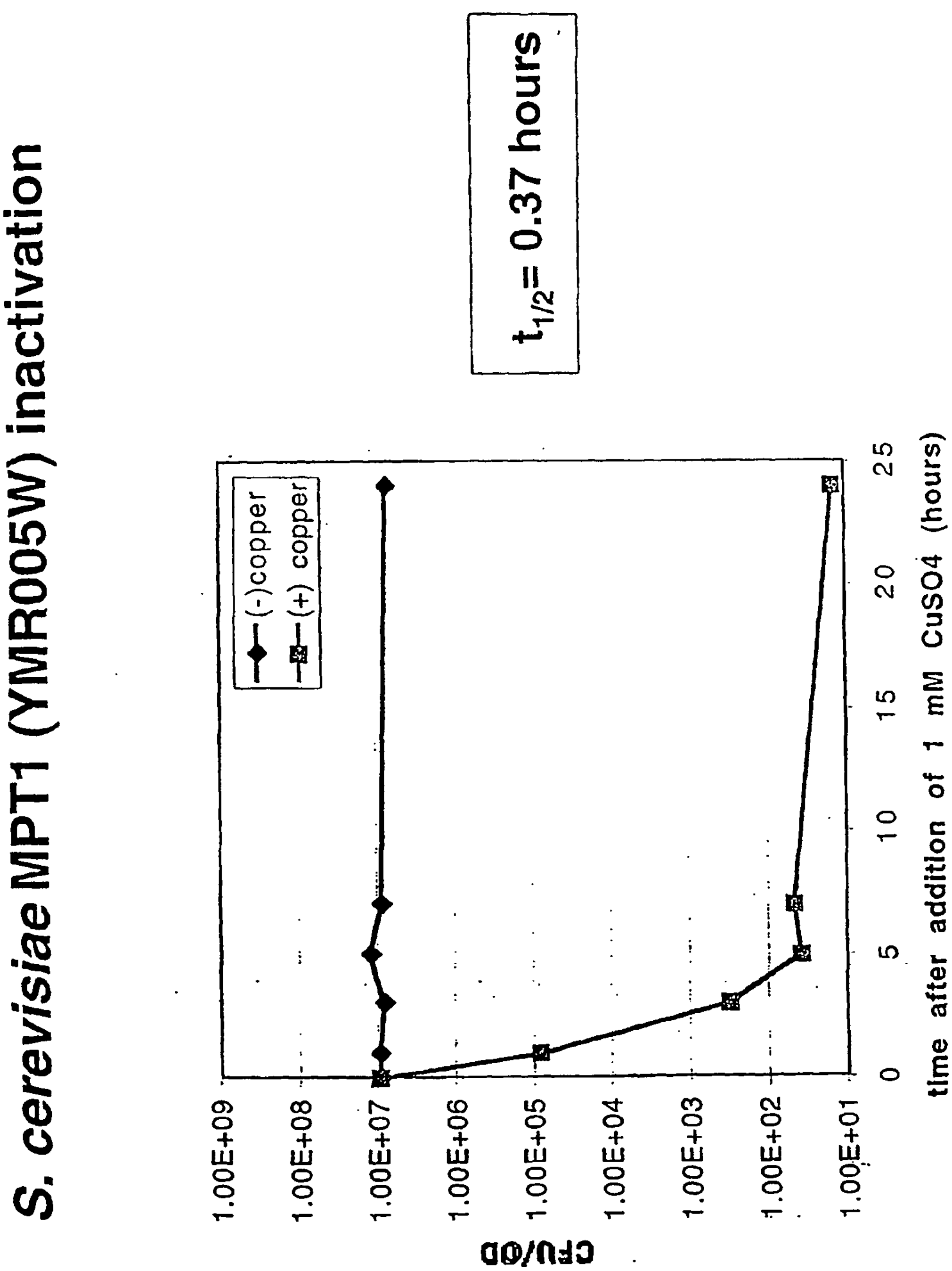

S. cerevisiae MPT1 (YMR005W) inactivation
t1/2= 0.37 hours
(-)copper
(+) copper
CFU/OD
1.00E+09
1.00E+08
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
1.00E+01
0
5
10
15
20
25
time after addition of 1 mM CuSO4 (hours)

Figure 31

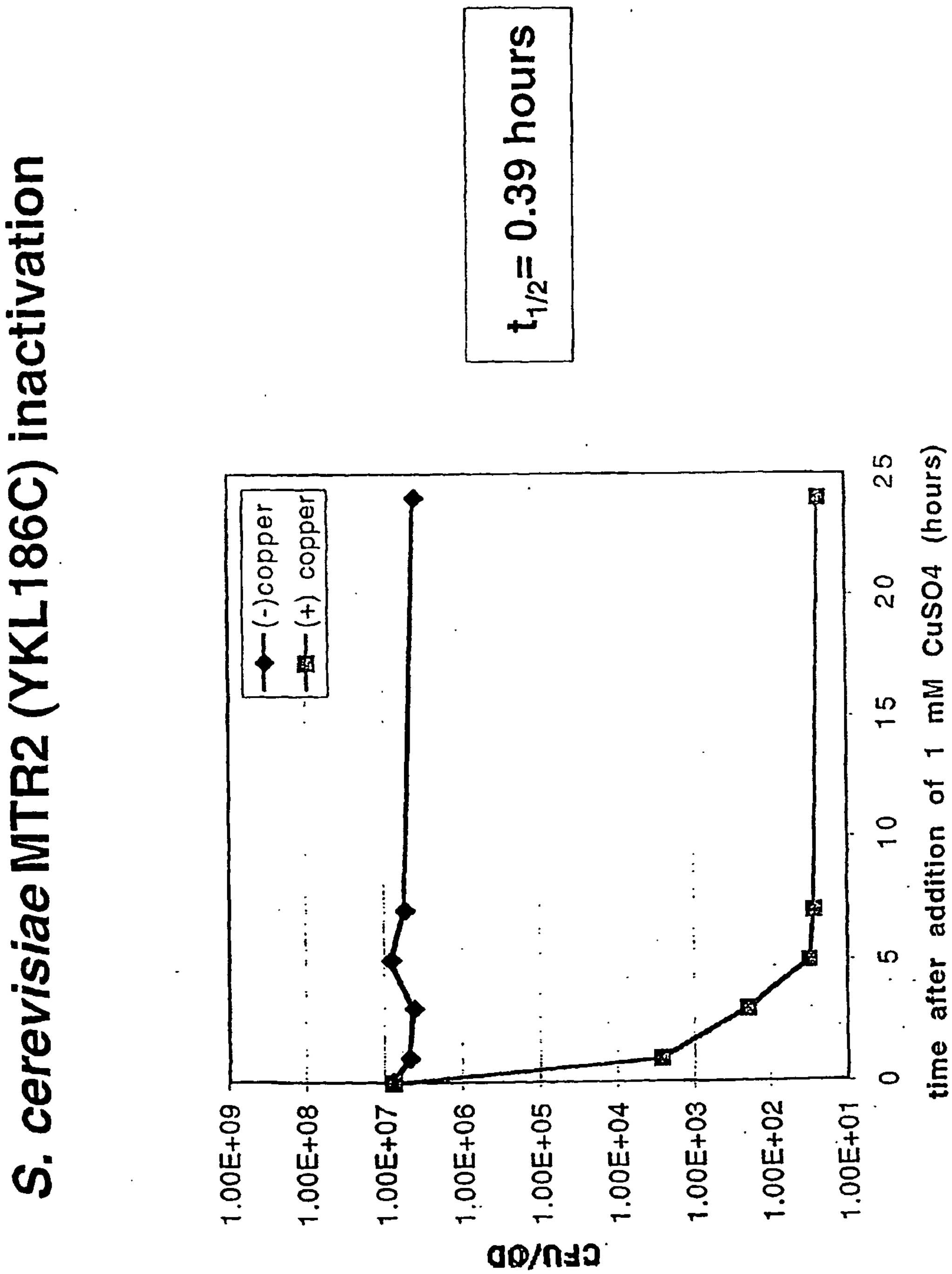

S. cerevisiae MTR2 (YKL186C) inactivation
t1/2= 0.39 hours
(-)copper
(+) copper
CFU/OD
1.00E+09
1.00E+08
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
1.00E+01
0
5
10
15
20
25
time after addition of 1 mM CuSO4 (hours)

Figure 32

S. cerevisiae BOS1 (YLR078C) inactivation

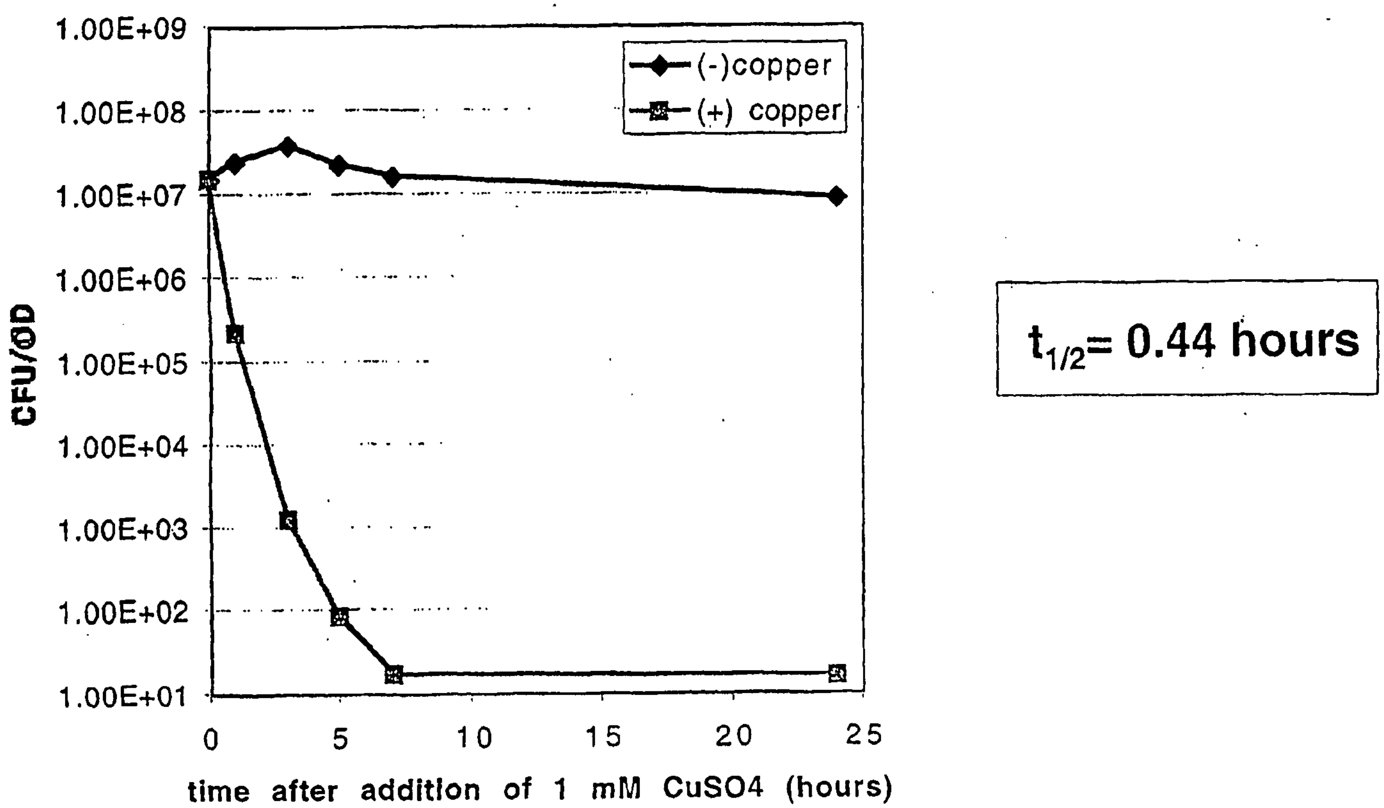


Figure 33

S. cerevisiae POL30 (YBR088C) inactivation

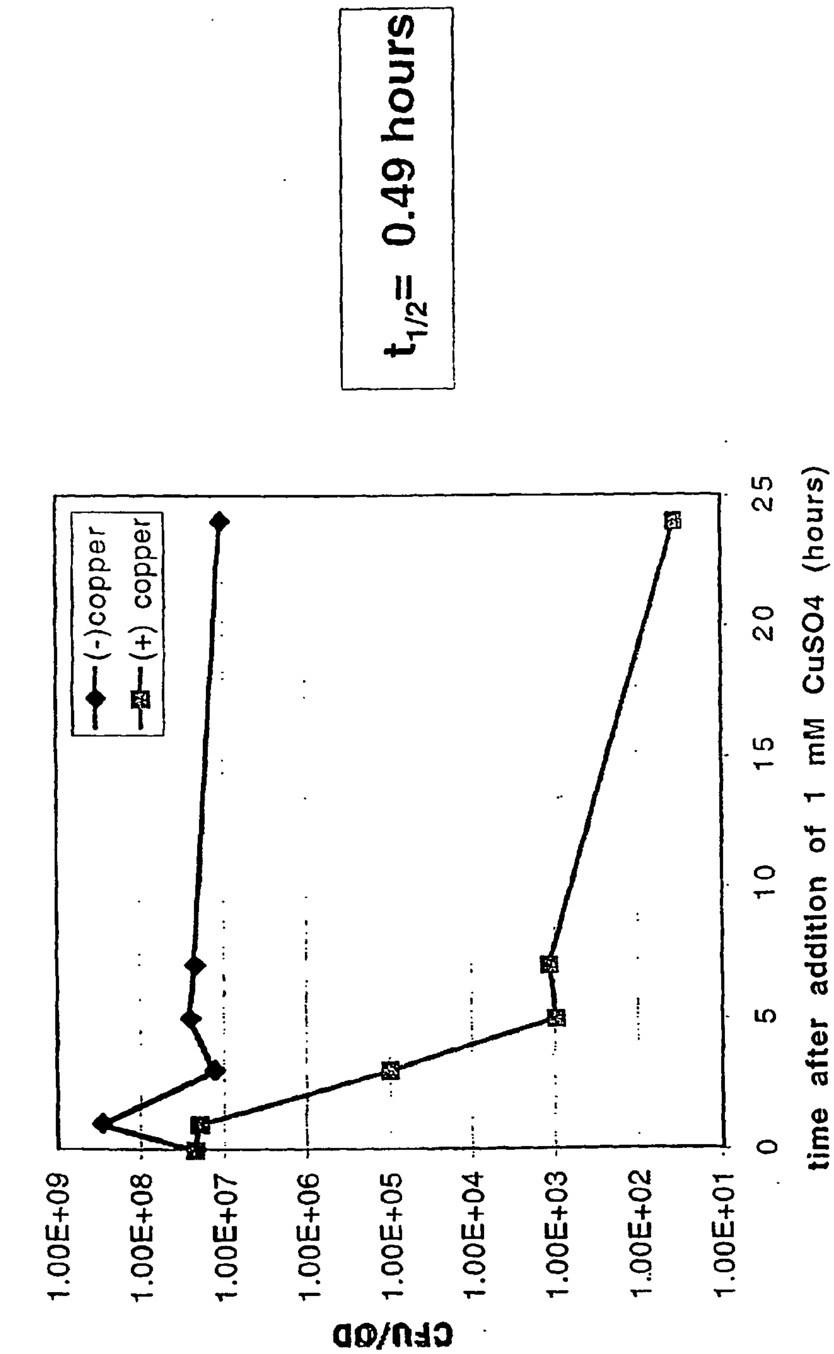


Figure 34

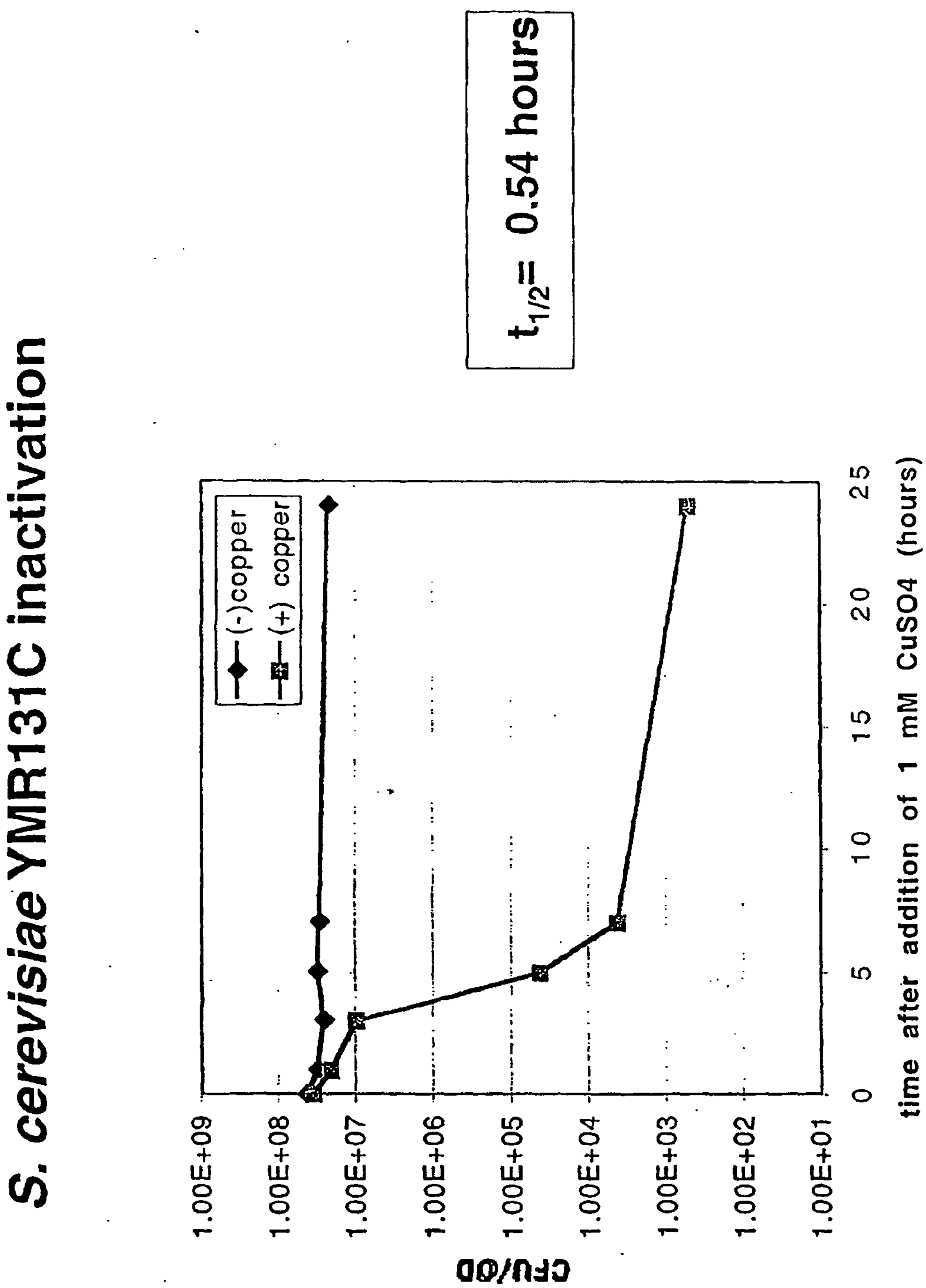

S. cerevisiae YMR131C inactivation
$t_{1/2}$= 0.54 hours
(-)copper
(+) copper
CFU/OD
1.00E+09
1.00E+08
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
1.00E+01
0
5
10
15
20
25
time after addition of 1 mM CuSO4 (hours)

Figure 35

S. cerevisiae SQT1 (YIR012W) inactivation

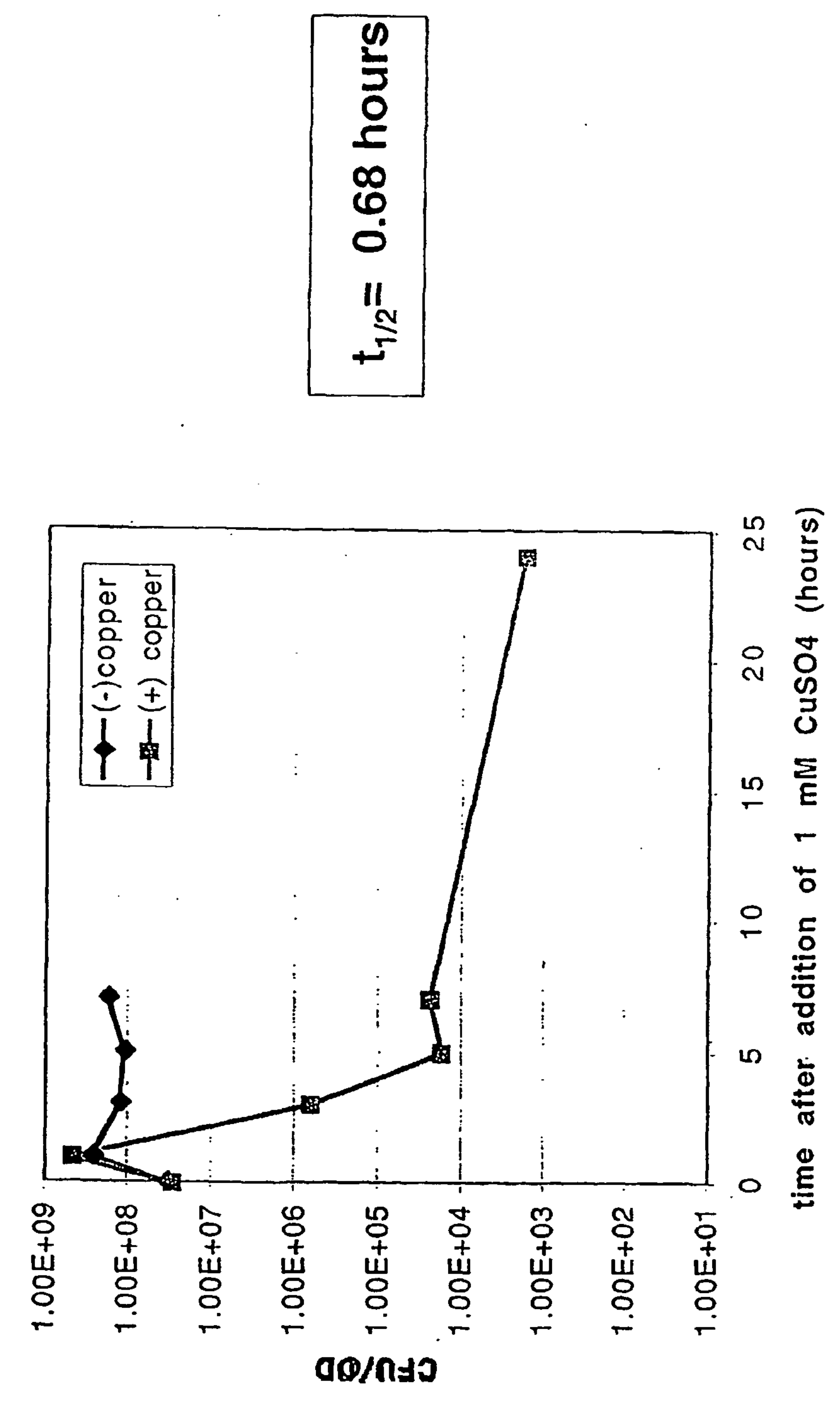
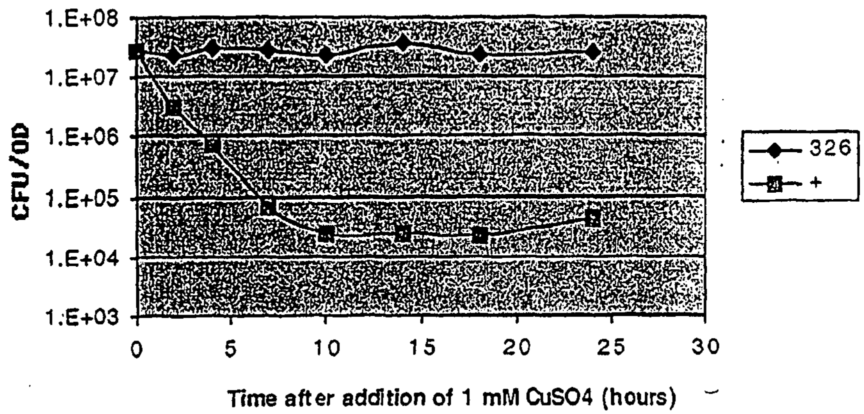


Figure 36

S. cerevisiae MTW1 (YAL034W-A) inactivation



$t_{1/2}$= 0.81 hours

Figure 37

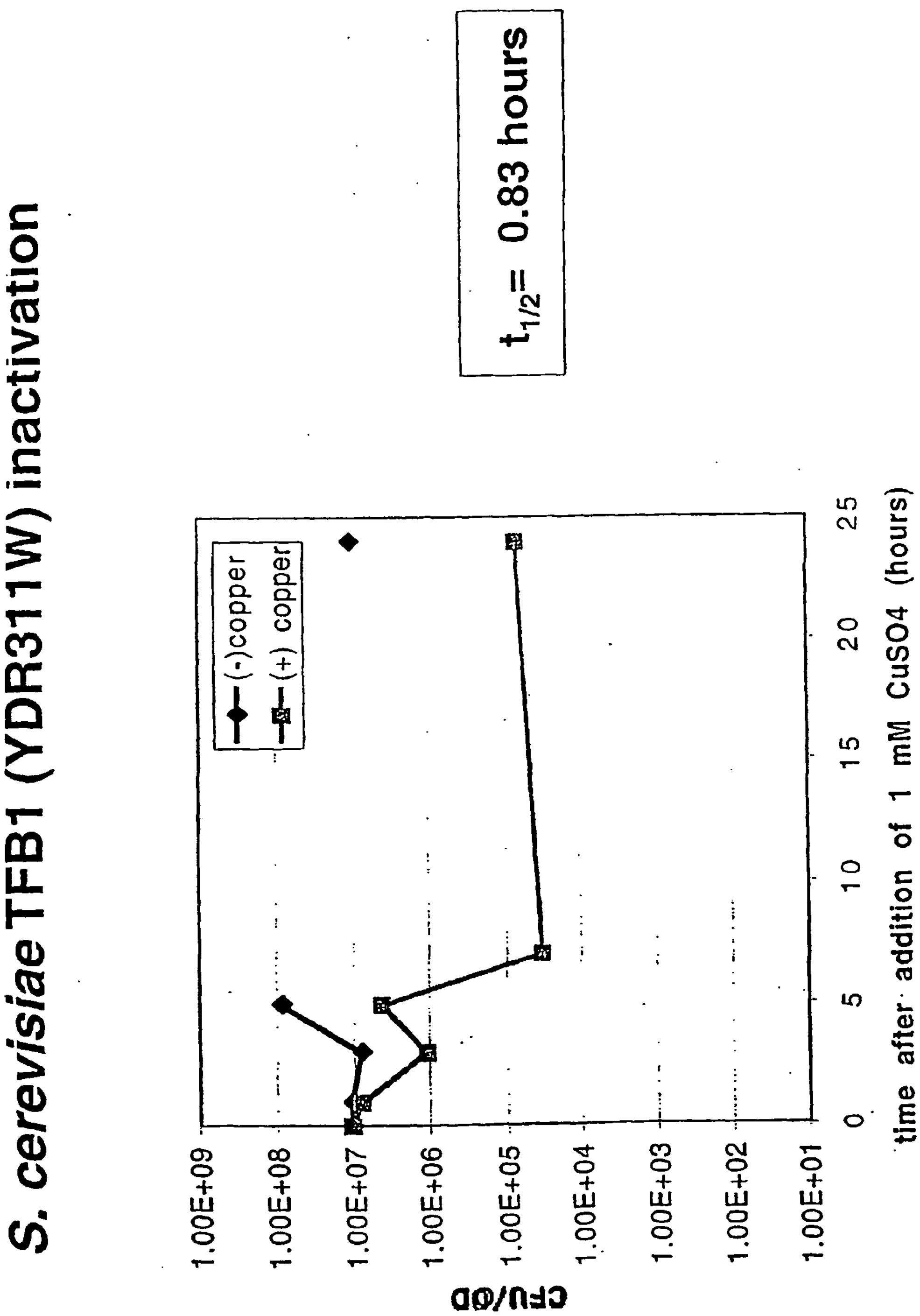

S. cerevisiae TFB1 (YDR311W) inactivation
$t_{1/2}$= 0.83 hours
(-)copper
(+) copper
CFU/OD
1.00E+09
1.00E+08
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
1.00E+01
0
5
10
15
20
25
time after addition of 1 mM CuSO4 (hours)

Figure 38

S. cerevisiae SPC98 (YNL126W) inactivation

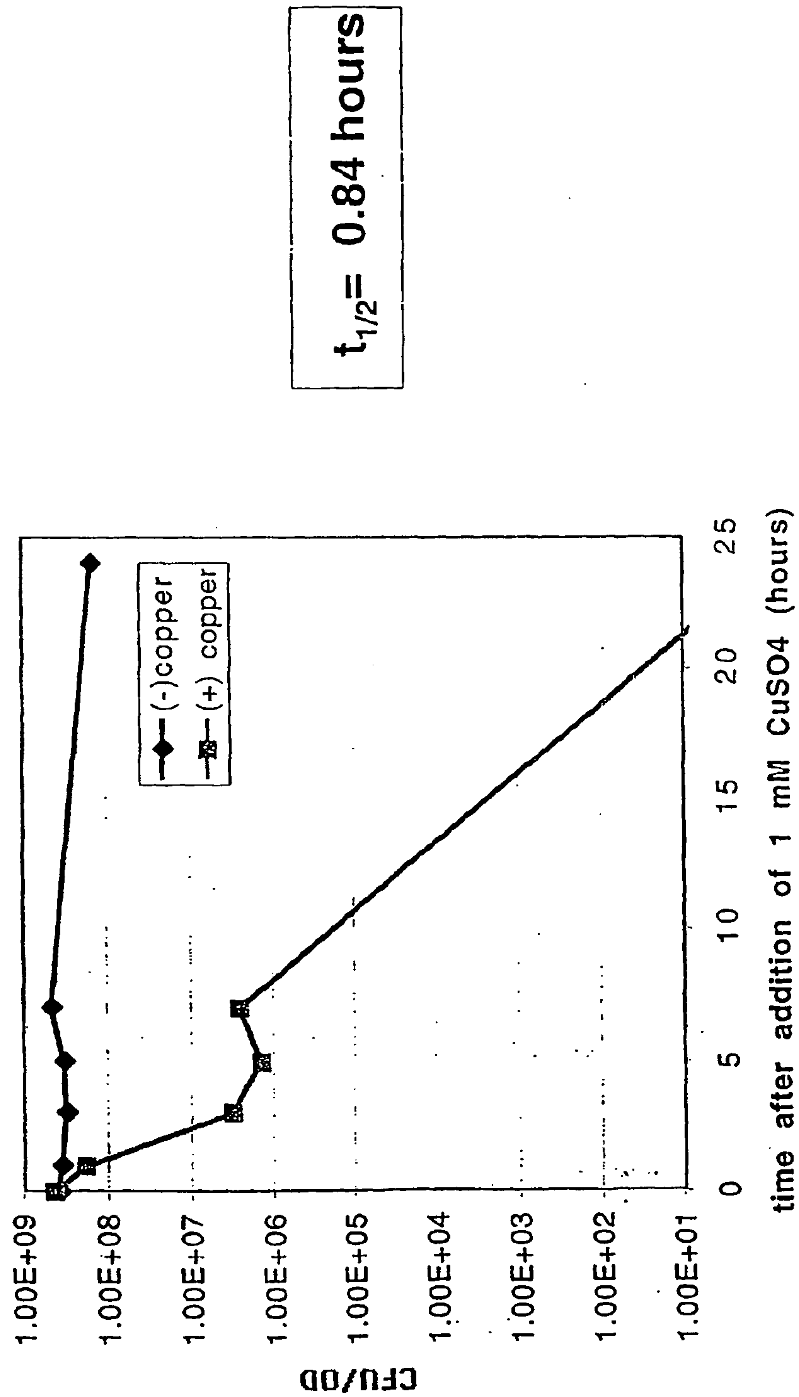


Figure 39

S. cerevisiae BFR2 (YDR299W) inactivation

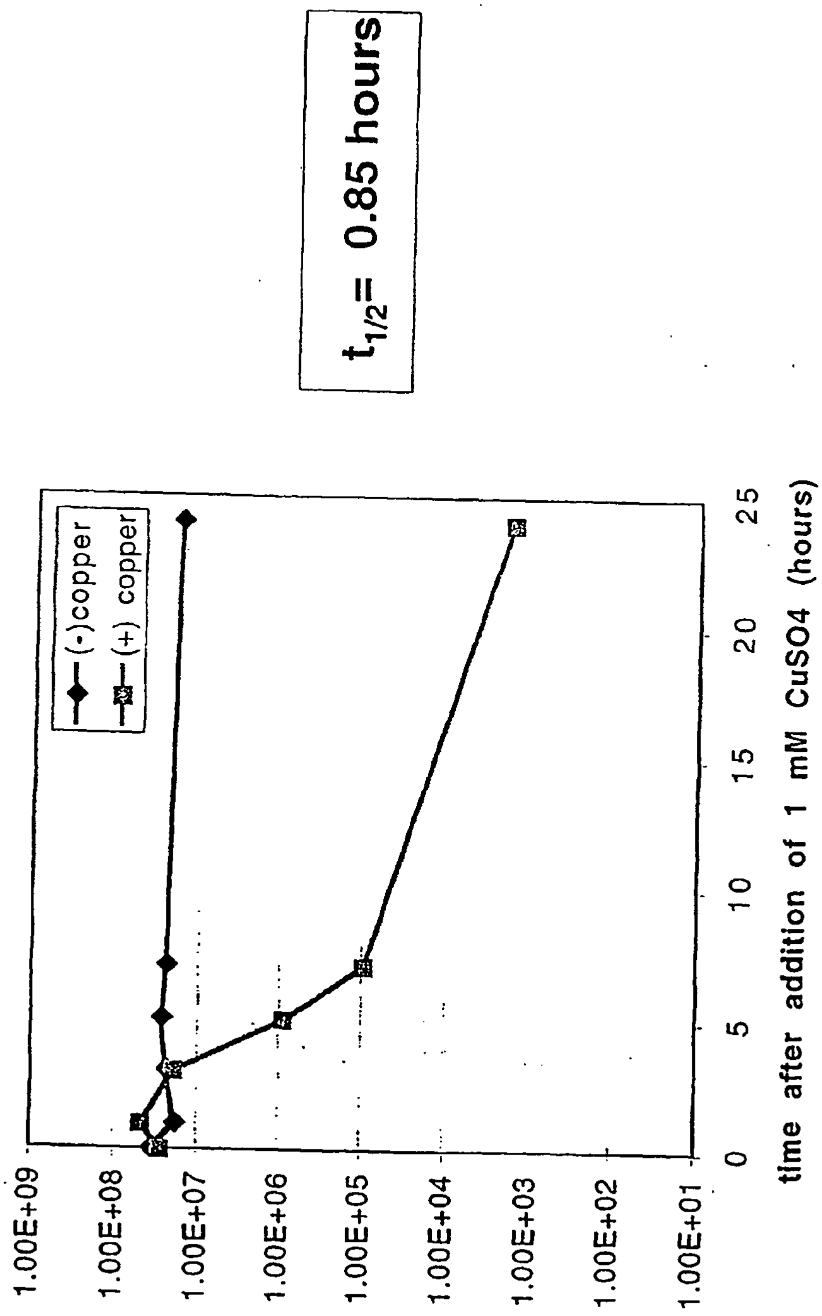


Figure 40

S. cerevisiae RNA1 (YMR235C) inactivation

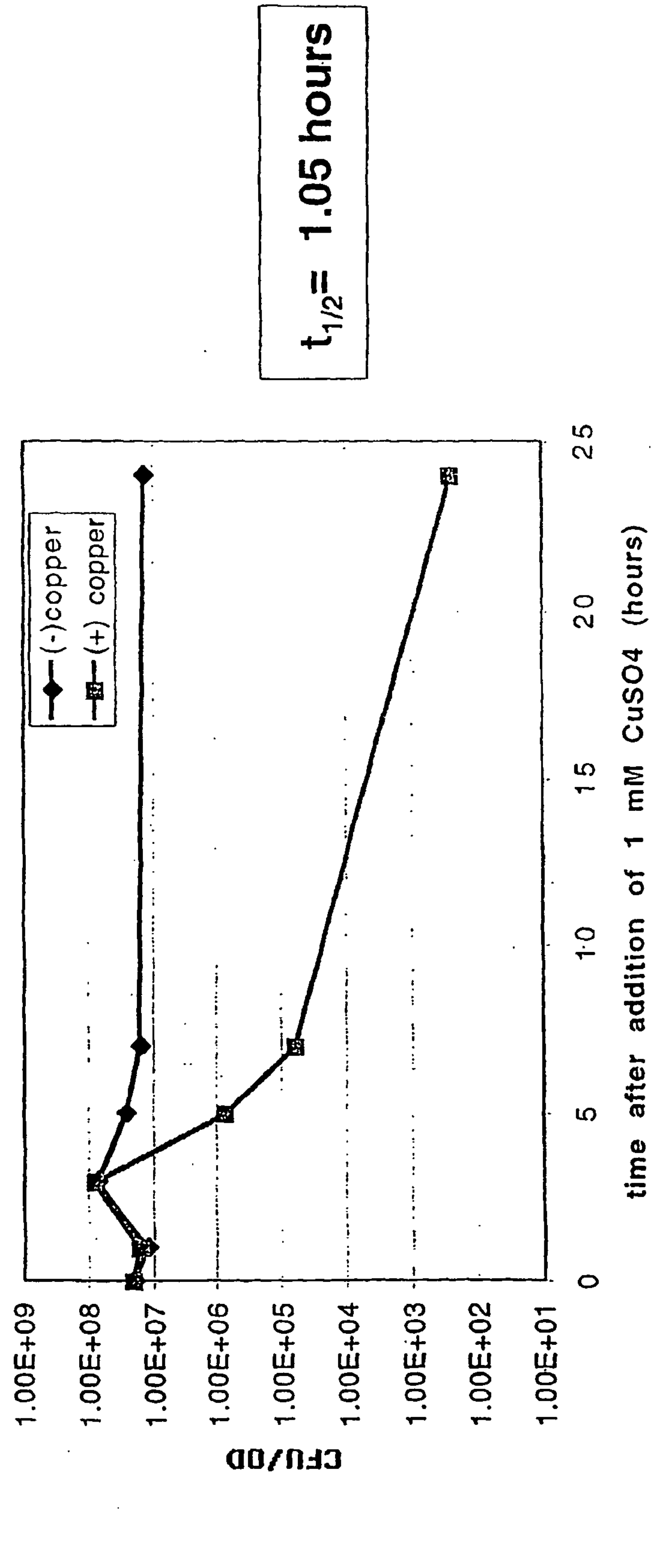


Figure 41

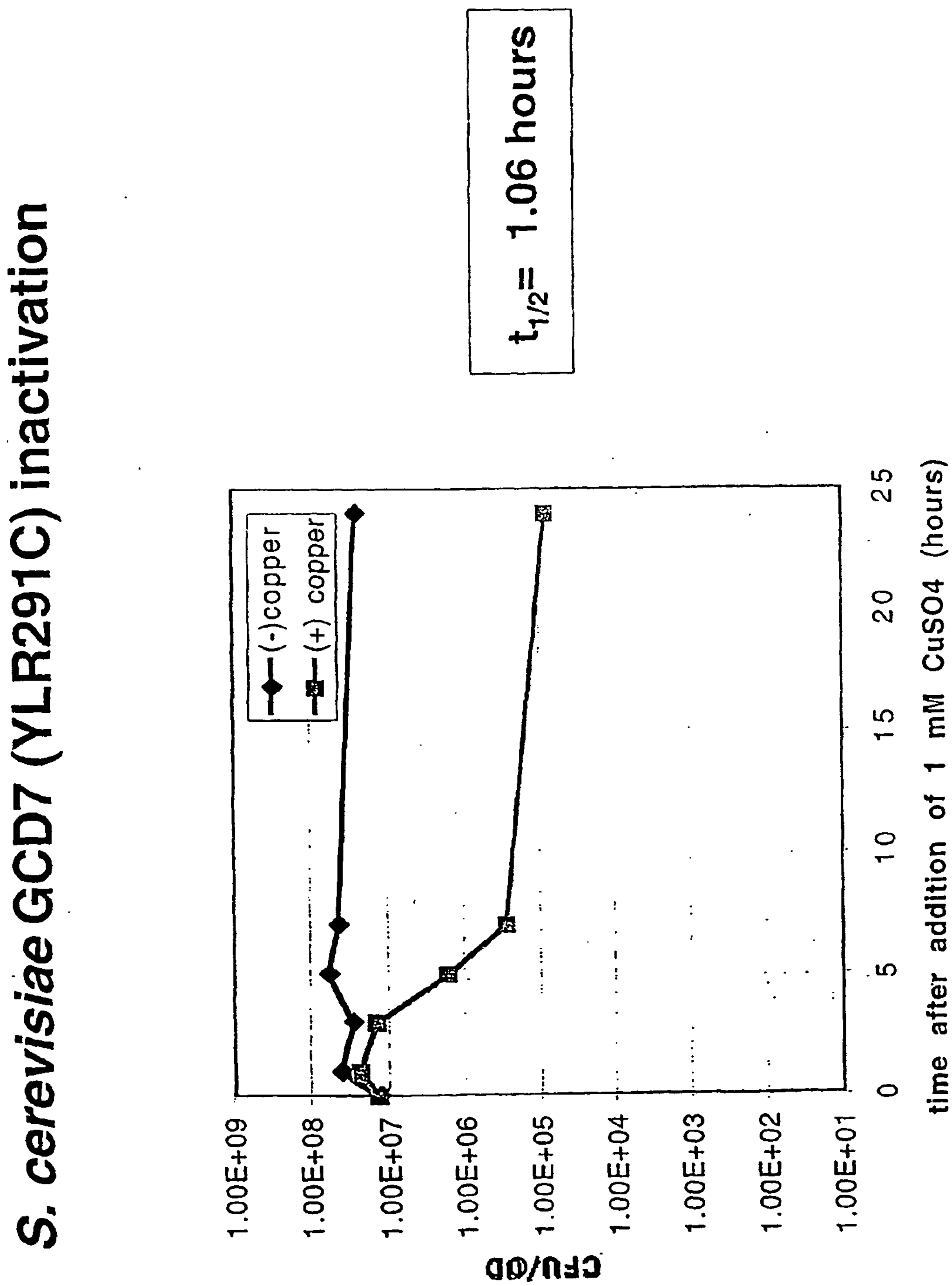

S. cerevisiae GCD7 (YLR291C) inactivation
$t_{1/2}$= 1.06 hours
(-)copper
(+) copper
CFU/OD
1.00E+09
1.00E+08
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
1.00E+01
0
5
10
15
20
25
time after addition of 1 mM CuSO4 (hours)

Figure 42

S. cerevisiae SKI6 (YGR195W) inactivation

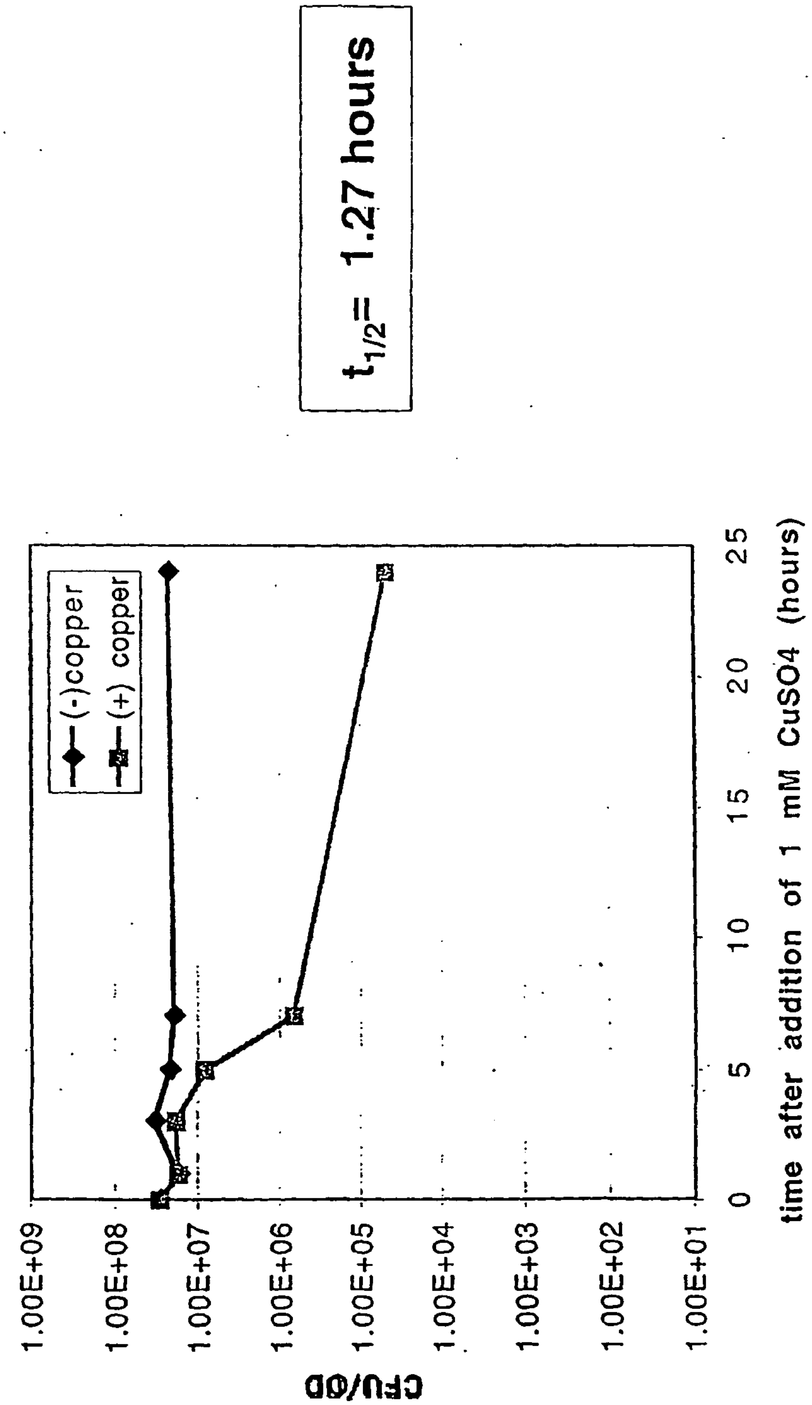
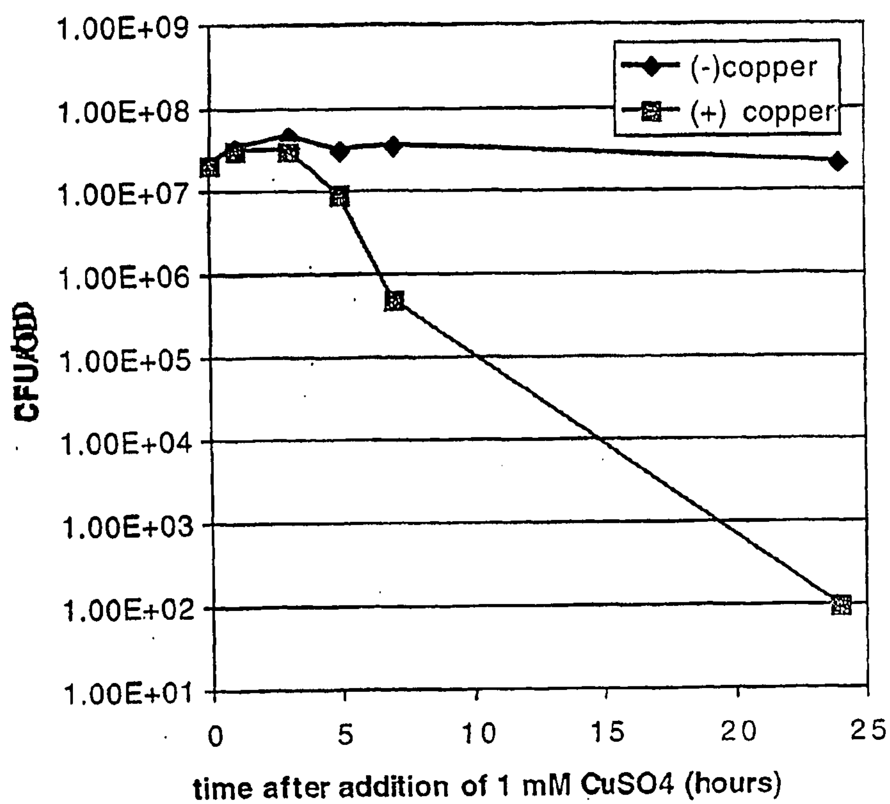


Figure 43

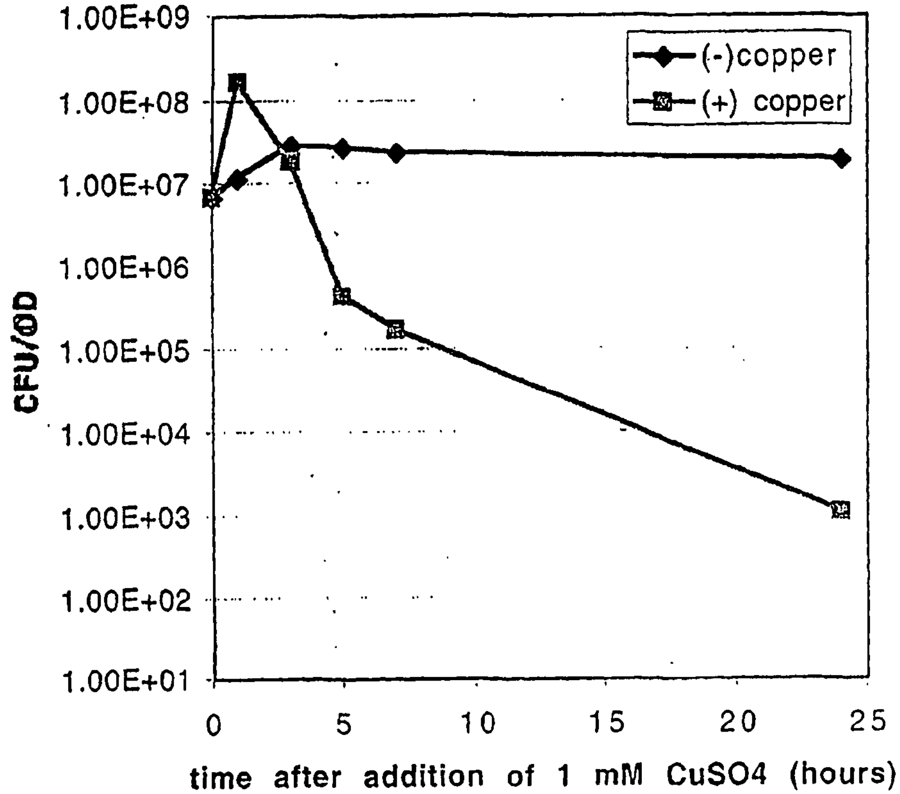
S. cerevisiae NIP1 (YMR309C) inactivation



$t_{1/2}$= 1.28 hours

Figure 44

S. cerevisiae LCP5 (YER127W) inactivation



$t_{1/2}$= 1.32 hours

Figure 45

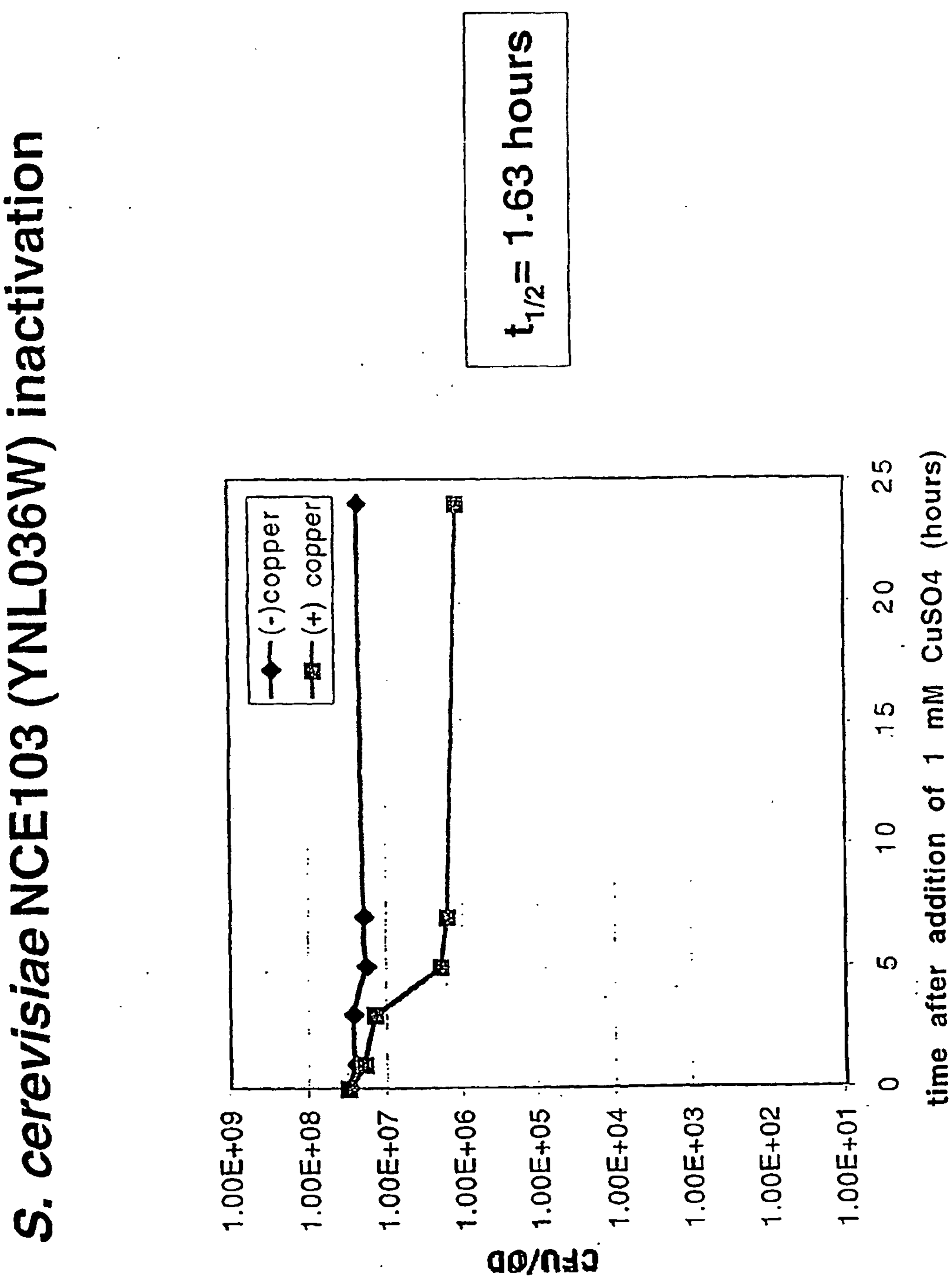

S. cerevisiae NCE103 (YNL036W) inactivation
$t_{1/2}$= 1.63 hours
(-)copper
(+) copper
1.00E+09
1.00E+08
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
1.00E+01
CFU/OD
0
5
10
15
20
25
time after addition of 1 mM CuSO4 (hours)

Figure 46

S. cerevisiae ECO1 (YFR027W) inactivation

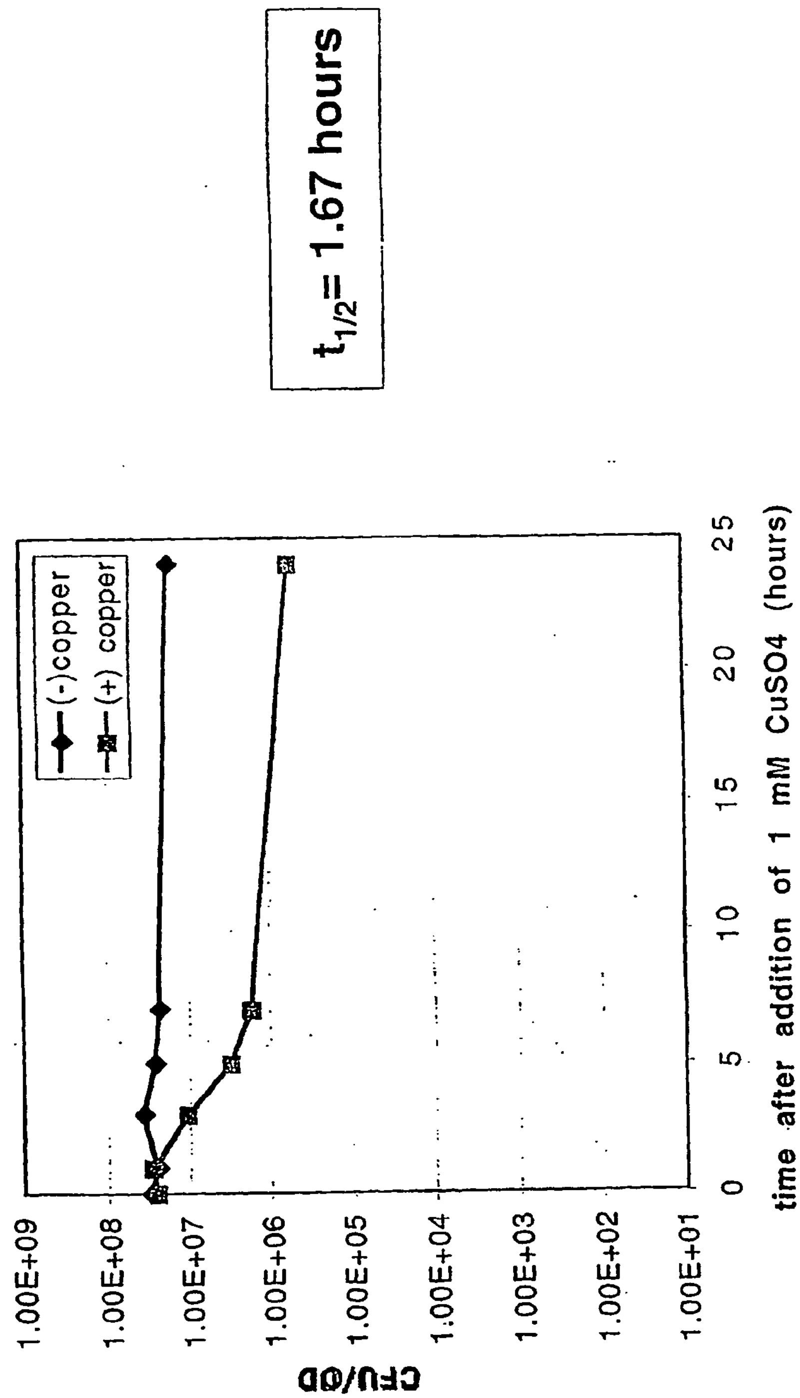


Figure 47

S. cerevisiae ORC2 (YBR060C) inactivation

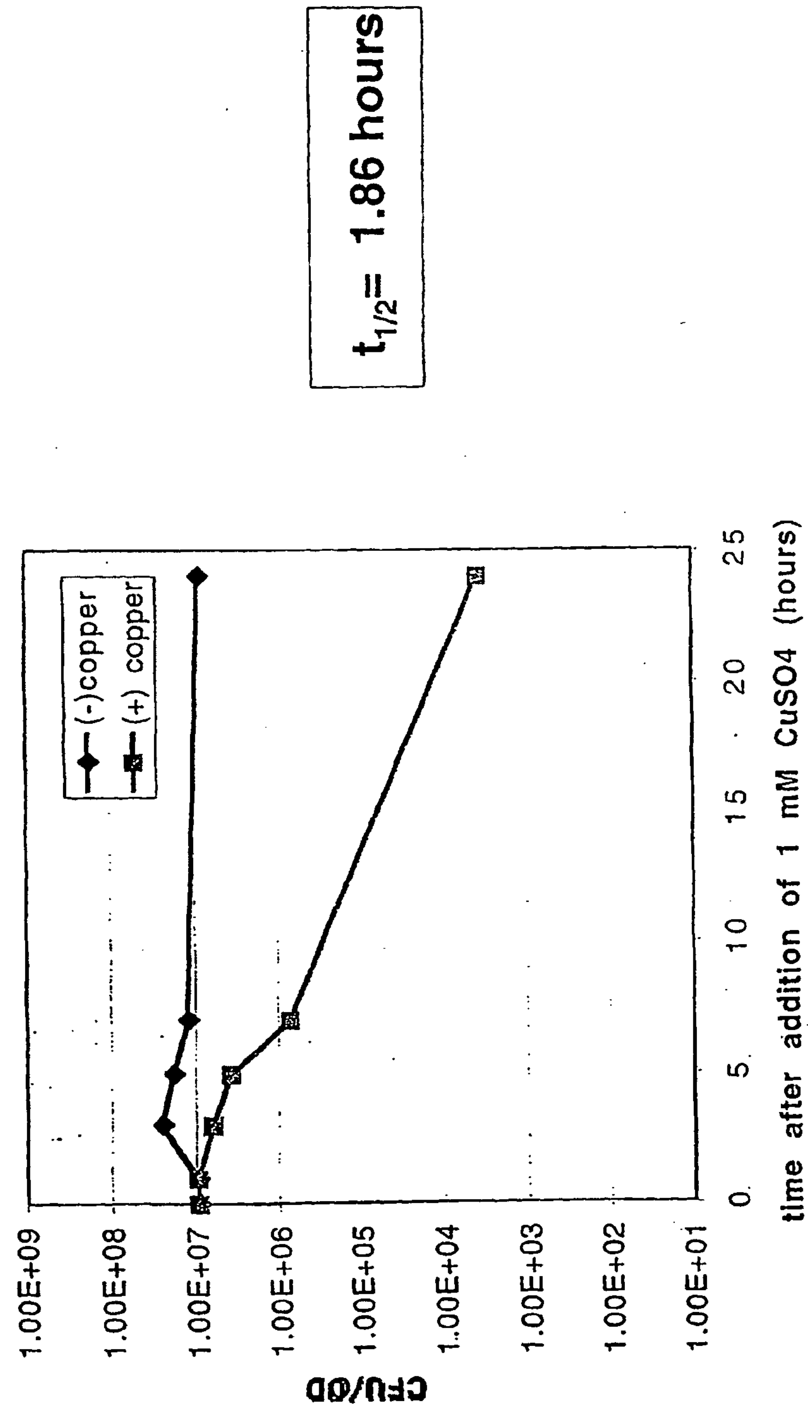
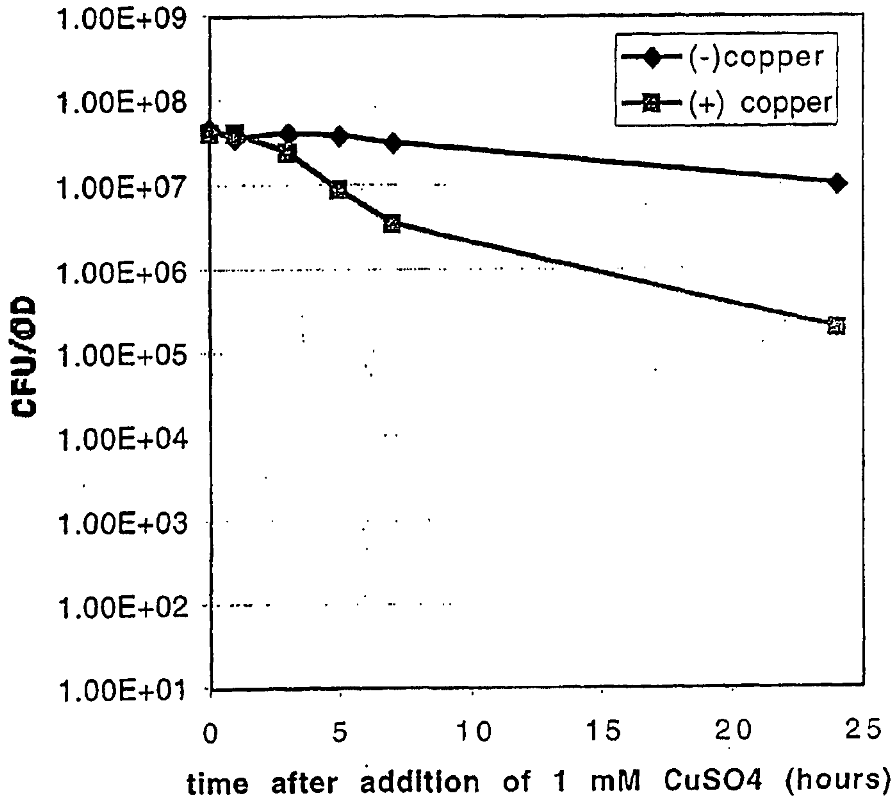


Figure 48

S. cerevisiae CNS1 (YBR155W) inactivation



$t_{1/2}$= 1.93 hours

Figure 49

S. cerevisiae YPD1 (YDL235C) inactivation

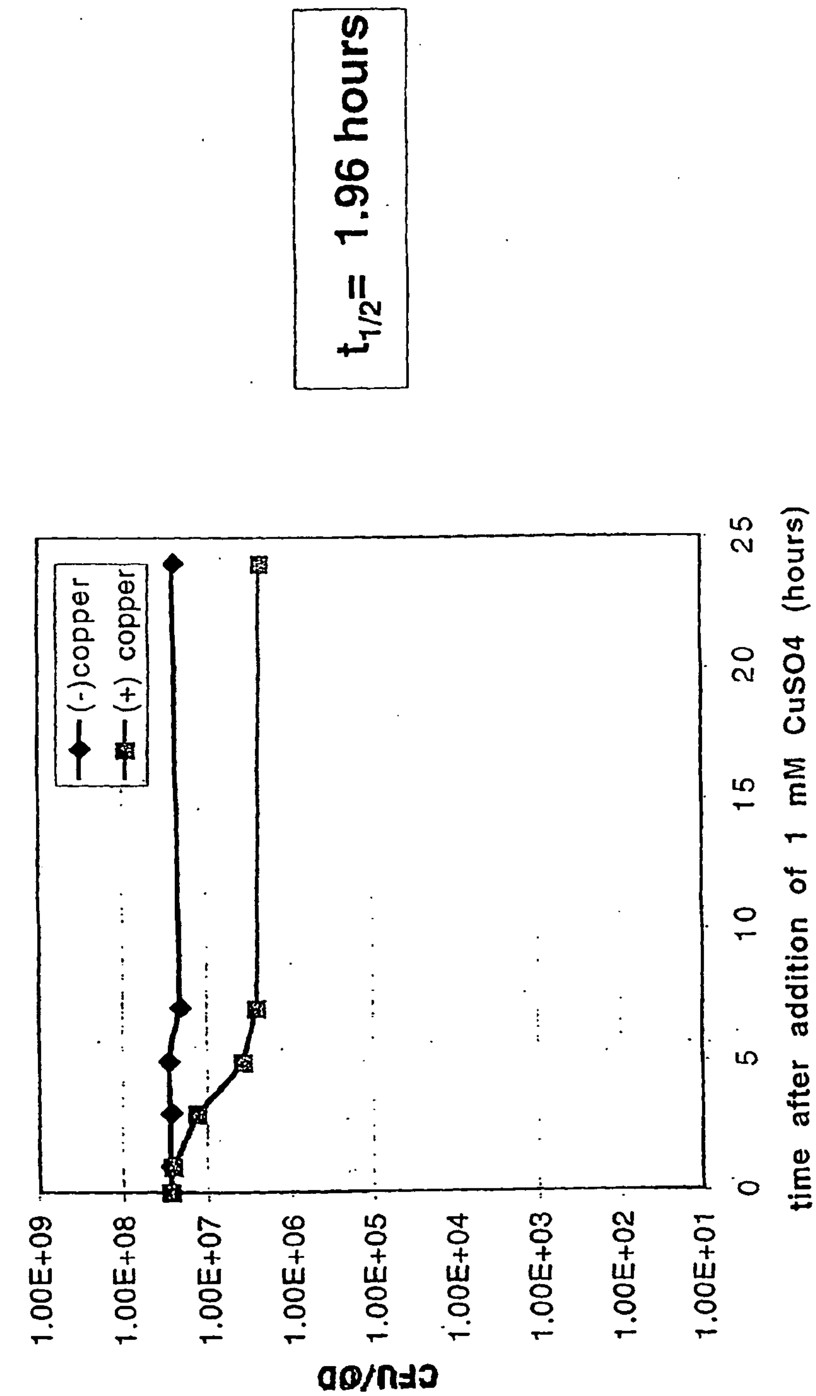
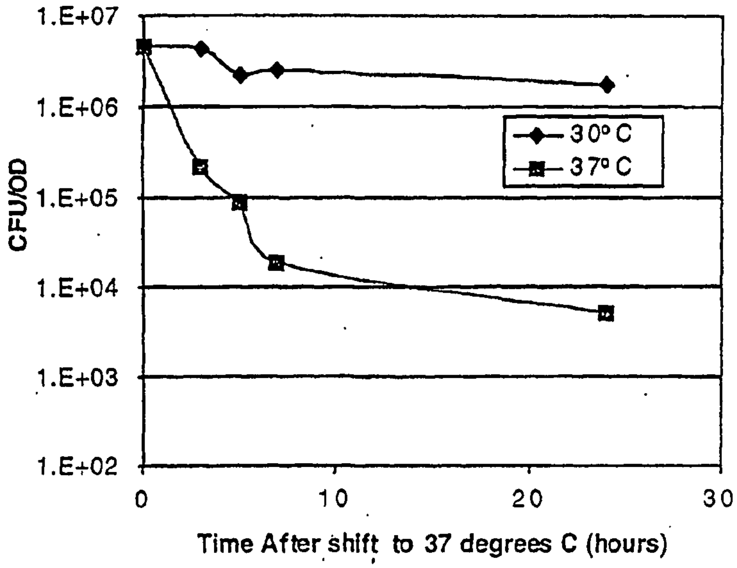


Figure 50

S. cerevisiae TIM10 (YHR005C-A) inactivation



$t_{1/2}$= 0.88 hours

Figure 51

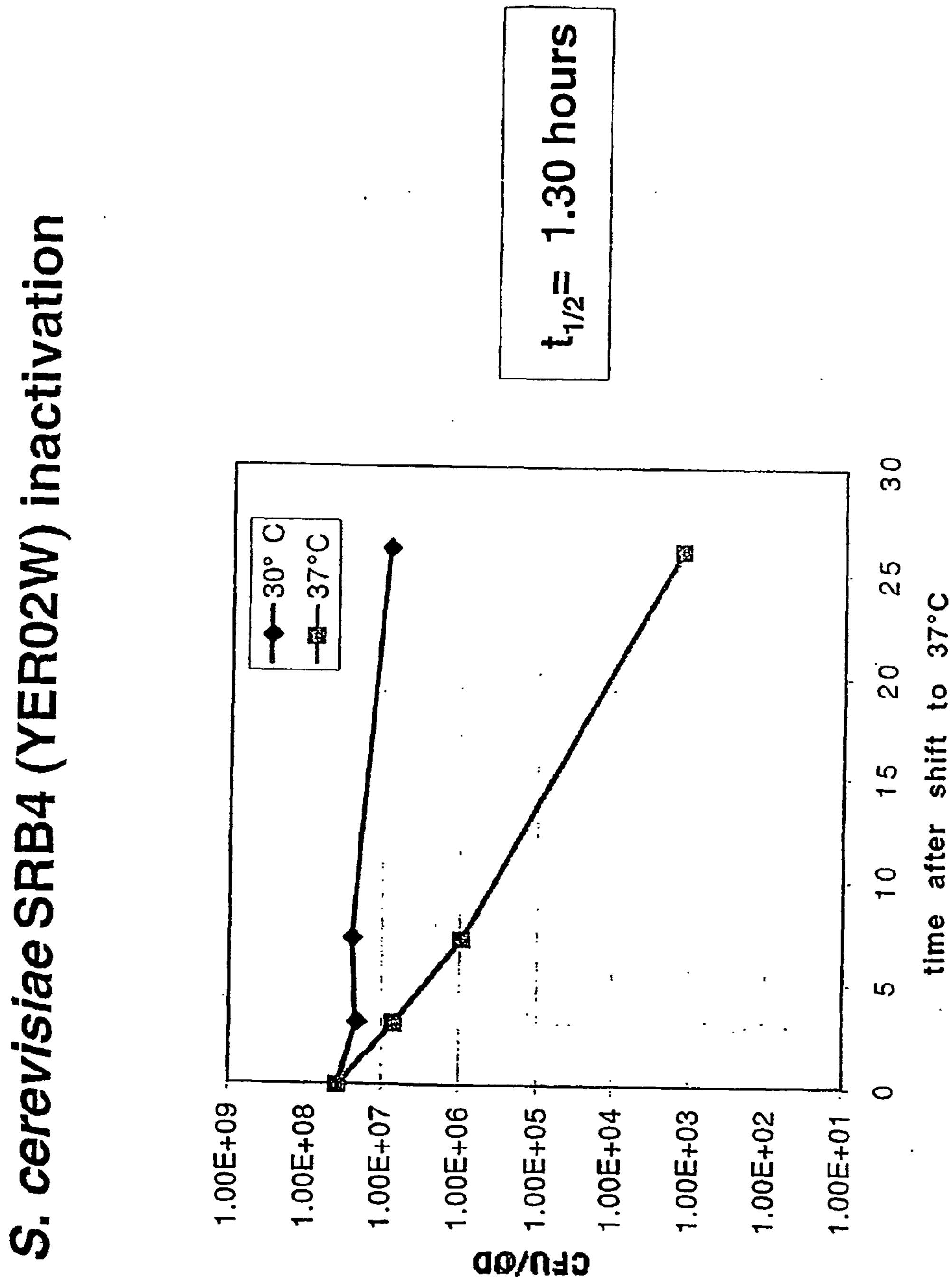

S. cerevisiae SRB4 (YER02W) inactivation
$t_{1/2}$= 1.30 hours
CFU/OD
1.00E+09
1.00E+08
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
1.00E+01
0
5
10
15
20
25
30
time after shift to 37°C
30° C
37°C

Figure 52

C. albicans RPC34 deletion analysis

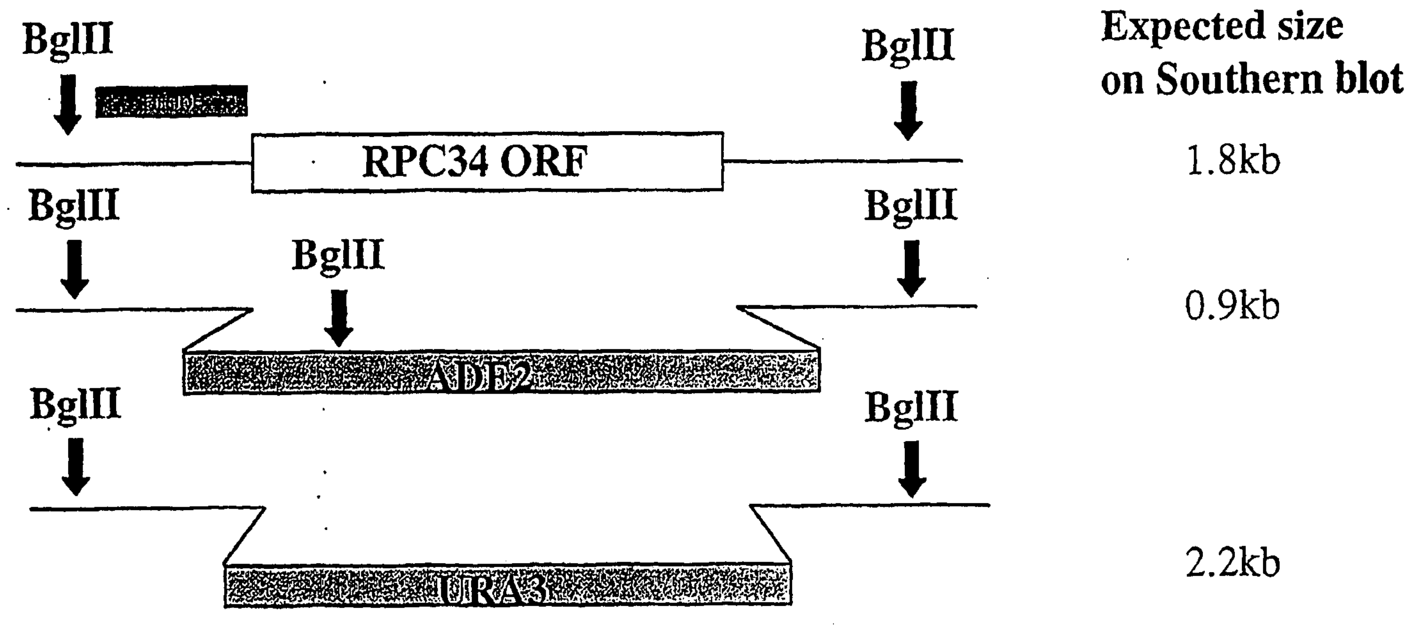
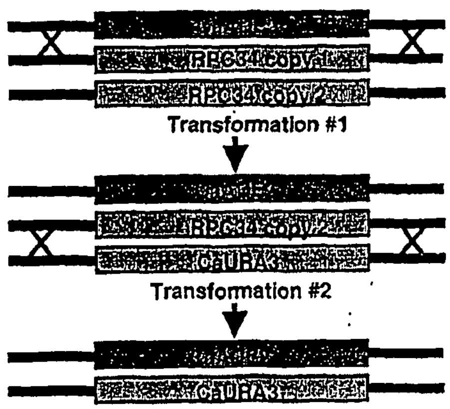


Figure 53A

C. albicans RPC34 deletion analysis

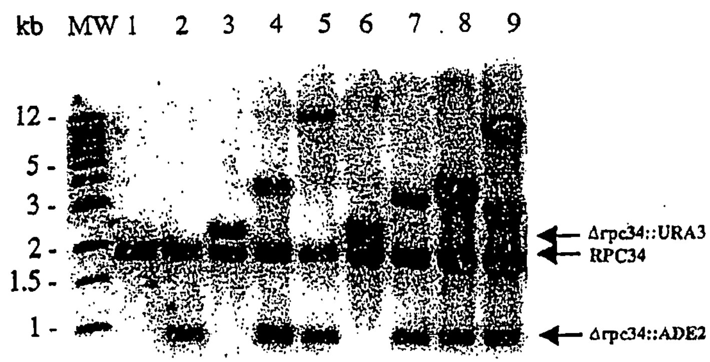


CAI8
(Ura-, Ade-)

Δrpc34::ADE2 / RPC34
(Ura-, Ade+)

Δrpc34::ADE2 / RPC34::URA3???
(Ura+, Ade+)

>20 Transformants examined
by Southern blot



Lane	
1	RPC34/RPC34 (CAI8)
2	Δrpc34::ADE2 / RPC34
3	RPC34 / Δrpc34::URA3
4-9	Δrpc34::ADE2 / RPC34, Ura+

<u>Unable to delete second copy of RPC34</u>

Figure 53B

C. albicans POP3 deletion analysis

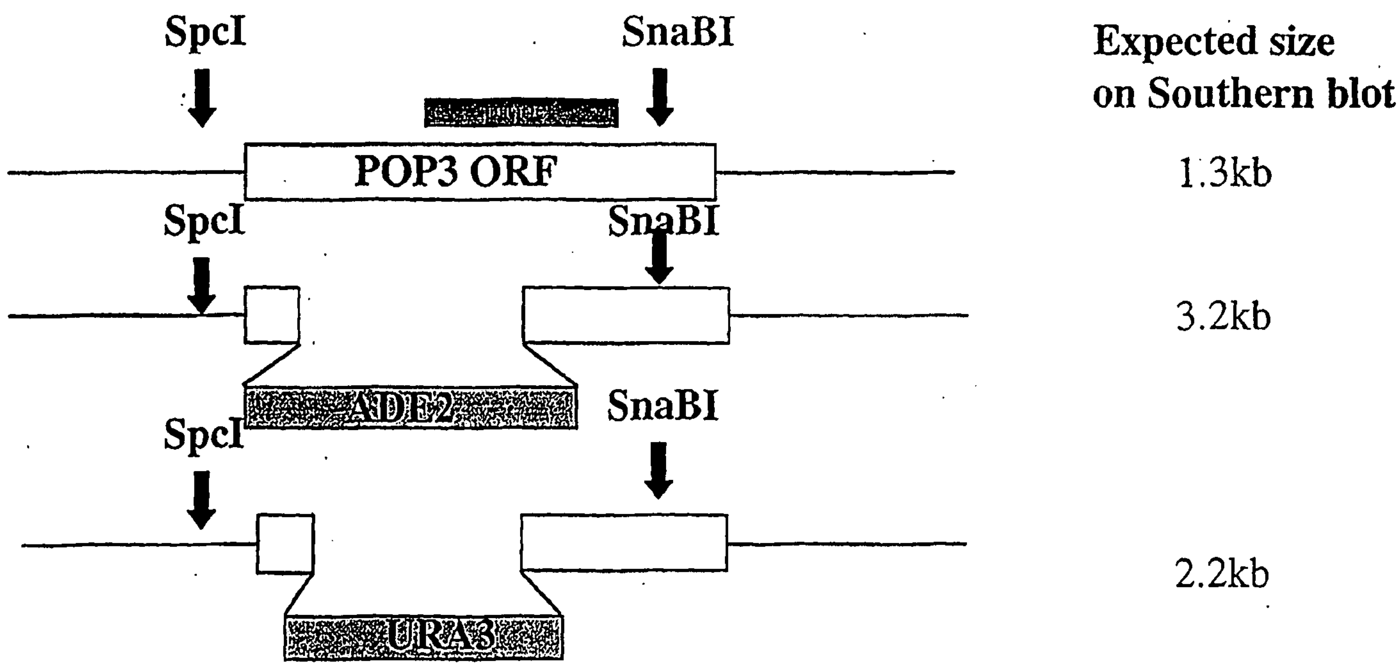
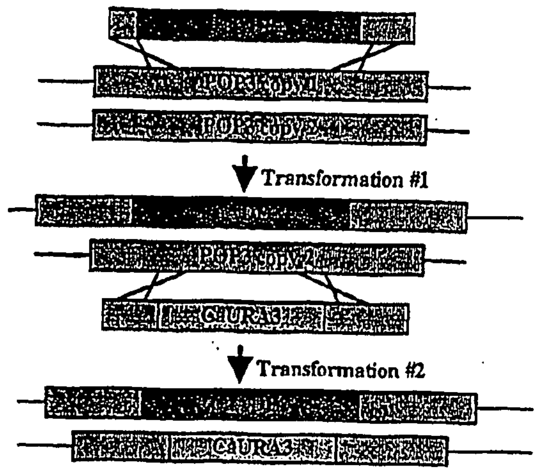


Figure 54A

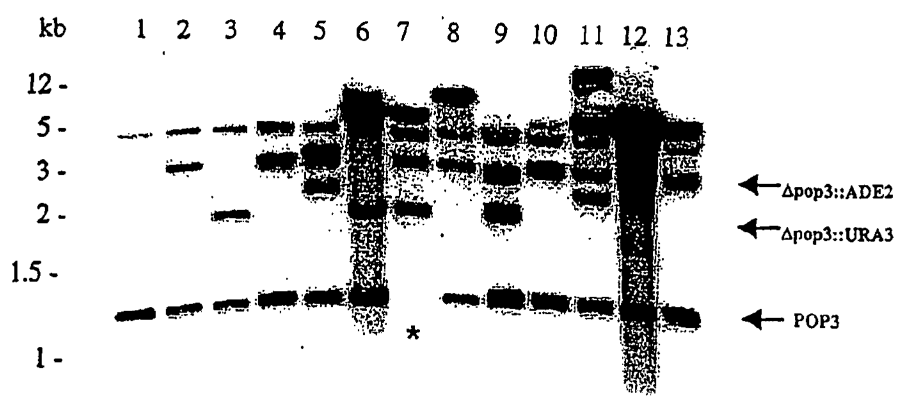
C. albicans POP3 deletion analysis



CAI8 (Ura-, Ade-)

Δpop3::ADE2 / POP3 (Ura-, Ade+)

Δpop3::ADE2 / Δ pop3::URA3??? (Ura+, Ade+)
>20 Transformants examined by Southern blot



Lane	
1	POP3/POP3 (CAI8)
2	Δpop3::ADE2 / POP3
3	POP3 / Δpop3::URA3
4-13	Δpop3::ADE2 / POP3, Ura+

* presence of wild-type confirmed by PCR (2 examples)

Unable to delete second copy of POP3

Figure 54B

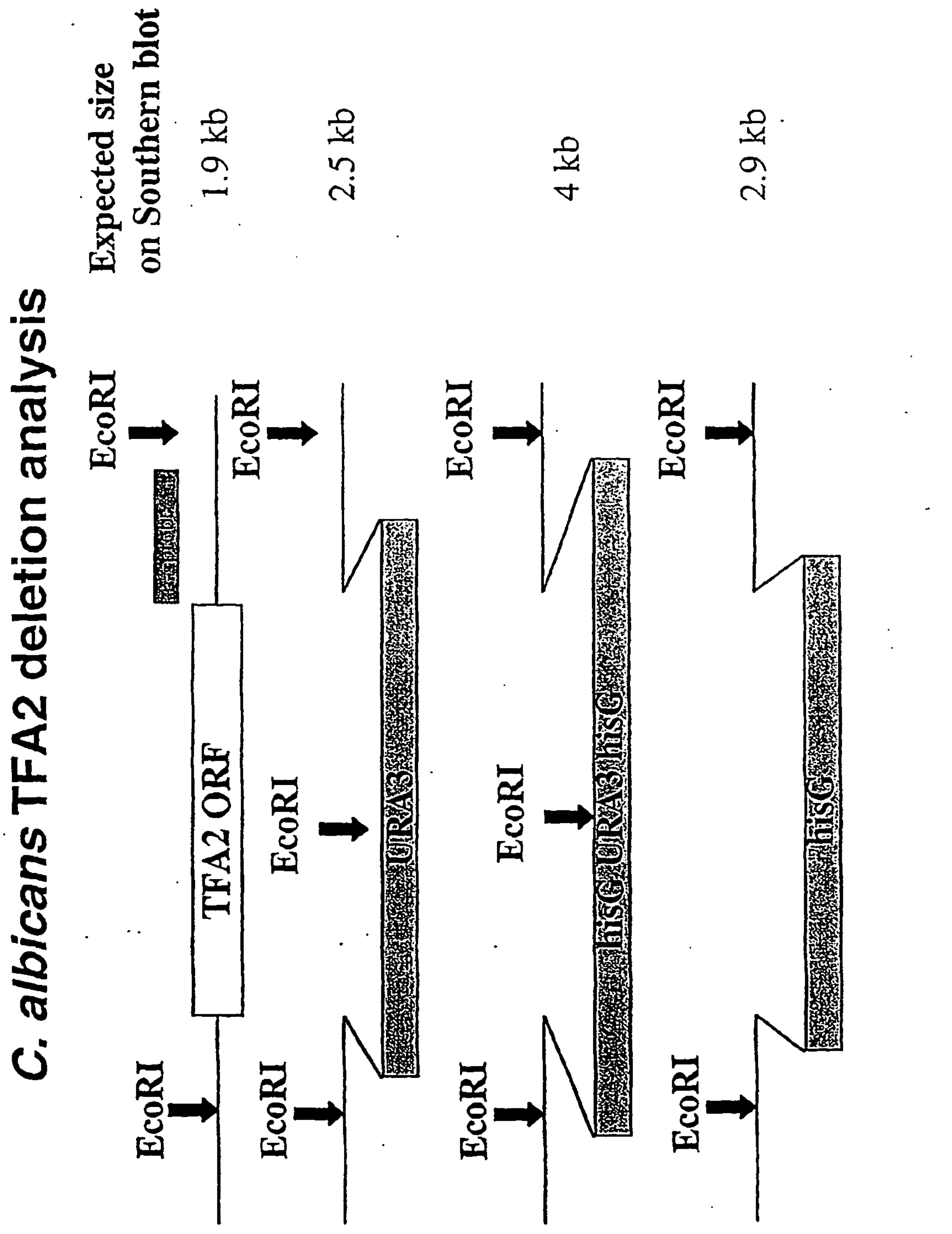
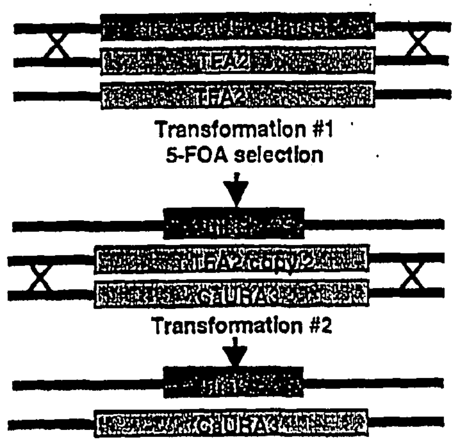

C. albicans TFA2 deletion analysis
Expected size on Southern blot
EcoRI
TFA2 ORF
1.9 kb
URA3
2.5 kb
hisG URA3 hisG
4 kb
hisG
2.9 kb

Figure 55A

C. albicans TFA2 deletion analysis

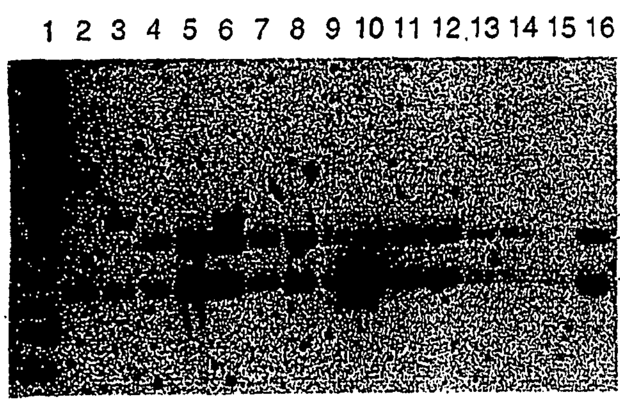


CAI4
(Ura-)

Δtfa2::hisG / TFA2
(Ura-)

Δtfa2::hisG / Δtfa2::CaURA3???
(Ura+)

>50 transformants examined
by Southern blot



Δtfa2::hisG-URA3-hisG	4.0 kb
ΔTFA2::hisG	2.9 kb
Δtfa2::URA3	2.6 kb
TFA2	0.9 kb

Lane	
15	TFA2/TFA2 (CAI4)
16	TFA2/tfa2::URA3
2	TFA2/tfa2::hisG-URA3-hisG
3	TFA2/tfa2::hisG
4 - 14	TFA2/tfa2::hisG, Ura+
	=>TFA2/tfa2::URA3

Unable to delete second copy of *CaTFA2*

Figure 55B

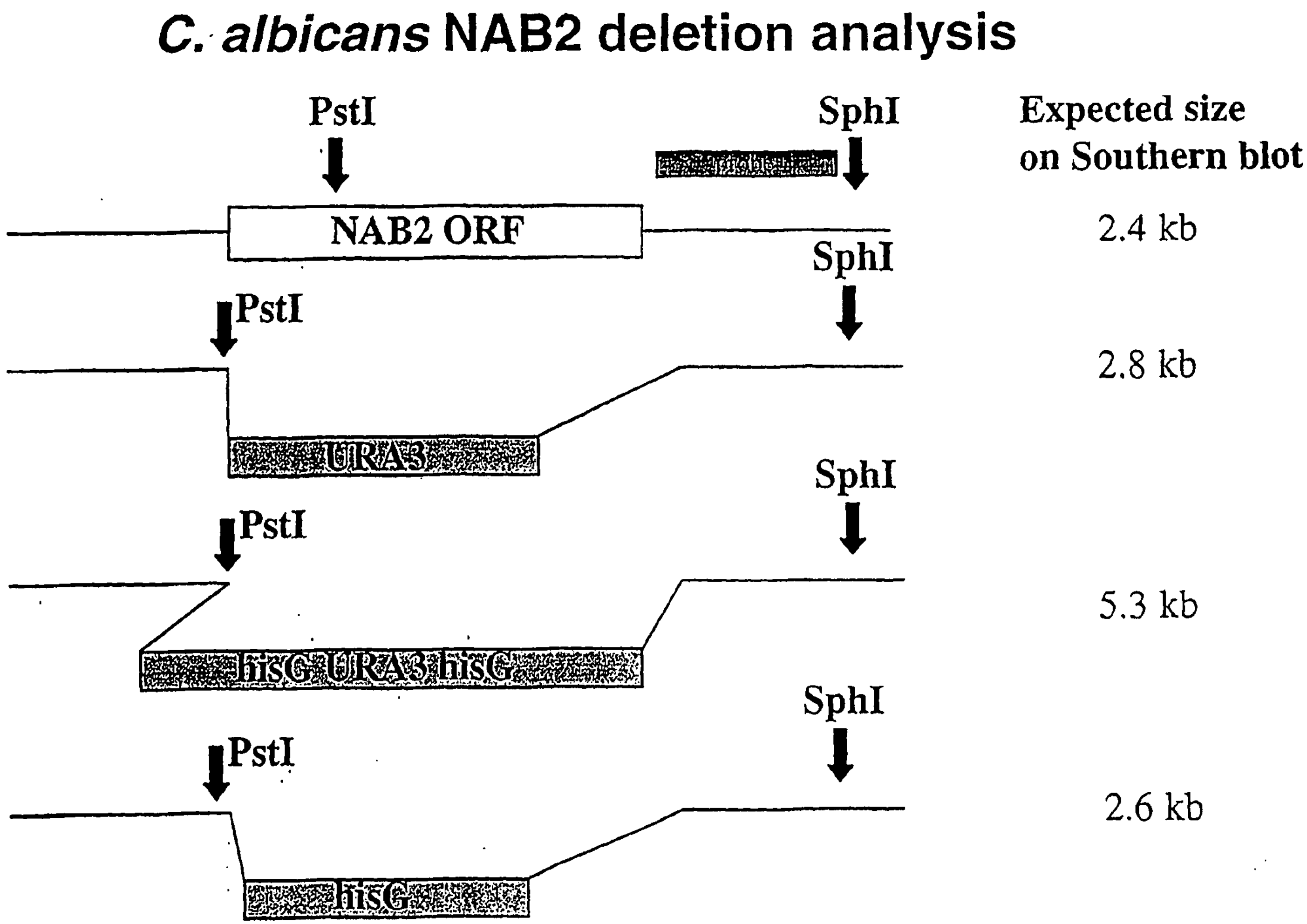
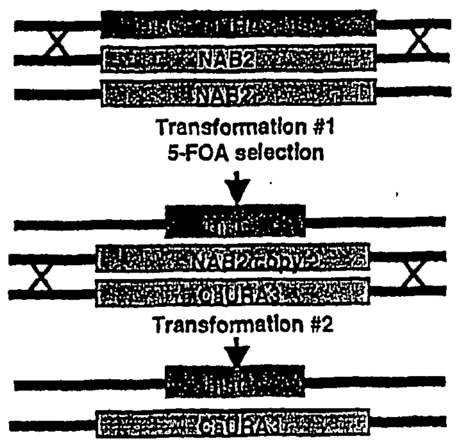

C. albicans NAB2 deletion analysis
PstI
SphI
Expected size on Southern blot
NAB2 ORF
2.4 kb
SphI
PstI
URA3
2.8 kb
SphI
PstI
hisG URA3 hisG
5.3 kb
SphI
PstI
hisG
2.6 kb

Figure 56A

C. albicans NAB2 deletion analysis

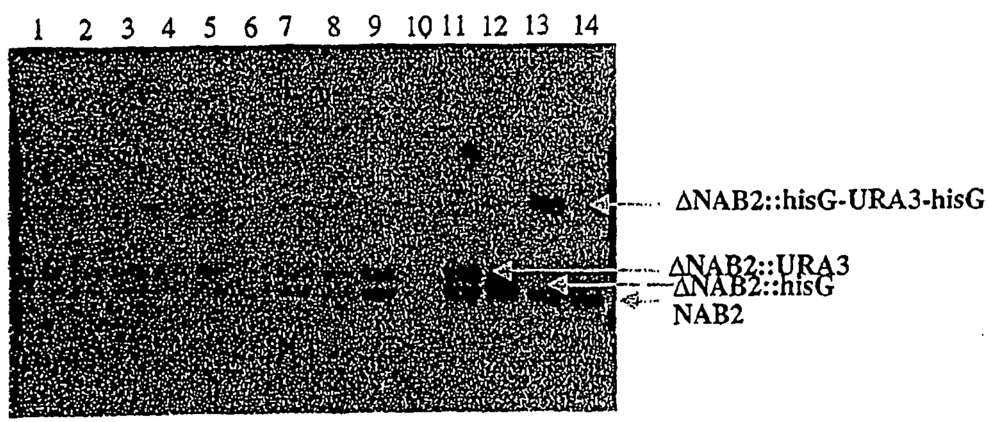


CAI4
(Ura-)

Δnab2::hisG / NAB2
(Ura-)

Δnab2::hisG / ΔNAB2::CaURA3???
(Ura+)

>20 Transformants examined by Southern blot



Lane	
14	NAB2/NAB2 (CAI4)
13	NAB2/nab2::hisG-URA3-hisG
12	NAB2/nab2::hisG
11	NAB2/nab2::URA3
1-10	NAB2/nab2::hisG, Ura+ =>NAB2/nab2::URA3 (20/20 transformants)

<u>Unable to delete second copy of *CaNAB2*</u>

Figure 56B

C. albicans MPT1 deletion analysis

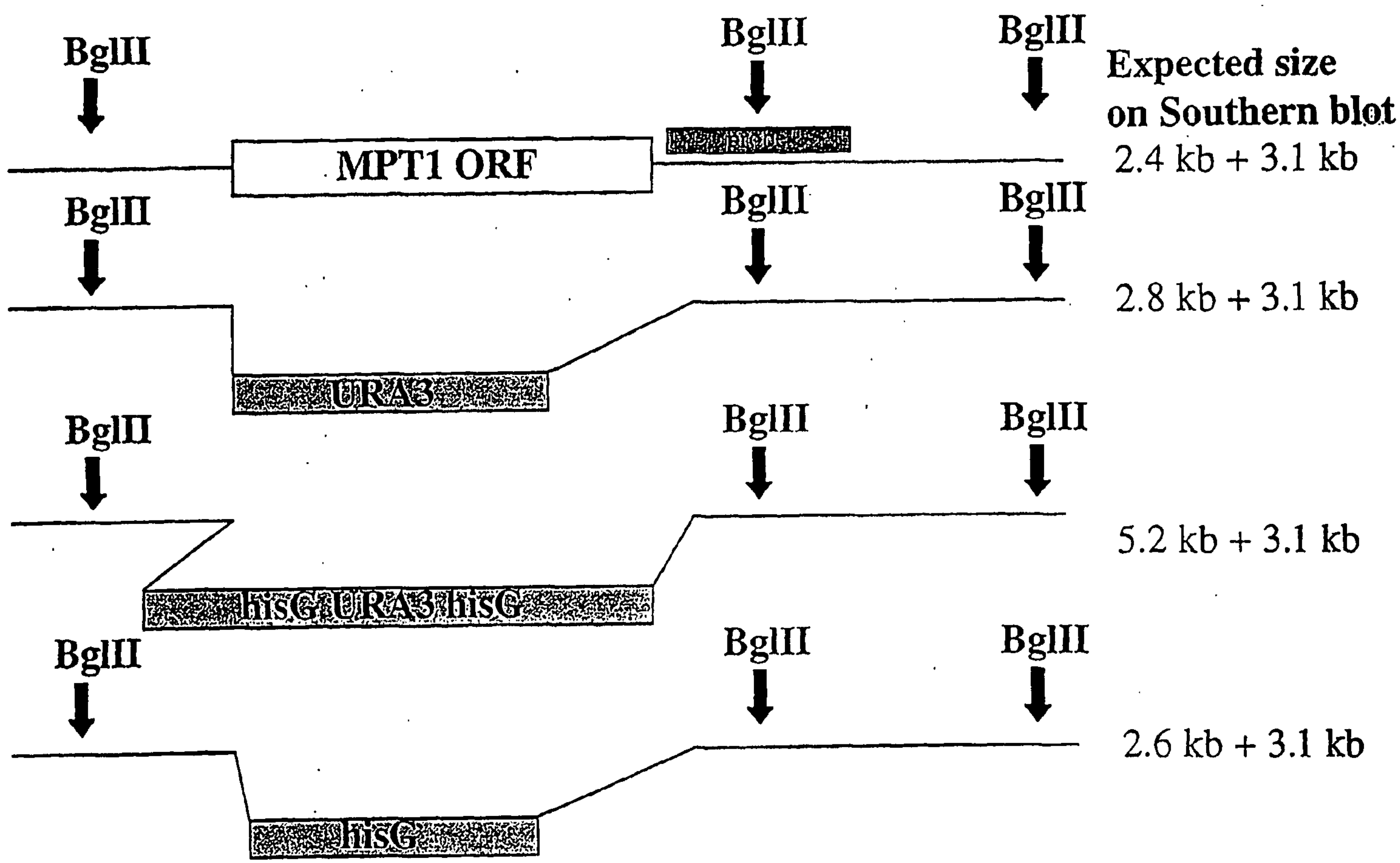
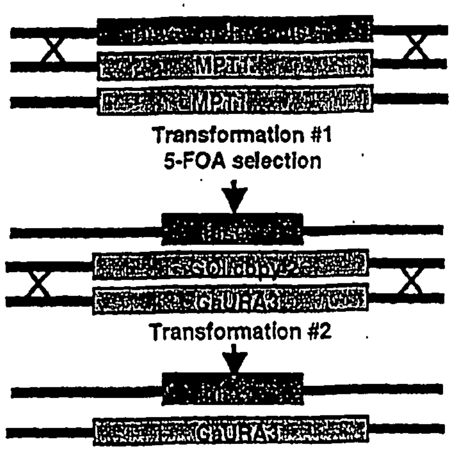


Figure 57A

C. albicans MPT1 deletion analysis

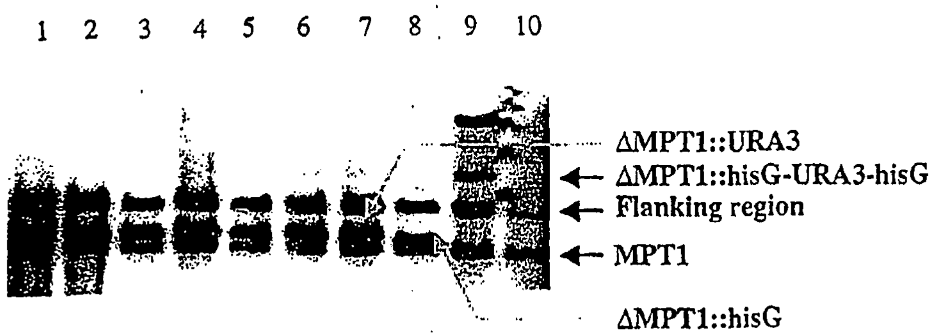


CAI4
(Ura-)

Δmpt1::hisG / MPT1
(Ura-)

Δmpt1::hisG / ΔMPT1::CaURA3???
(Ura+)

20 Transformants examined
by Southern blot



Lane	
10	MPT1/MPT1 (CAI4)
9	MPT1/mpt1::hisG-URA3-hisG
8	MPT1/mpt1::hisG
1-7	MPT1/mpt1::hisG, Ura+ =>MPT1/mpt1::URA3 (20/20 transformants)

<u>Unable to delete second copy of *CaMPT1*</u>

Figure 57B

C. albicans MTR2 deletion analysis

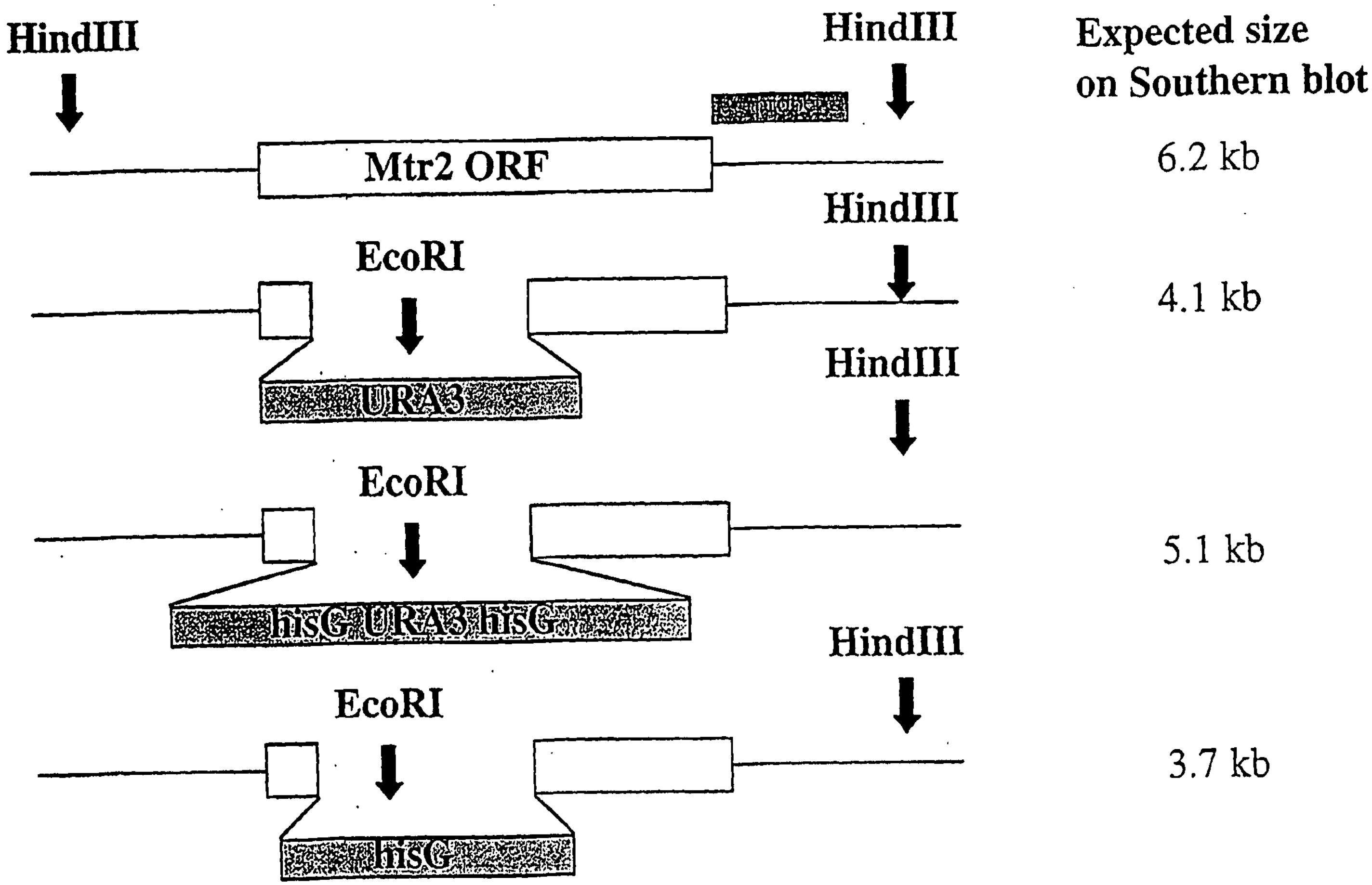
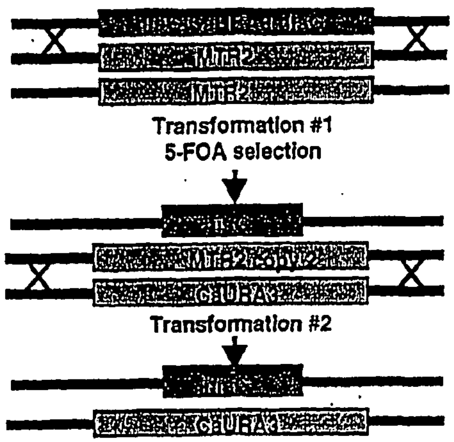


Figure 58A

C. albicans MTR2 deletion analysis

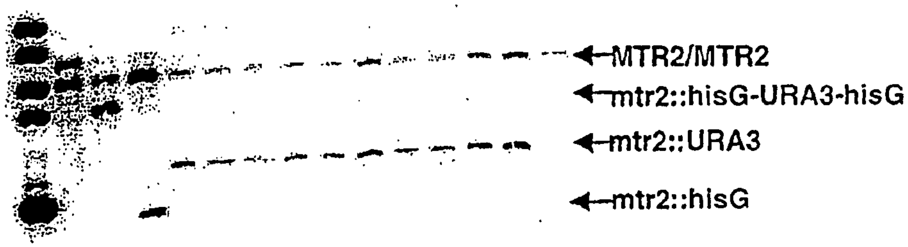


CAI4
(Ura-)

Δmtr2::hisG / MTR2
(Ura-)

Δmtr2::hisG / ΔMTR2::CaURA3???
(Ura+)

>20 Transformants examined
by Southern blot



Lane	
2	MTR2/MTR2 (CAI4)
3	MTR2/mtr2::hisG-URA3-hisG
4	MTR2/mtr2::hisG
5-15	MTR2/mtr2::hisG, Ura+ =>MTR2/mtr2::URA3

<u>Unable to delete second copy of *CaMTR2*</u>

Figure 58B

C. albicans BOS1 deletion analysis

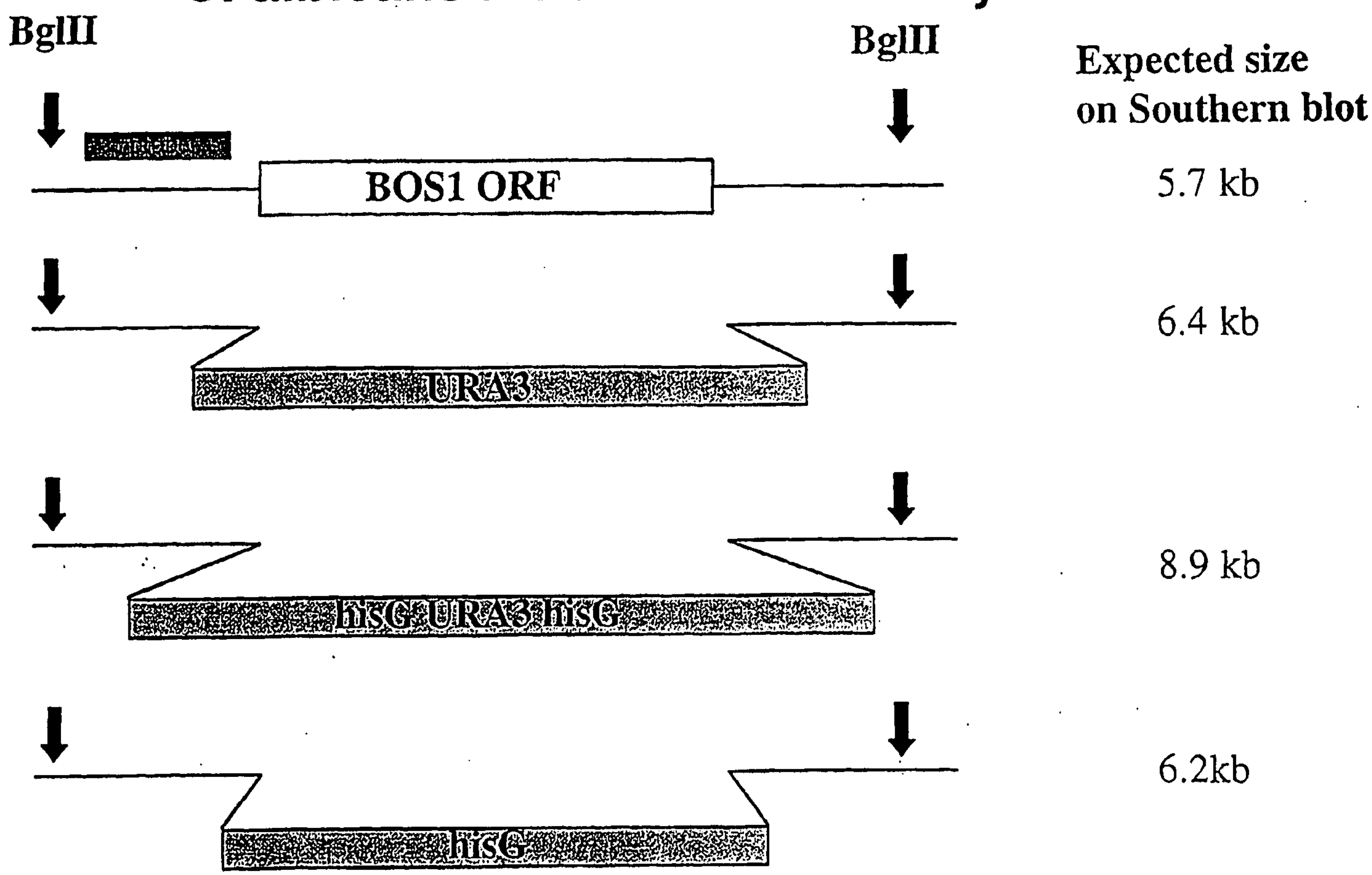
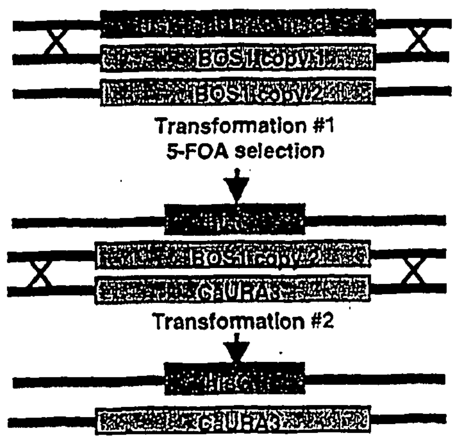


Figure 59A

C. albicans BOS1 deletion analysis

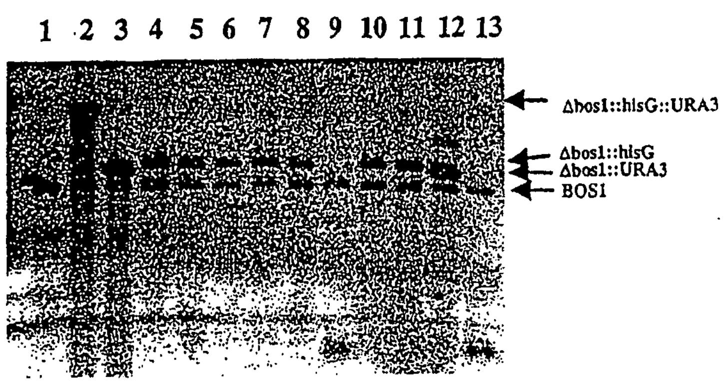


CAI4
(Ura-)

Δbos1::hisG / BOS1
(Ura-)

Δbos1::hisG / Δbos1::URA3???
(Ura+)

>20 Transformants examined
by Southern blot



Lane	
1	BOS1/BOS1(CAI4)
2	Δbos1::hisG::URA3 / BOS1
3	Δbos1::hisG/BOS1
4	Δbos1::URA3 / BOS1
5-13	Δbos1::hisG/Δbos1::URA3 ?

<u>Unable to delete second copy of BOS1</u>

Figure 59B

C. albicans POL30 deletion analysis

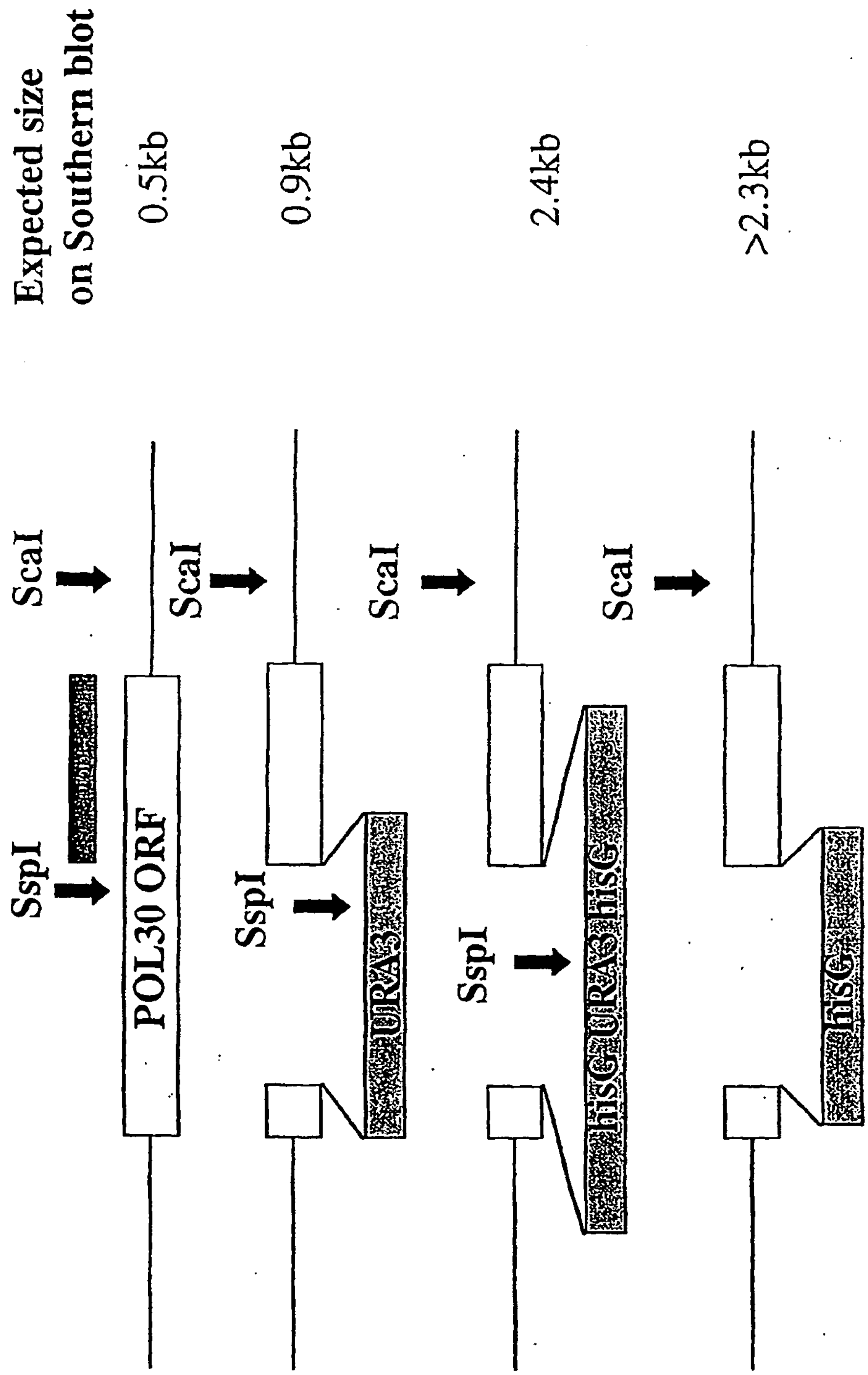
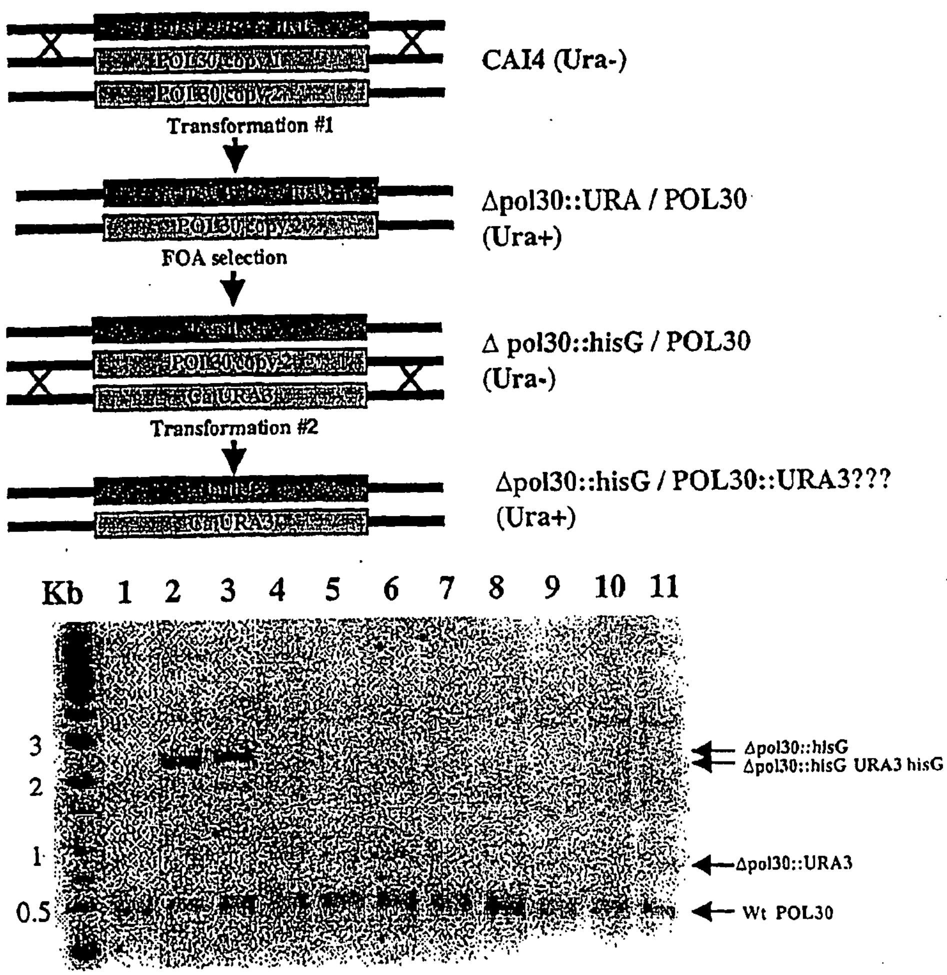


Figure 60A

C. albicans POL30 deletion analysis



20 Transformants examined by Southern blot

Lane

1 POL30/POL30 (CAI4)
2 POL30/Δpol30::hisG URA3 hisG
3 POL30/ Δpol30::hisG
4 Δpol30::URA3/POL30
5–11 Δpol30::hisG / POL30, Ura+

Unable to delete second copy of POL30

Figure 60B

C. albicans YMR131C deletion analysis

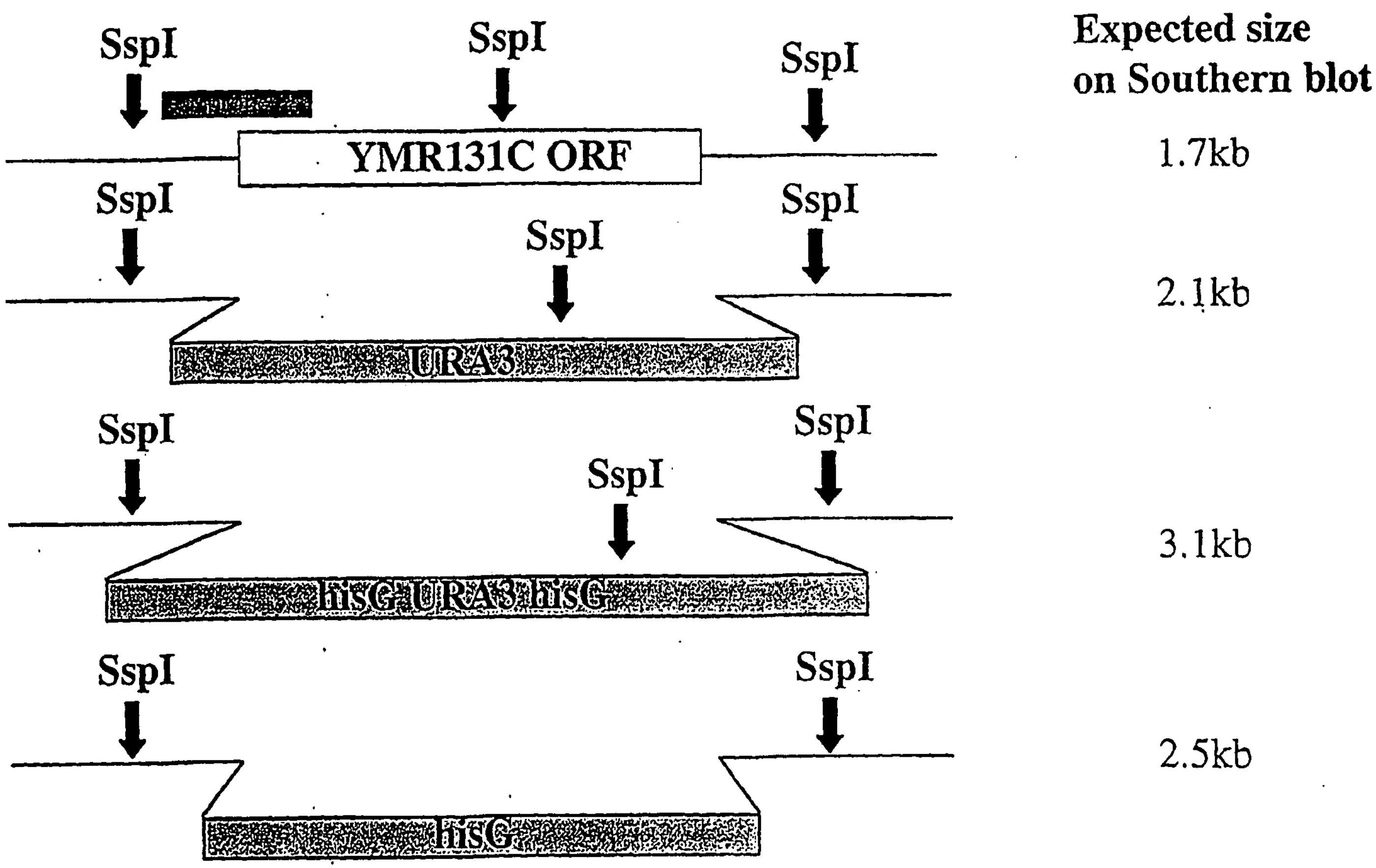
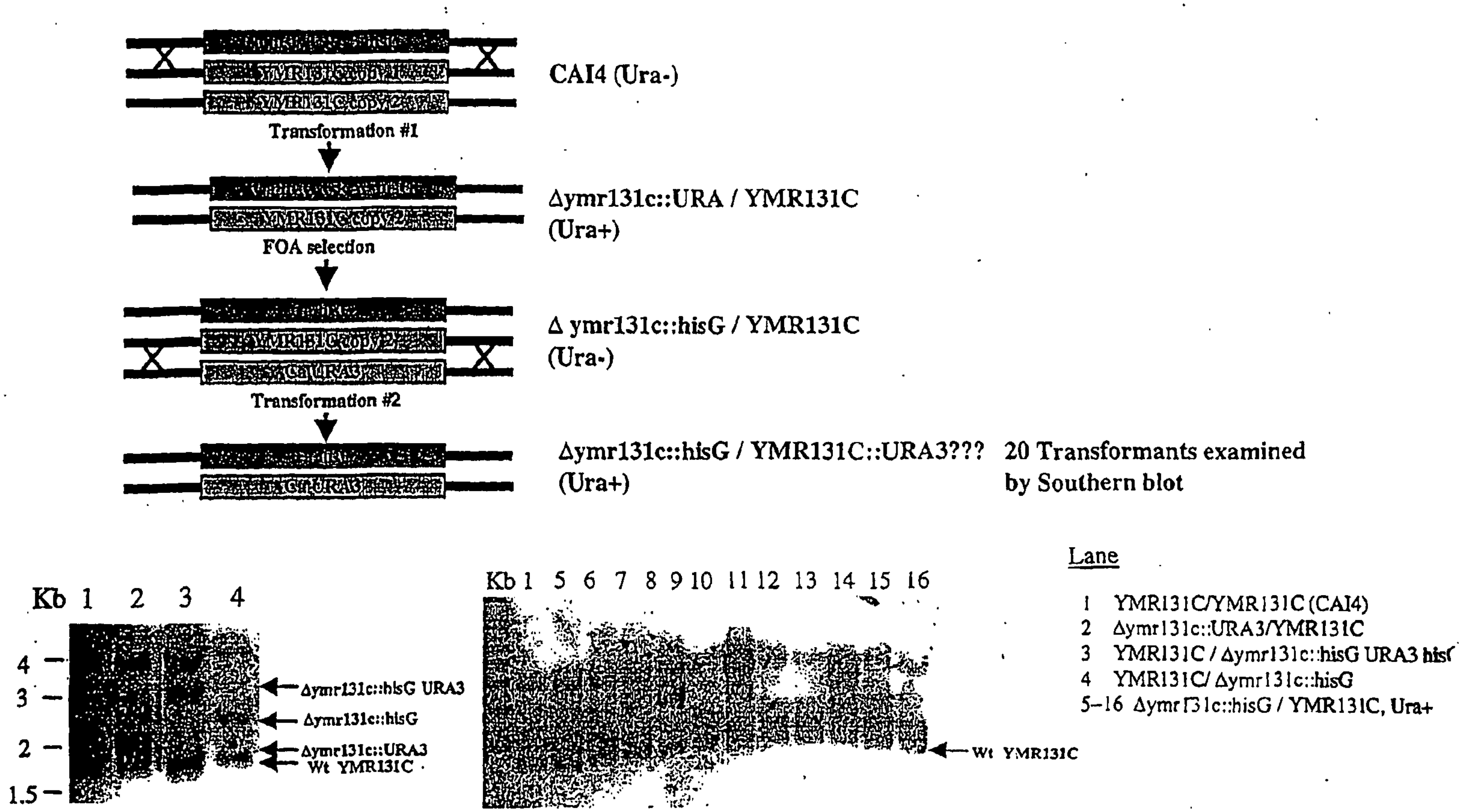


Figure 61A

C. albicans YMR131C deletion analysis



Unable to delete second copy of YMR131C

Figure 61B

C. albicans SQT1 deletion analysis

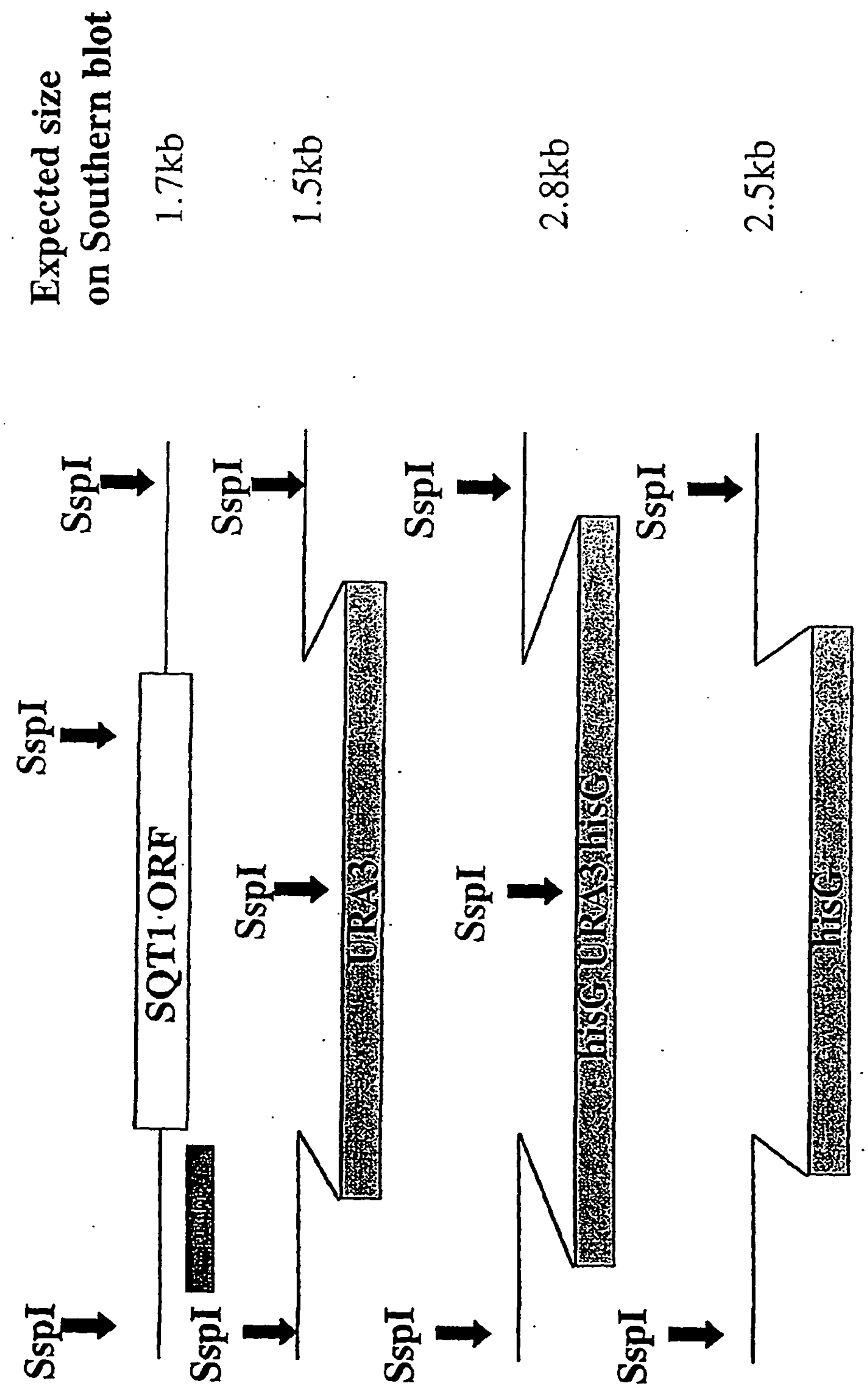
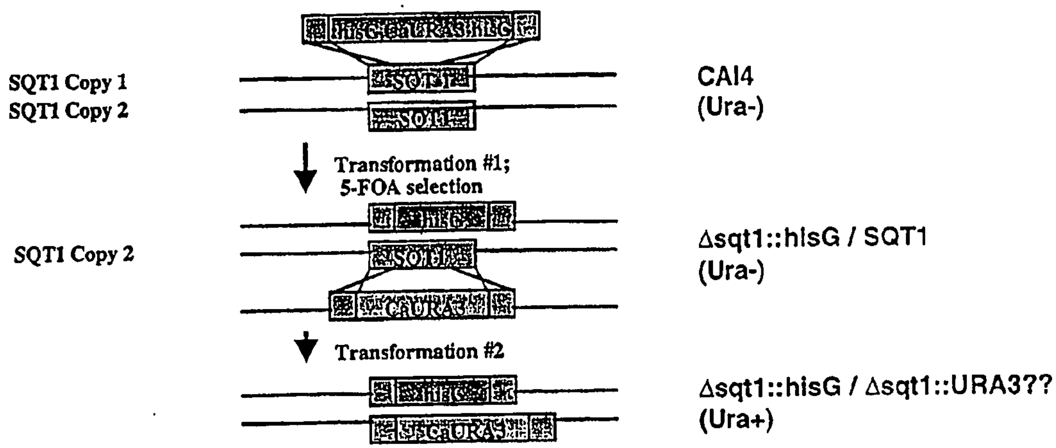
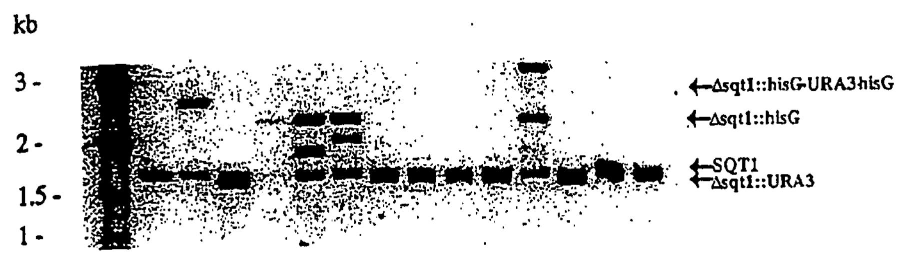


Figure 62A

C. albicans SQT1 deletion analysis



20 Transformants examined by Southern blot



Lane	
1	SQT1 / SQT1 (CAI4)
2	Δsqt1::hisG-URA3-hisG / SQT1
3	Δsqt1::URA3/ SQT1
4	Δsqt1::hisG/ SQT1
5-14	Δsqt1::hisG / Δsqt1::URA3

Unable to delete second copy of SQT1 in 20/20 transformants

Figure 62B

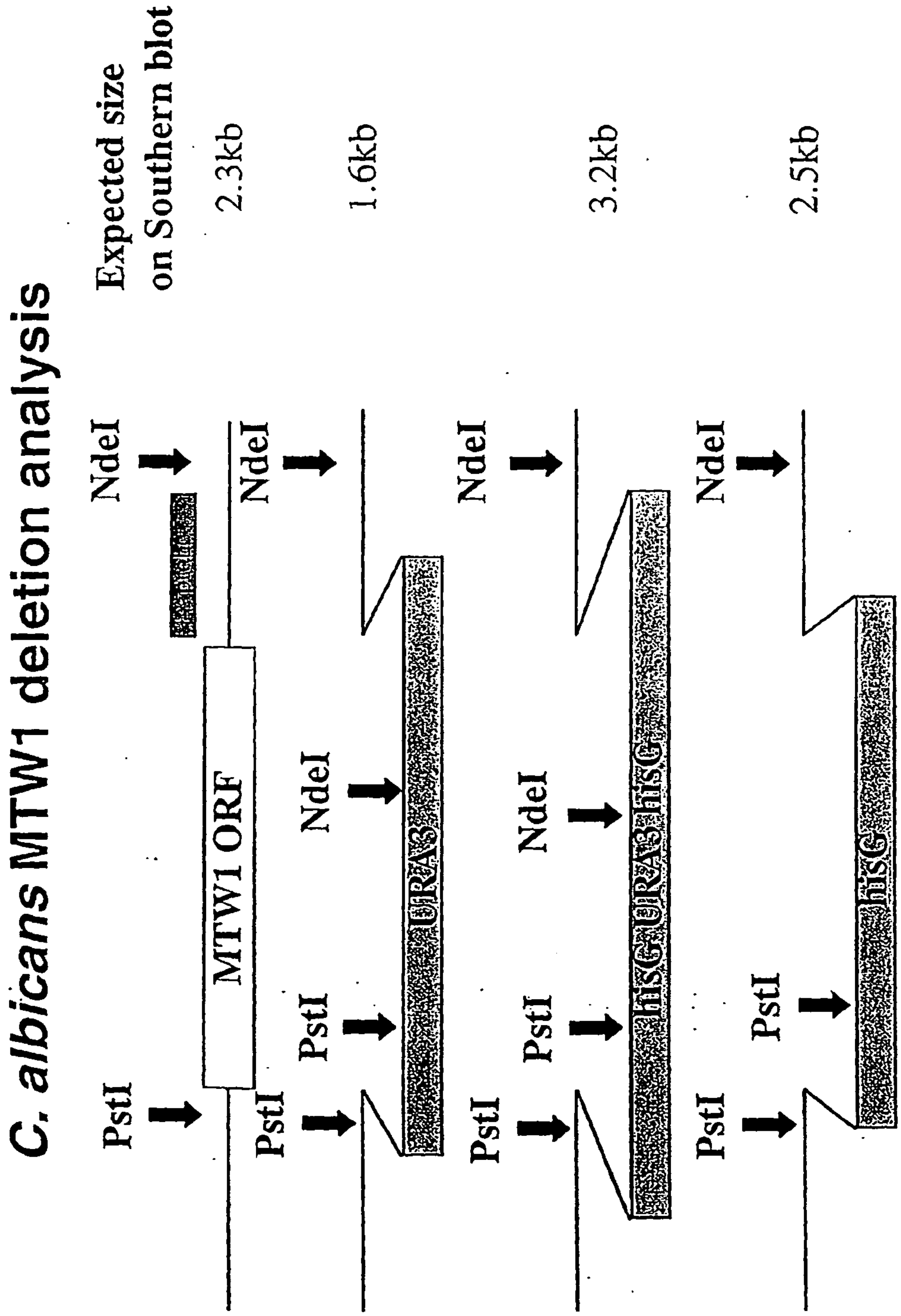
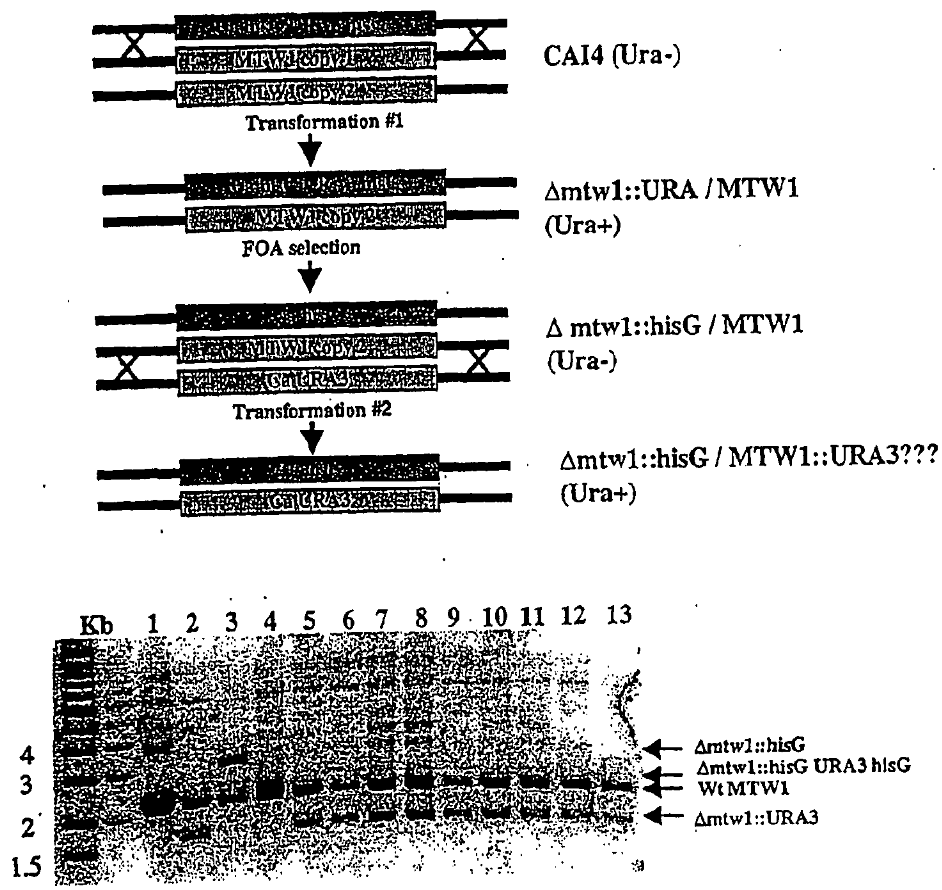

C. albicans MTW1 deletion analysis
Expected size on Southern blot
PstI
NdeI
MTW1 ORF
2.3kb
PstI
PstI
NdeI
NdeI
URA3
1.6kb
PstI
PstI
NdeI
NdeI
hisG URA3 hisG
3.2kb
PstI
PstI
NdeI
hisG
2.5kb

Figure 63A

C. albicans MTW1 deletion analysis



20 Transformants examined by Southern blot

Lane

1 MTW1/MTW1 (CAI4)
2 Δmtw1::URA3/MTW1
3 MTW1 / Δmtw1::hisG URA3 hisG
4 MTW1/ Δmtw1::hisG
5–16 Δmtw1::hisG / MTW1, Ura+

<u>Unable to delete second copy of MTW1</u>

Figure 63B

C. albicans TFB1 deletion analysis

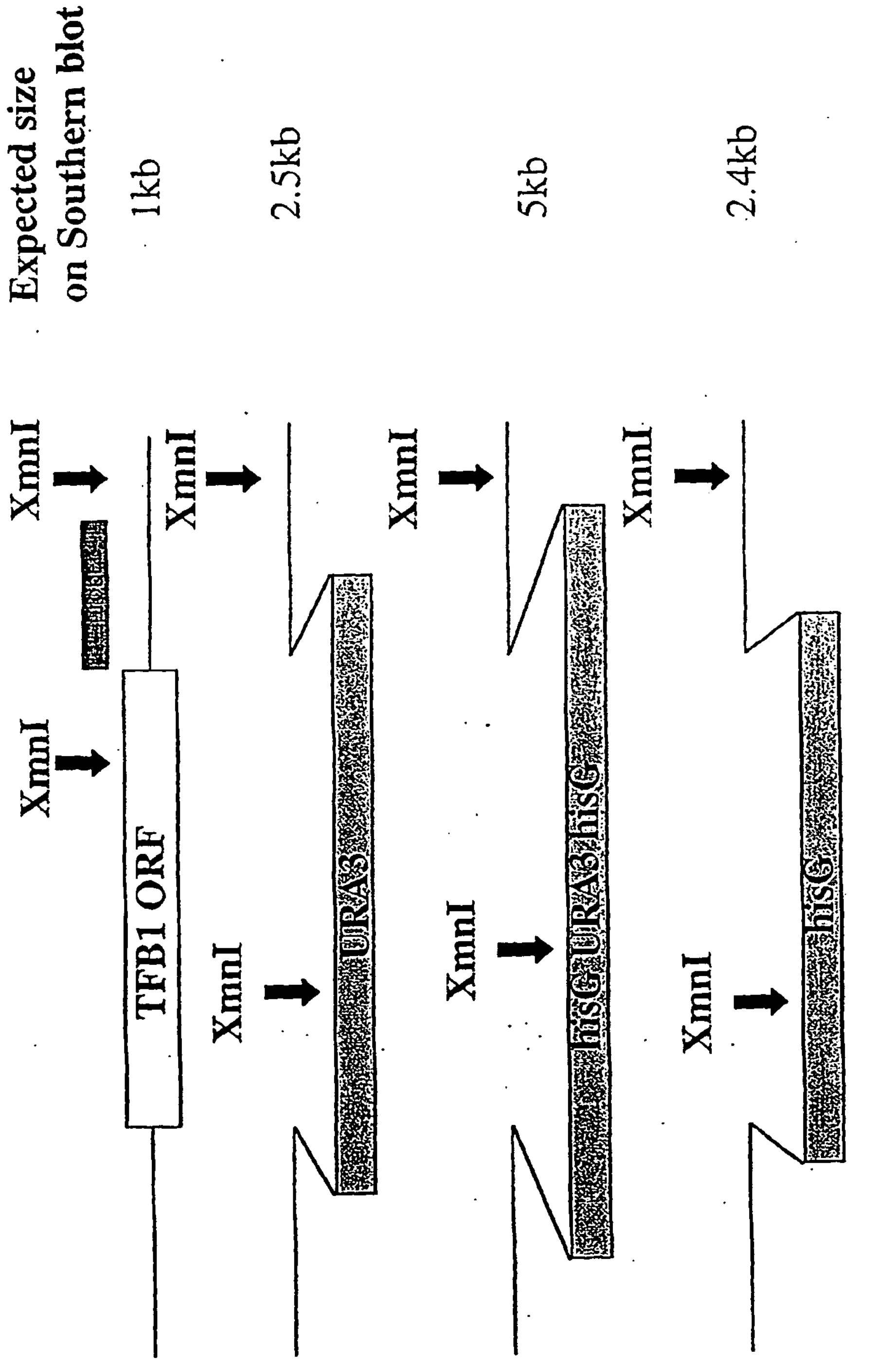
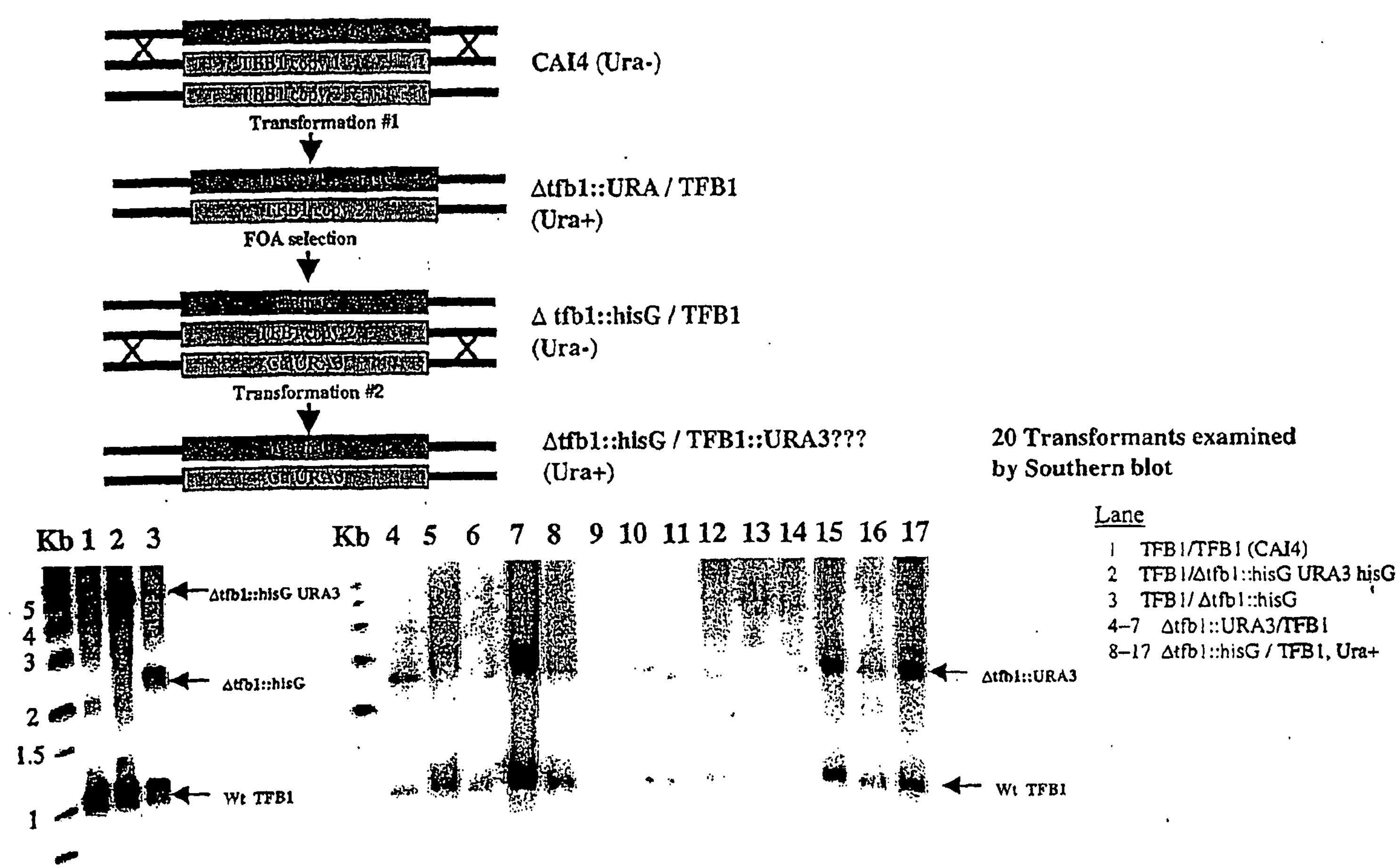


Figure 64A

C. albicans TFB1 deletion analysis



Unable to delete second copy of TFB1

Figure 64B

C. albicans SPC98 deletion analysis

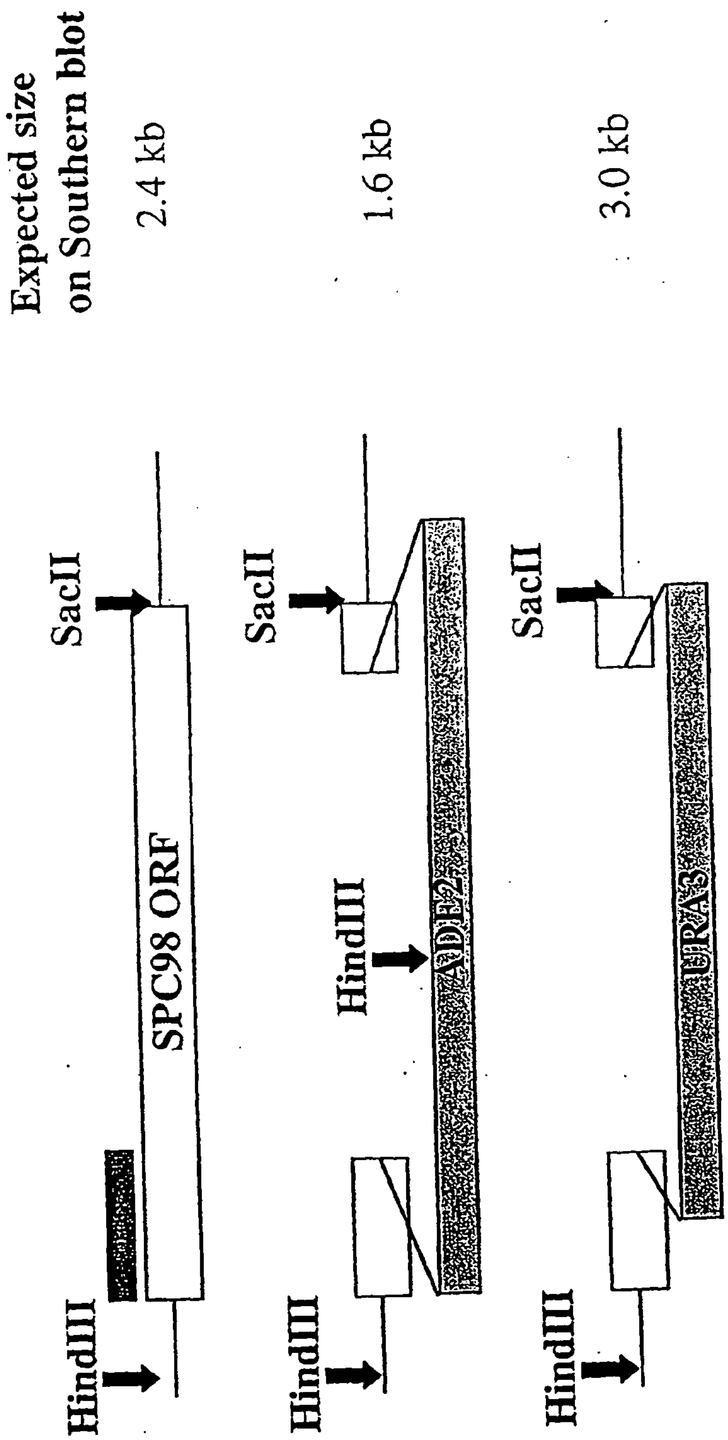
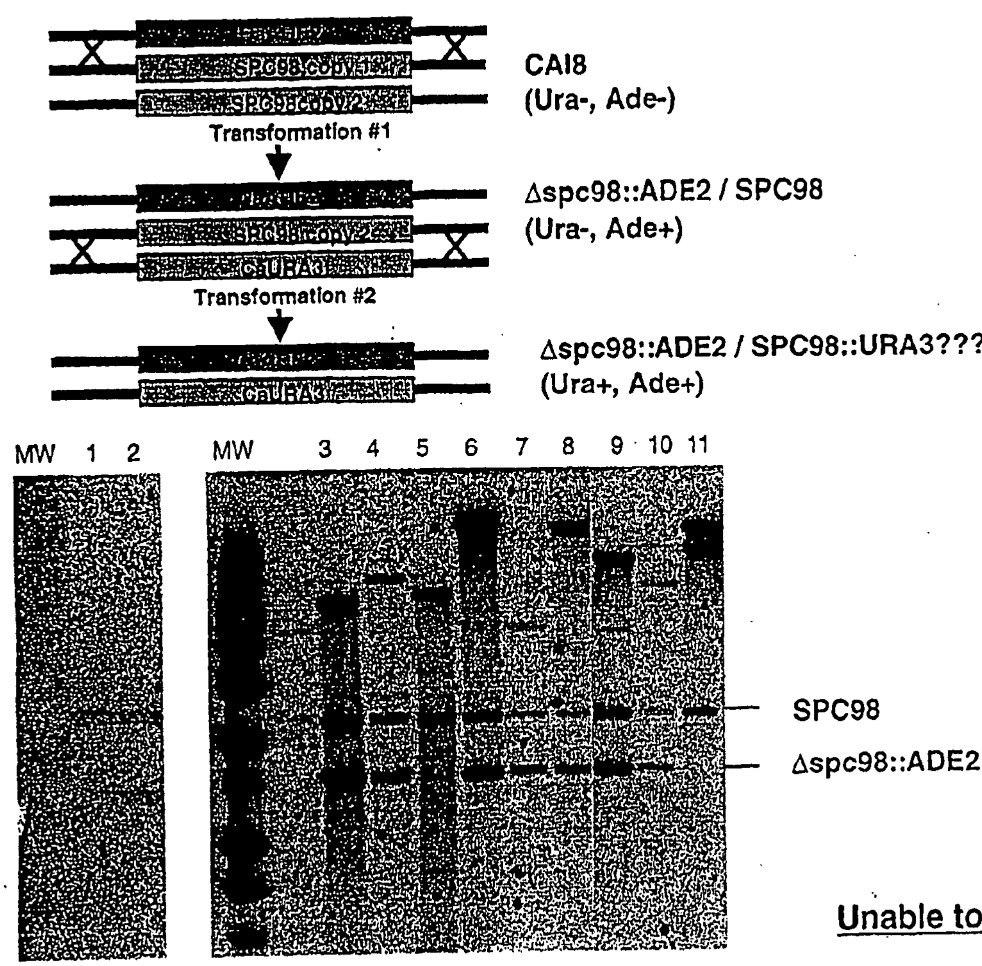


Figure 65A

C. albicans SPC98 deletion analysis



>20 Transformants examined by Southern blot

Lane	
1	SPC98/SPC98 (CAI8)
2	Δspc98::ADE2 / SPC98
3-11	Δspc98::ADE2 / SPC98, Ura+

<u>Unable to delete second copy of SPC98</u>

Figure 65B

C. albicans BFR2 deletion analysis

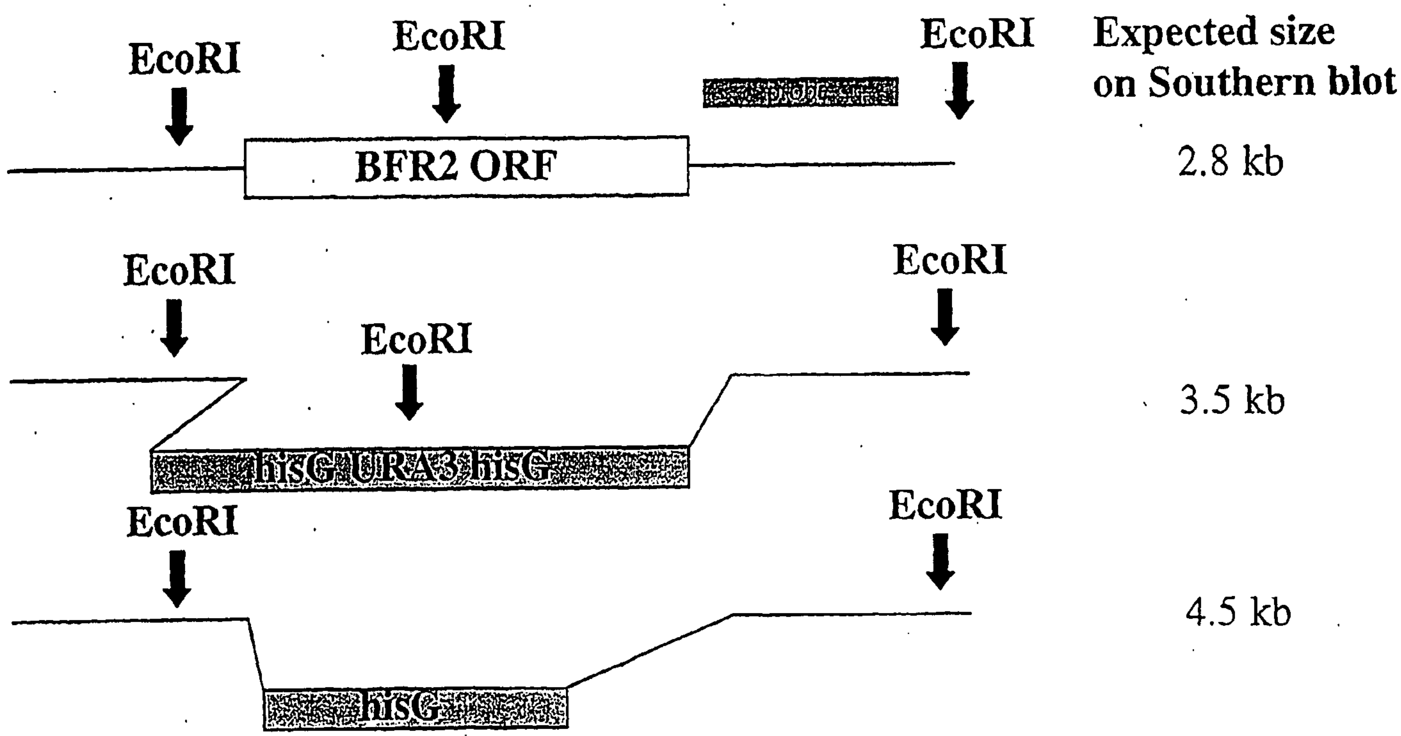
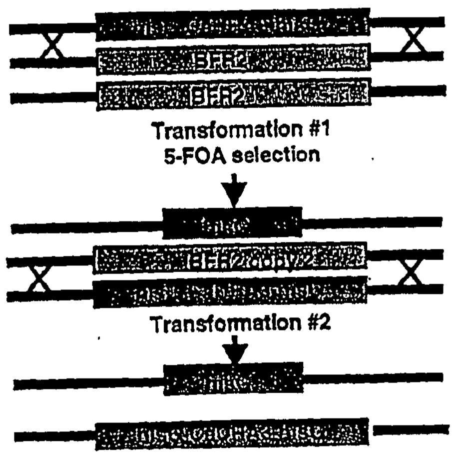


Figure 66A

C. albicans BFR2 deletion analysis

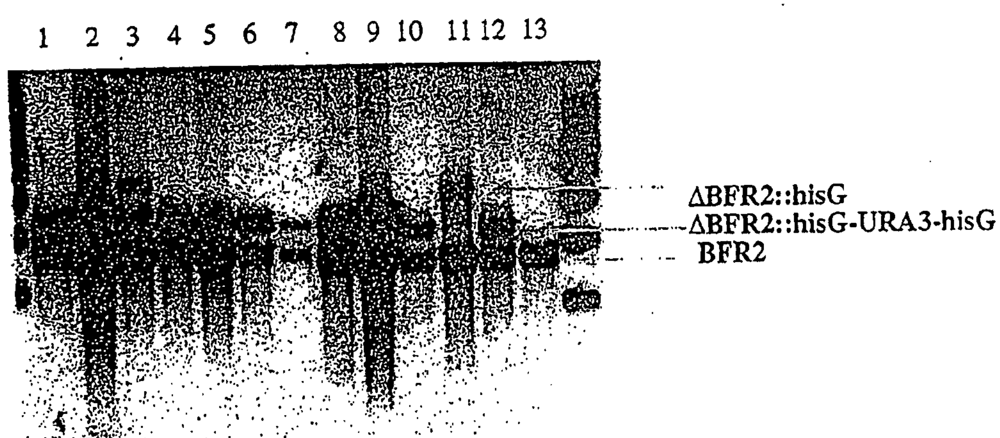


CAI4
(Ura-)

Δbfr2::hisG / BFR2
(Ura-)

Δbfr2::hisG / Δbfr2::hisG-CaURA3-hisG???
(Ura+)

>20 Transformants examined by Southern blot



Lane	
13	BFR2/BFR2 (CAI4)
12	BFR2/bfr2::hisG-URA3-hisG
11	BFR2/bfr2::hisG
1-10	BFR2/bfr2::hisG, Ura+

<u>Unable to delete second copy of *CaBFR2*</u>

Figure 66B

C. albicans RNA1 deletion analysis

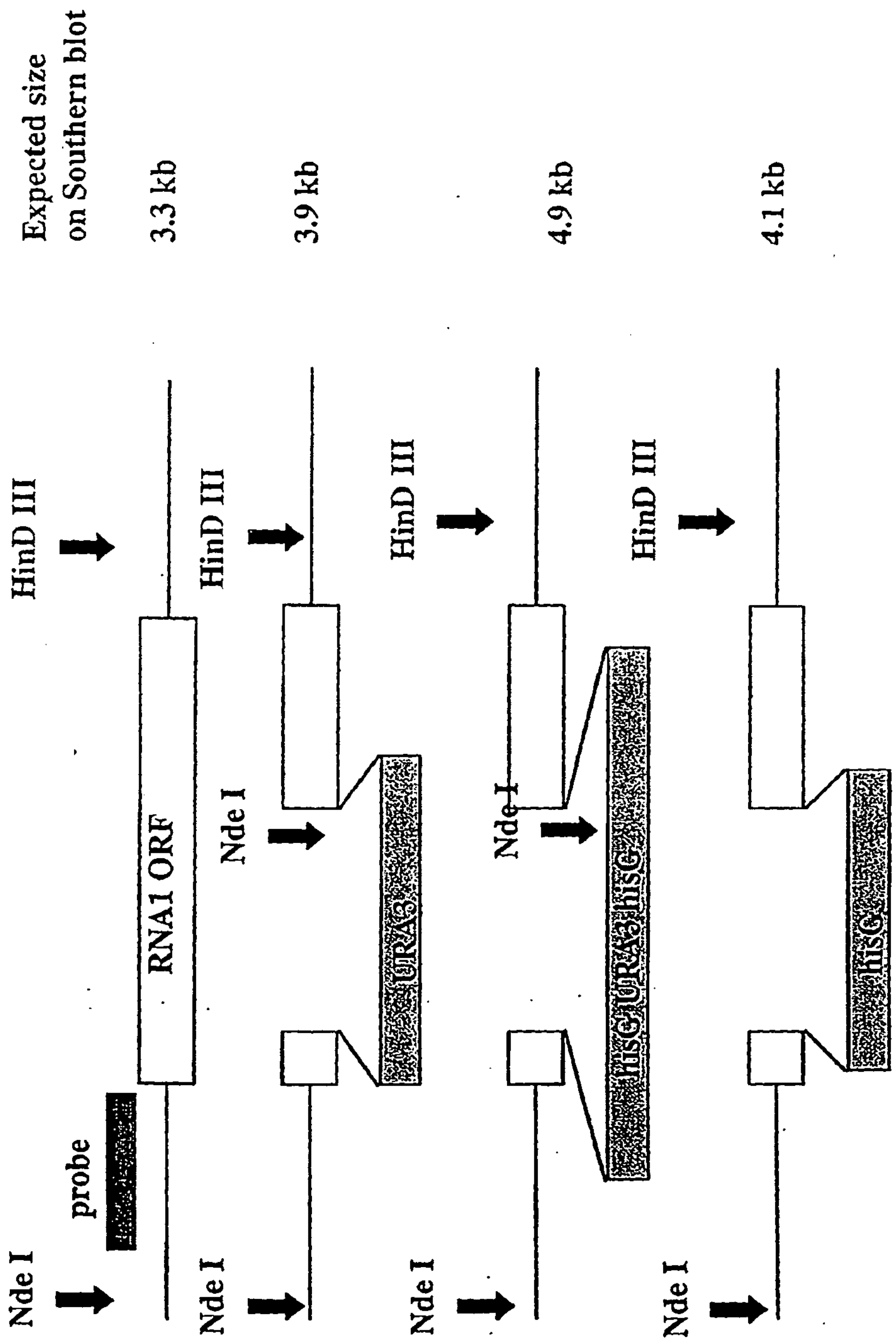
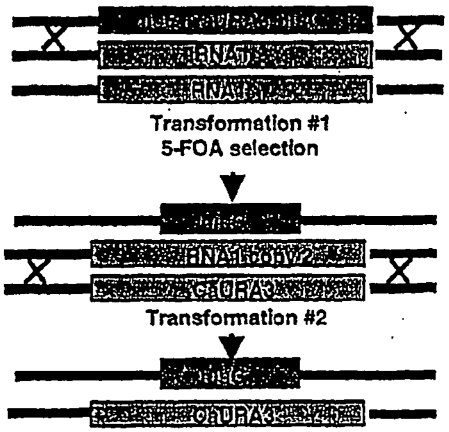
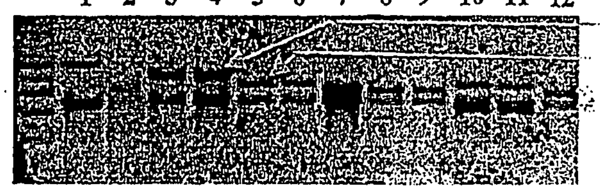


Figure 67A

C. albicans RNA1 deletion analysis



Lane	Sample
1	RNA1/RNA1 (CAI4)
2	RNA1/rna1::URA3
3-4	RNA1/rna1::hisG-URA3-hisG
5-6	RNA1/rna1::hisG
7-12	RNA1/rna1::hisG, Ura+ => RNA1/rna1 ::URA3



Unable to delete second copy of *CaRNA1*

Figure 67B

C. albicans GCD7 deletion analysis

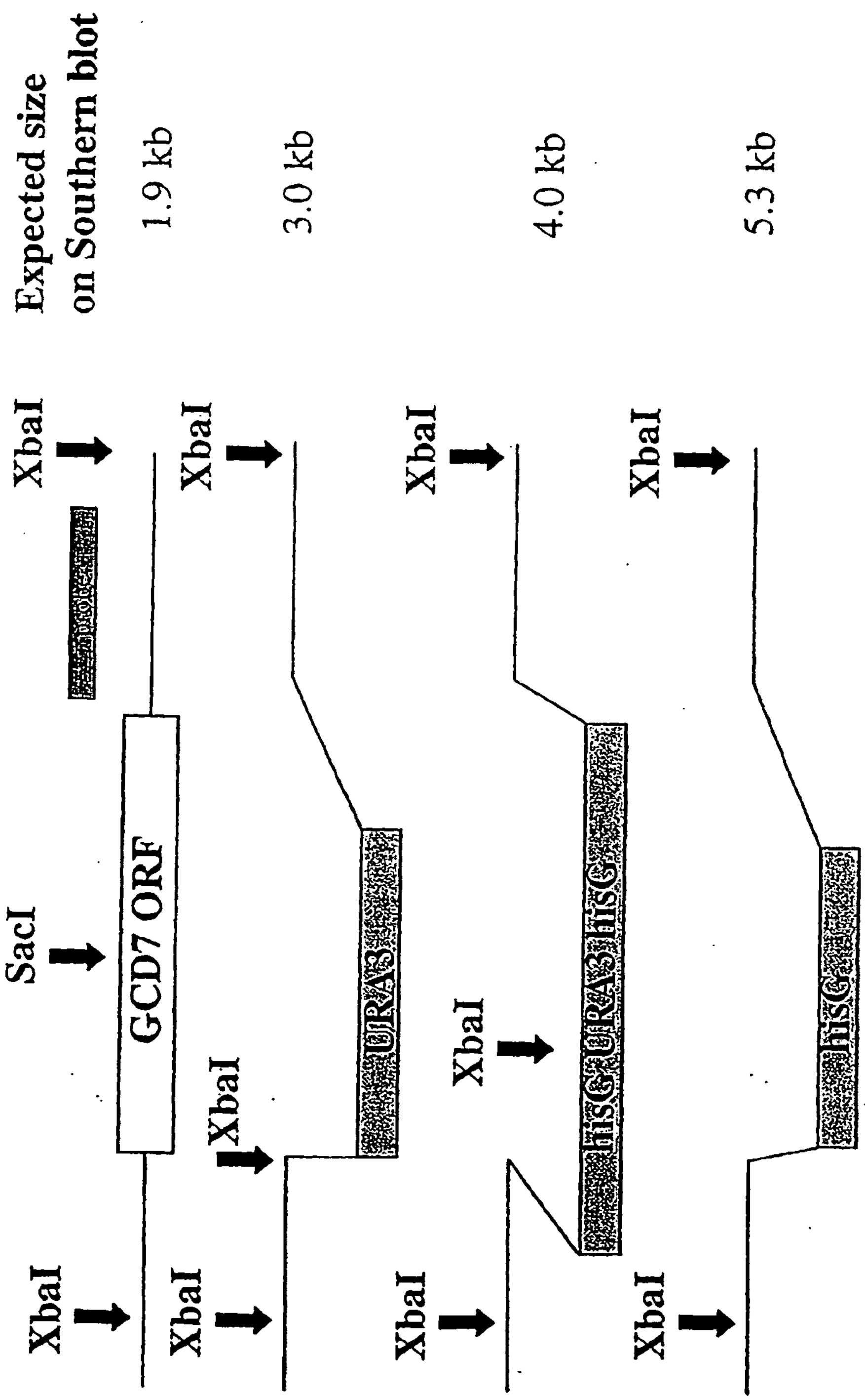
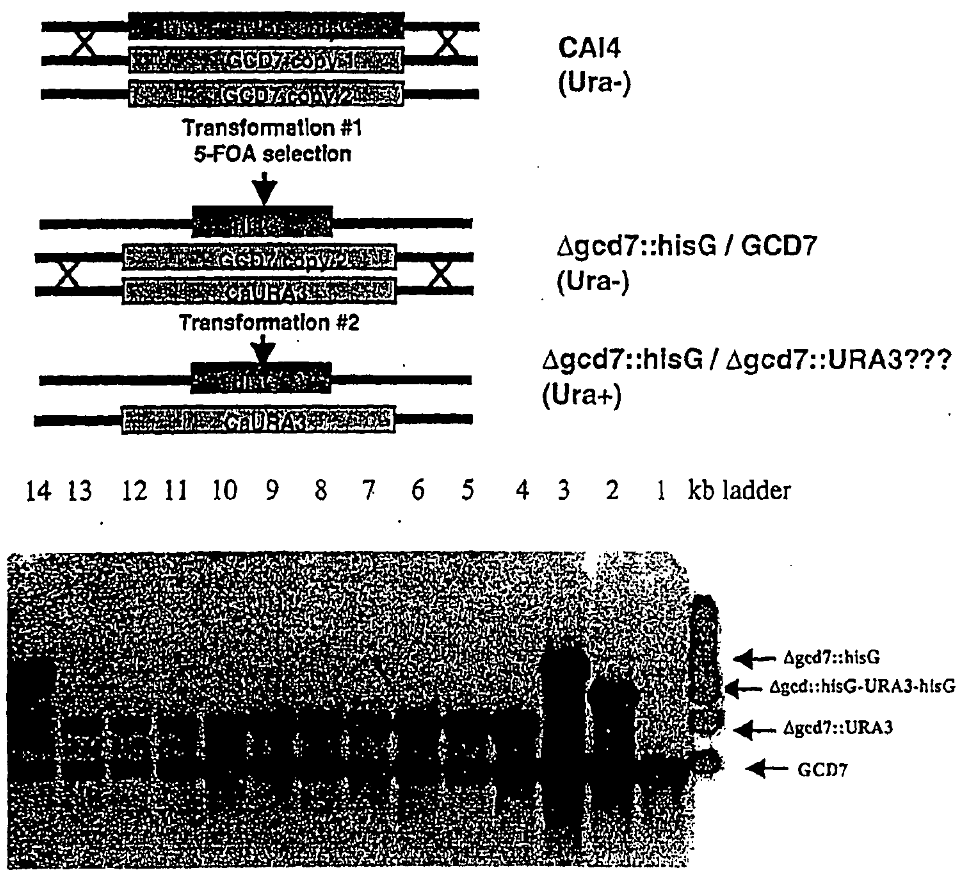


Figure 68A

C. albicans GCD7 deletion analysis



20 Transformants examined by Southern blot

Lane

1 GCD7/GCD7 (CAI4)

2 Δgcd7::hisG-URA3-hisG / GCD7

3 Δgcd7::hisG/GCD7

4 Δgcd7::URA3/GCD7

5-14 Δgcd7::hisG / GCD7, Ura+

<u>Unable to delete second copy of GCD7</u>

Figure 68B

C. albicans SKI6 deletion analysis

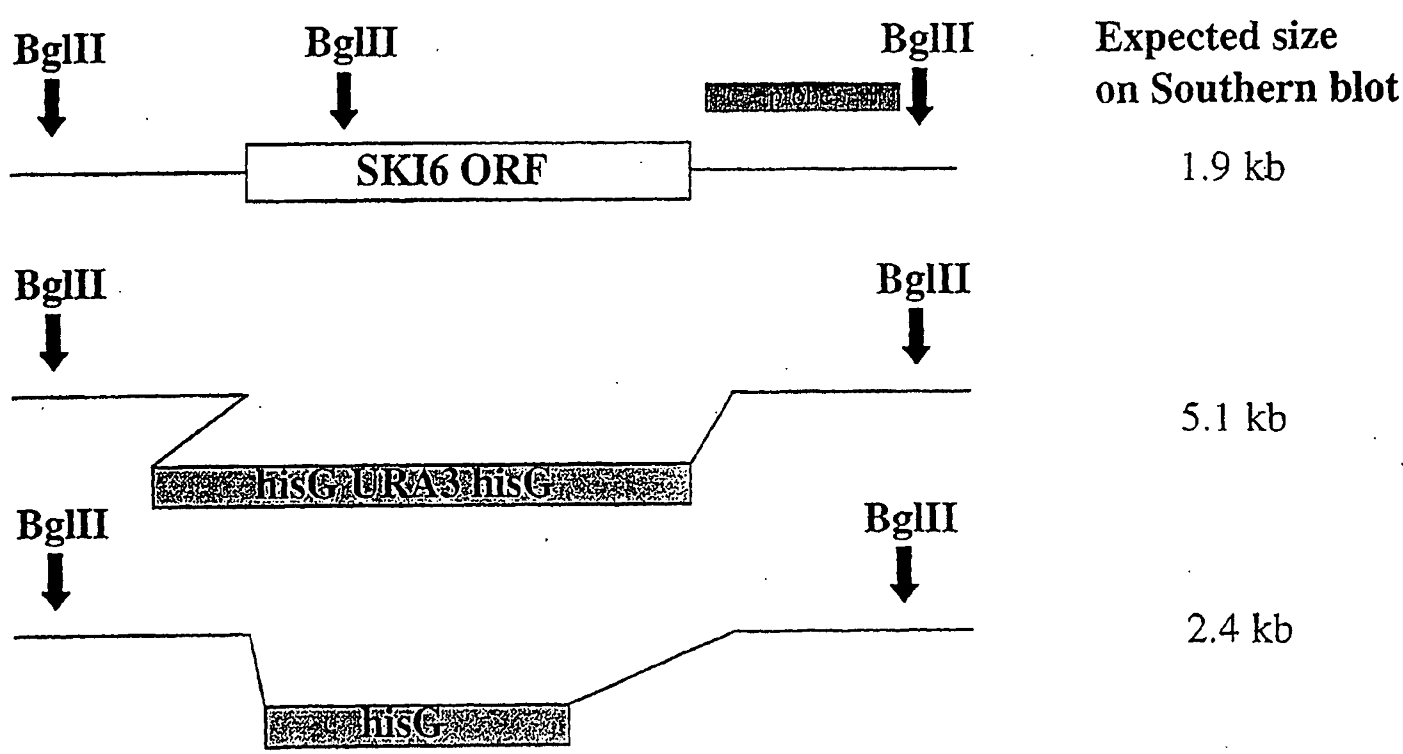
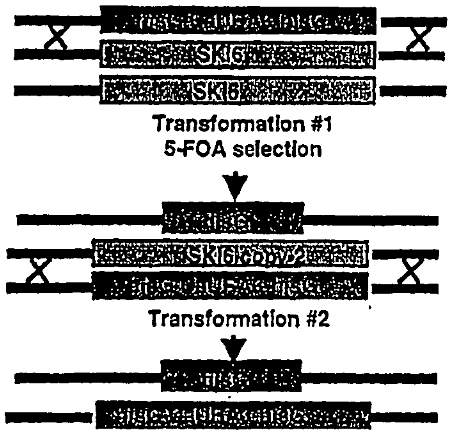


Figure 69A

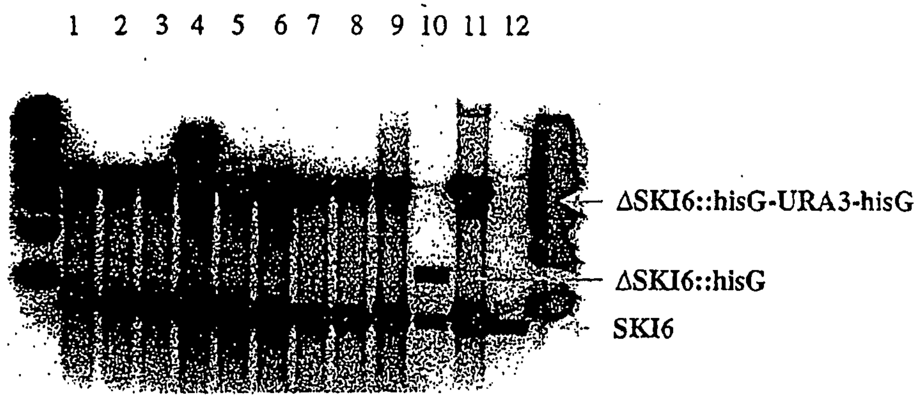
C. albicans SKI6 deletion analysis



CAI4
(Ura-)

Δski6::hisG / SKI6
(Ura-)

Δski6::hisG / ΔSKI6::hisG-CaURA3-hisG??? 20 Transformants examined by Southern blot
(Ura+)



Lane	
12	SKI6/SKI6 (CAI4)
11	SKI6/ski6::hisG-URA3-hisG
10	SKI6/ski6::hisG
1-9	SKI6/ski6::hisG, Ura+ =>SKI6/ski6::hisG-URA3-hisG (20/20 transformants)

<u>Unable to delete second copy of *CaSKI6*</u>

Figure 69B

C. albicans NIP1 deletion analysis

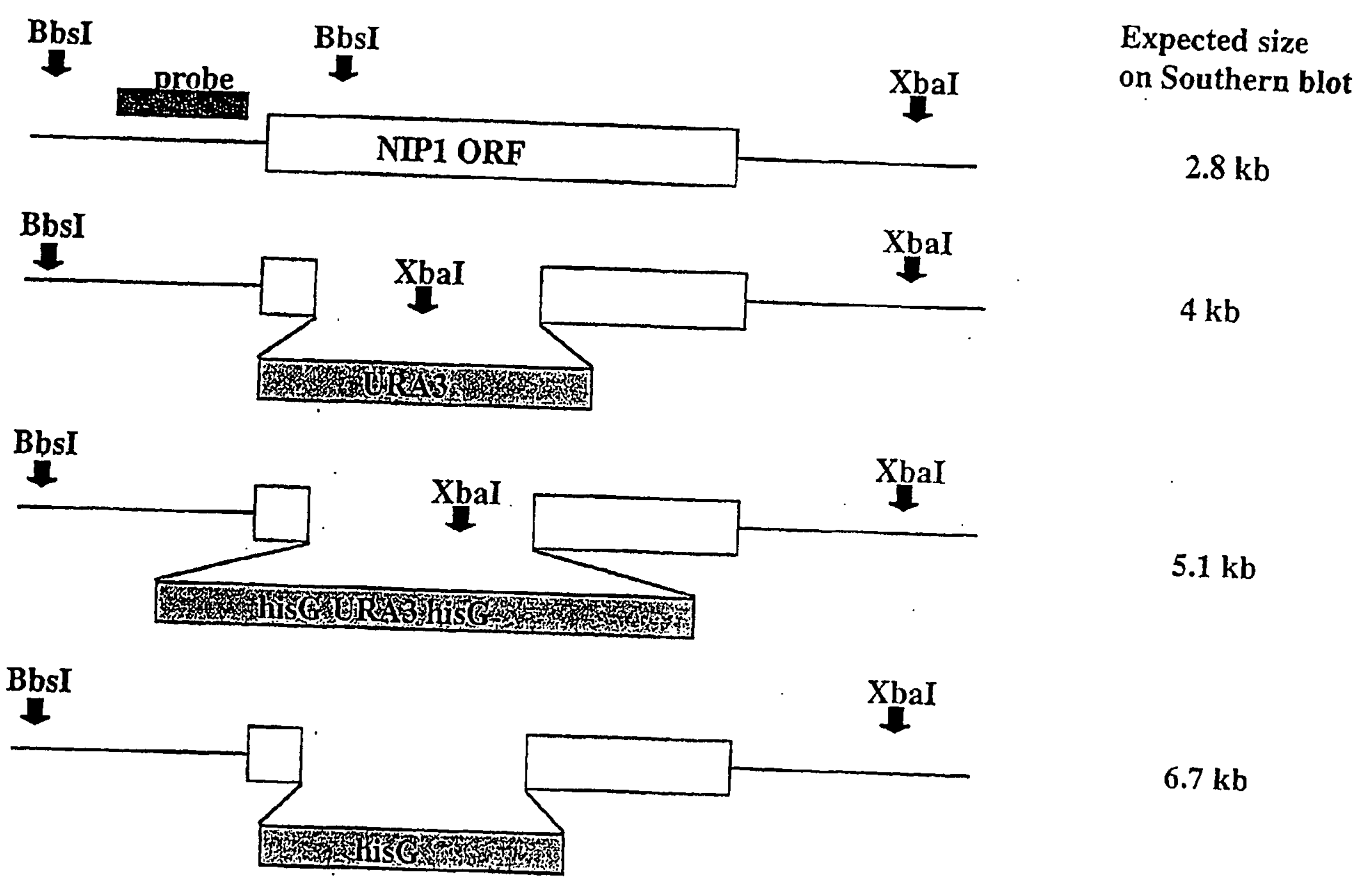
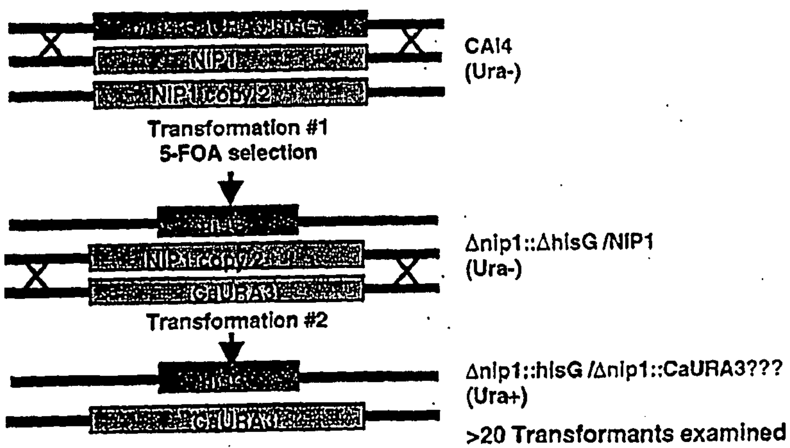


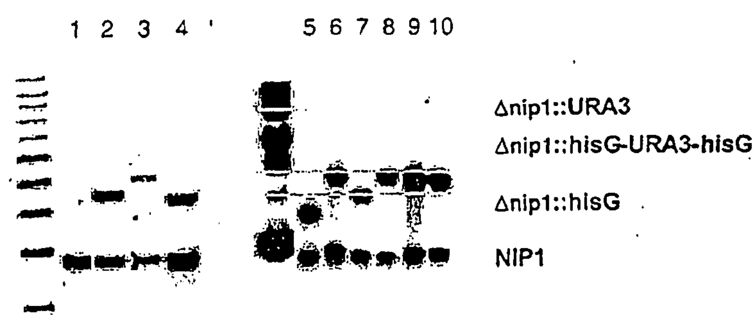
Figure 70A

C. albicans NIP1 deletion analysis



>20 Transformants examined by Southern blot, all contained the wild type copy of *CaNIP1*

Lane	
1	NIP1/NIP1 (CAI4)
2	NIP1/Δnip1 ::URA3
3	NIP1/Δnip1::hisG-URA3-hisG
4	NIP1/Δnip1::hisG
5-10	NIP1/Δnip1::hisG, Ura+ => NIP1/Δnip1::URA3



<u>Unable to delete second copy of *CaNIP1*</u>

Figure 70B

C. albicans LCP5 deletion analysis

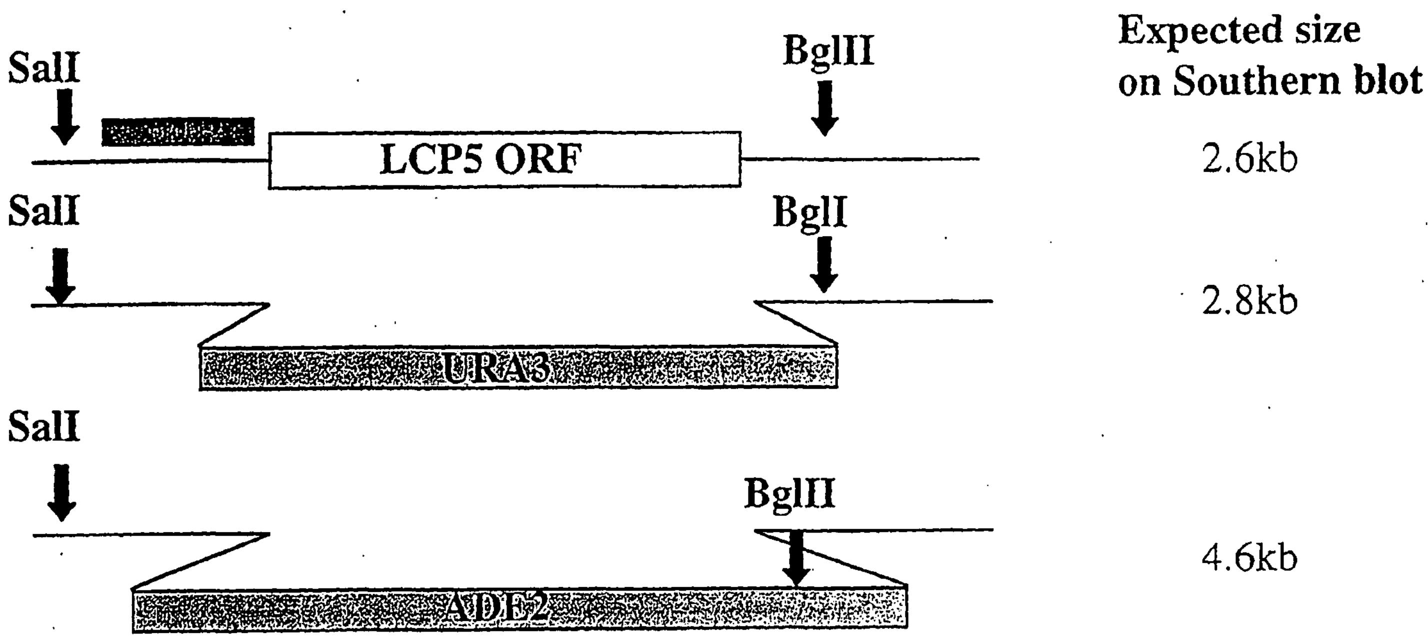
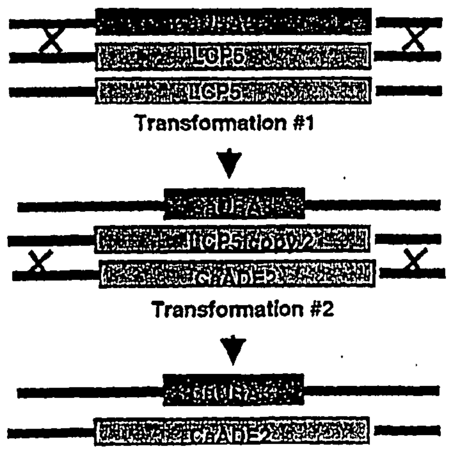


Figure 71A

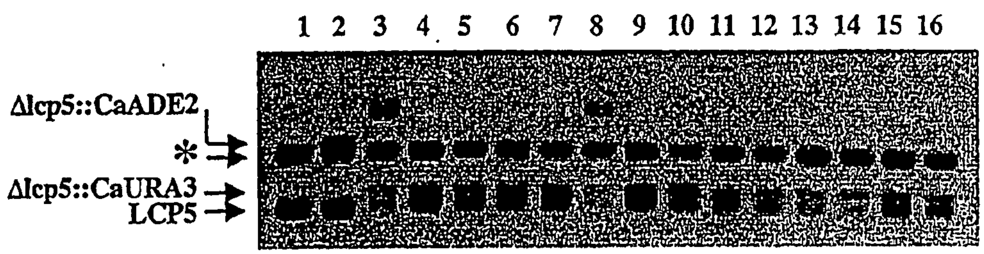
C. albicans LCP5 deletion analysis



CAI8 (Ura-, Ade-)

Δlcp5::CaURA3 / LCP5
(Ura+, Ade-)

Δlcp5::CaURA3 / Δlcp5::CaADE2???
(Ura+, Ade+)



Lane	
1	LCP5/LCP5 (CAI4)
2	LCP5/Δlcp5::CaADE2
3	LCP5/Δlcp5::CaURA3
4-16	Δlcp5::CaURA3/LCP5, Ade+

* Region 5′of LCP5 was used as probe
Region is repeated in genome (YER126)

<u>Unable to delete second copy of *CaLCP5*</u>

Figure 71B

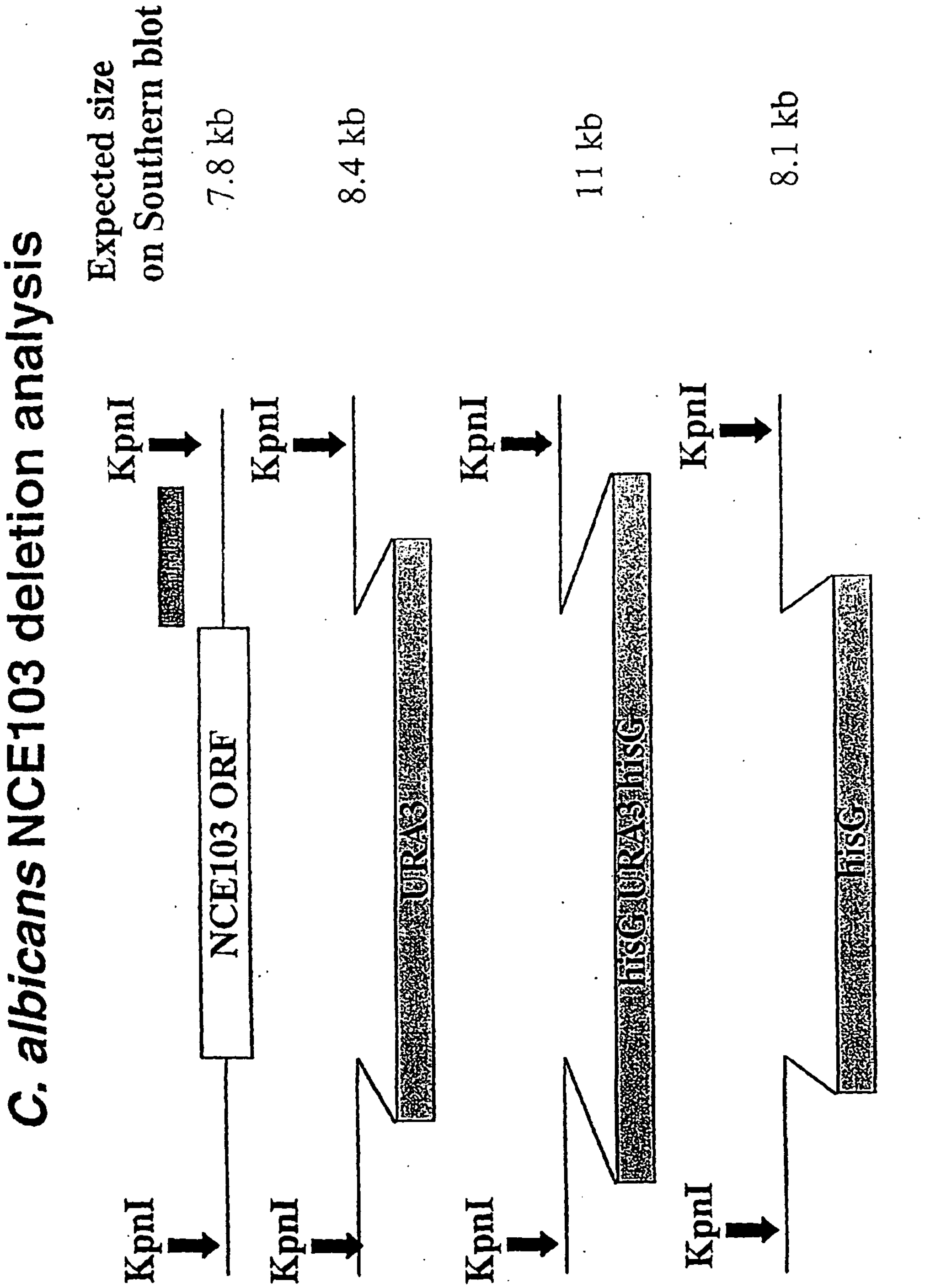
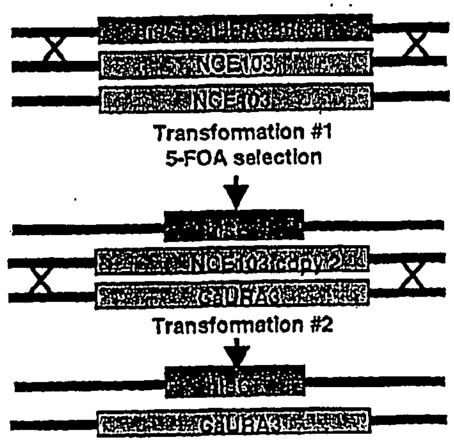

C. albicans NCE103 deletion analysis
Expected size on Southern blot
KpnI
NCE103 ORF
7.8 kb
URA3
8.4 kb
hisG URA3 hisG
11 kb
hisG
8.1 kb

Figure 72A

C. albicans NCE103 deletion analysis

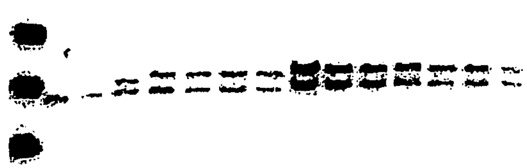


CAI4
(Ura-)

Δnce103::hisG /NCE103
(Ura-)

Δnce103::hisG / Δnce103::CaURA3???
(Ura+)

20 Transformants examined by Southern blot



nce103 ::hisG-URA3-hisG
nce103 ::URA3
nce103 ::hisG
NCE103/NCE103

Lane	
2	NCE103/NCE103 (CAI4)
3	NCE103/nce103::hisG-URA3-hisG
4	NCE103/nce103 ::hisG
5-14	NCE103/nce103 ::hisG, Ura+ => NCE103/nce103 ::URA3

<u>Unable to delete second copy of *CaNCE103*</u>

Figure 72B

C. albicans ECO1 deletion analysis

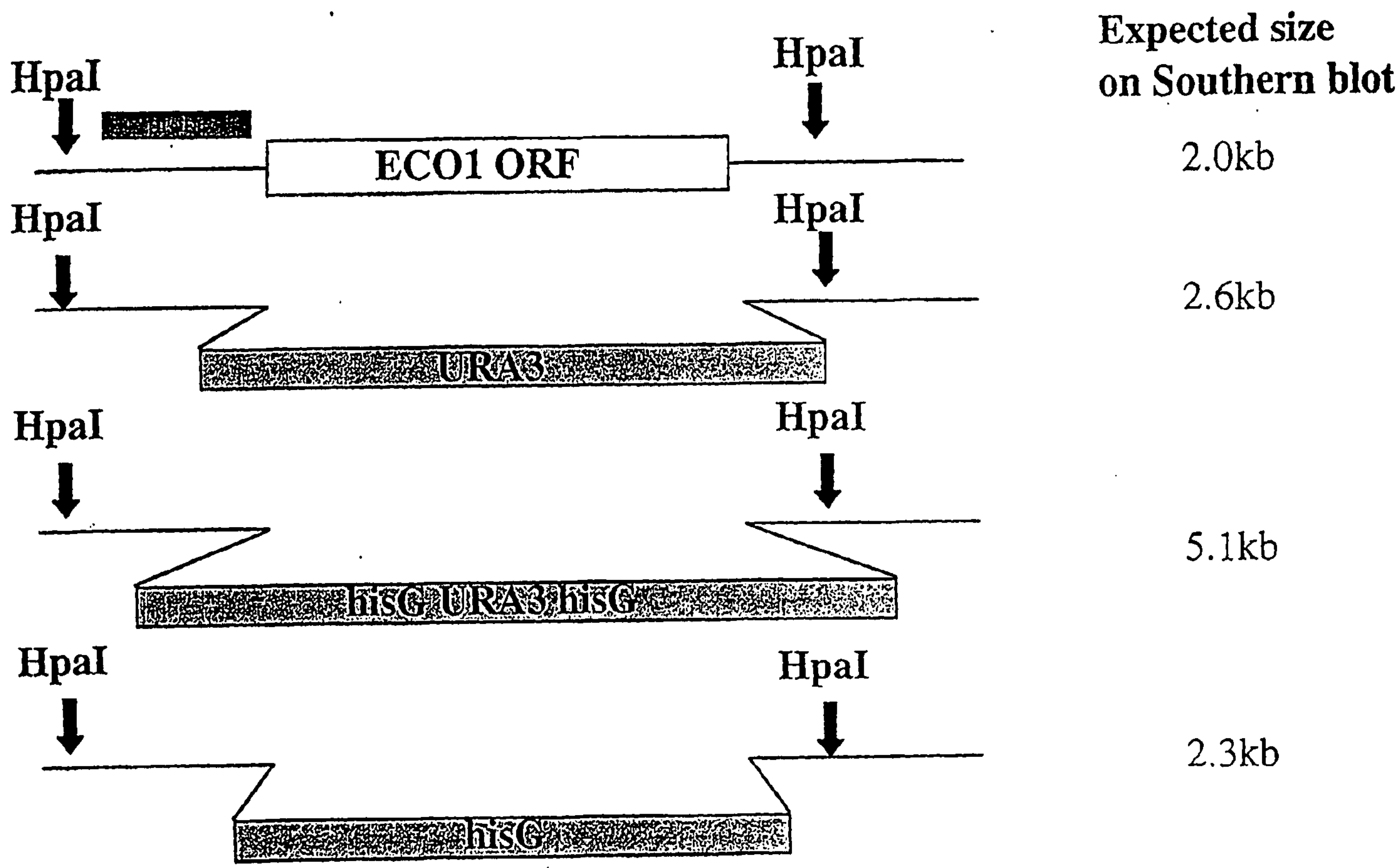
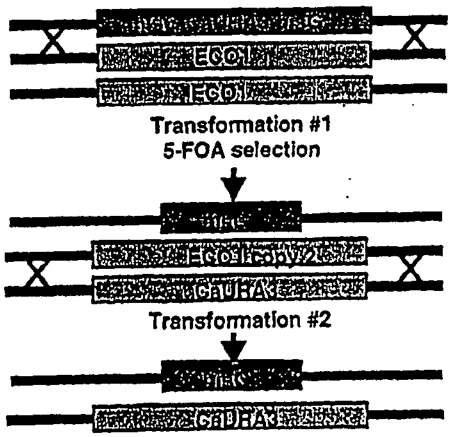


Figure 73A

C. albicans ECO1 deletion analysis

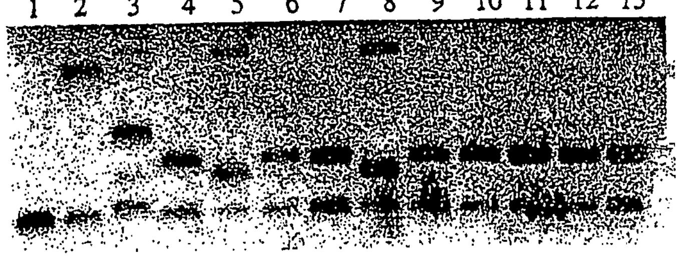


CAI4
(Ura-)

Δeco1::hisG / ECO1
(Ura-)

Δeco1::hisG / ΔECO1::CaURA3???
(Ura+)

>20 Transformants examined
by Southern blot



ΔECO1::hisG-URA3-hisG 3.1 kb
ΔECO1::URA3 2.6 kb
ΔECO1::hisG 2.3 kb
ECO1 2.0 kb

Lane	
1	ECO1/ECO1 (CAI4)
2	ECO1/eco1::hisG-URA3-hisG
3	ECO1/eco1::hisG
4-13	ECO1/eco1::hisG, Ura+ =>ECO1/eco1::URA3 (20/20 transformants)

<u>Unable to delete second copy of *CaECO1*</u>

Figure 73B

C. albicans ORC2 deletion analysis

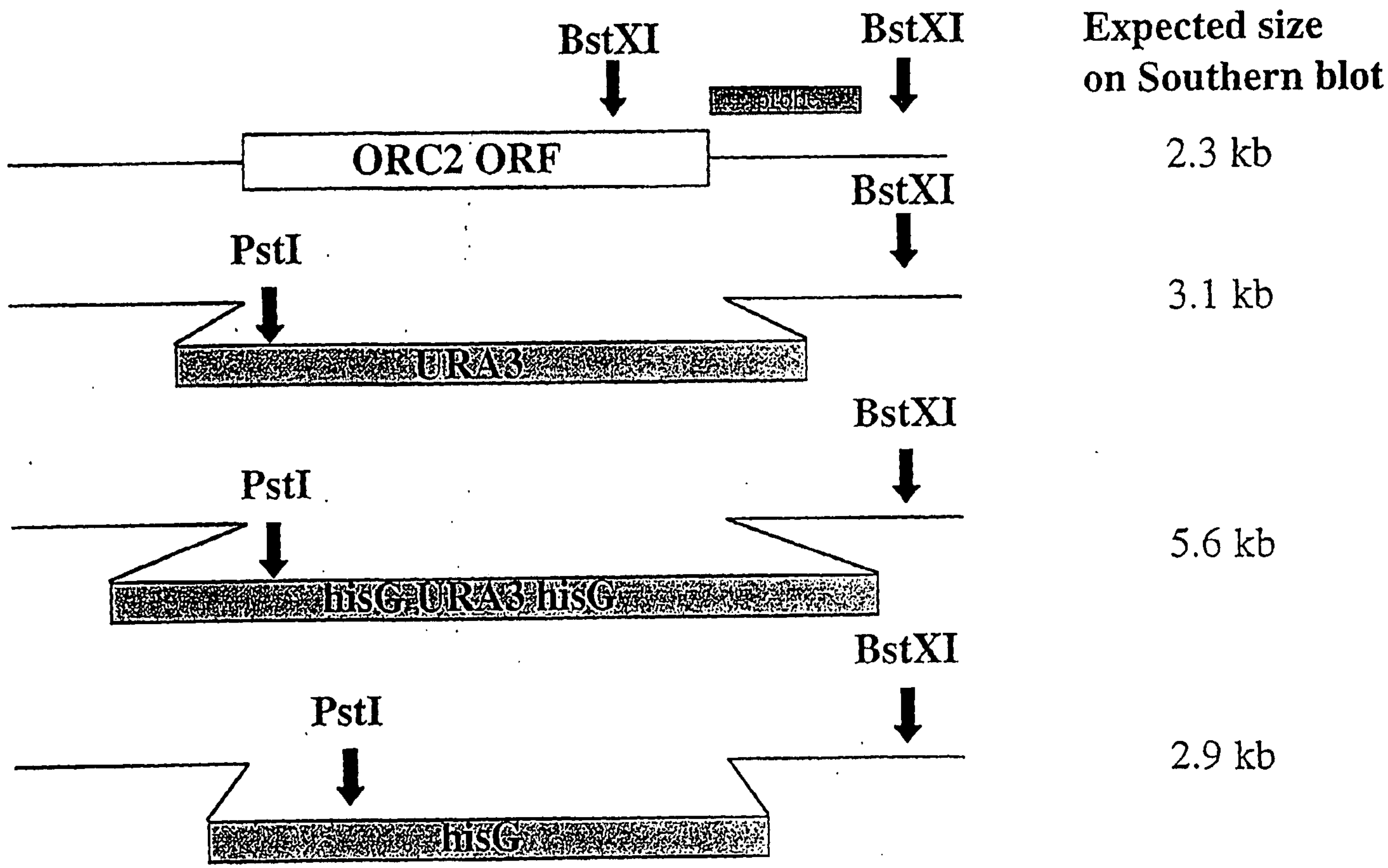
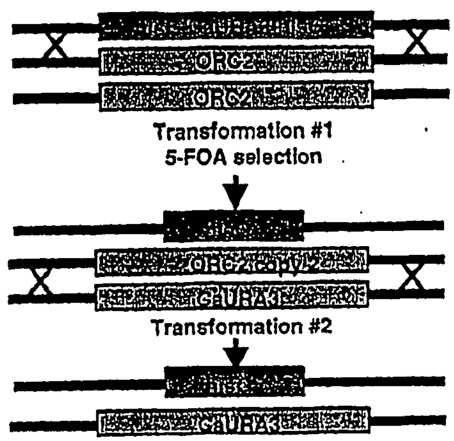


Figure 74A

C. albicans ORC2 deletion analysis

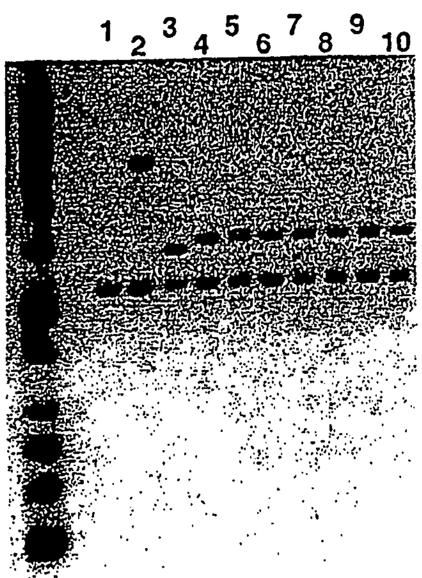


CAI4
(Ura-)

Δorc2::hisG / ORC2
(Ura-)

Δorc2::hisG / Δorc2::CaURA3 ???
(Ura+)

24 transformants were examined
-- all carried the ORC2⁺ locus



Δorc2::hisG-URA3-hisG	5.6 kb
Δorc2::URA3	3.1 kb
Δorc2::hisG	2.9 kb
ORC2	2.3 kb

Lane	Genotype
1	ORC2/ORC2 (CAI4)
2	ORC2/Δorc2::hisG-URA3-hisG
3	ORC2/Δorc2::hisG
4 - 9	ORC2/Δorc2::hisG, Ura+ =>ORC2/Δorc2::URA3
10	ORC2/Δorc2::URA3

<u>Unable to delete both copies of *CaORC2*</u>

Figure 74B

C. albicans CNS1 deletion analysis

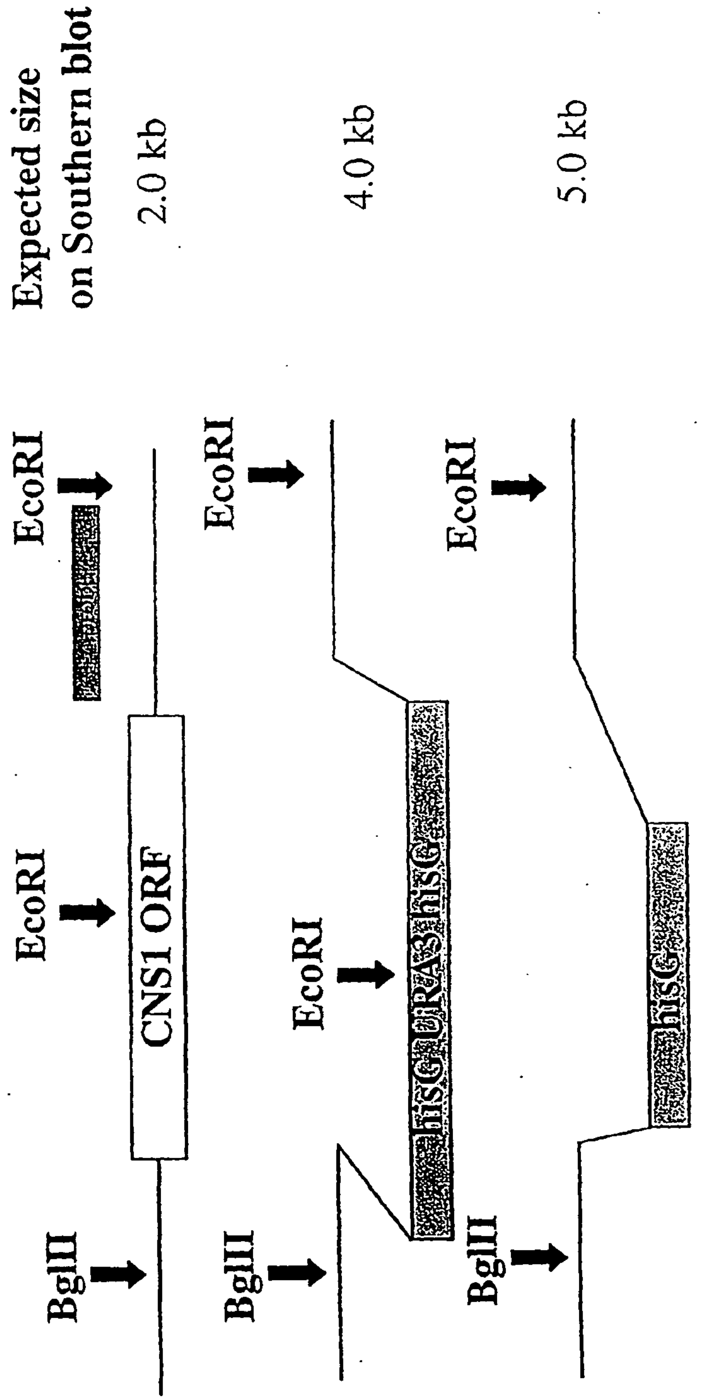
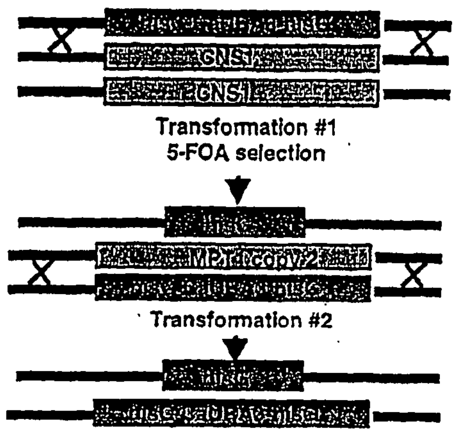


Figure 75A

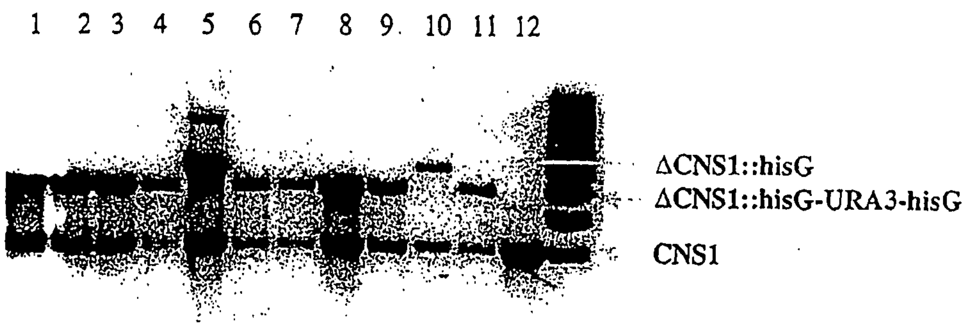
C. albicans CNS1 deletion analysis



CAI4
(Ura-)

Δcns1::hisG / cns1
(Ura-)

Δcns1::hisG / ΔCNS1::his G-CaURA3-hisG???
(Ura+)



Lane	
12	CNS1/CNS1 (CAI4)
11	CNS1/cns1::hisG-URA3-hisG
10	CNS1/cns1::hisG
1-9	CNS1/cns1::hisG, Ura+ =>CNS1/cns1::hisG-URA3-hisG (18/18 transformants)

<u>Unable to delete second copy of *CaCNS1*</u>

Figure 75B

C. albicans YPD1 deletion analysis

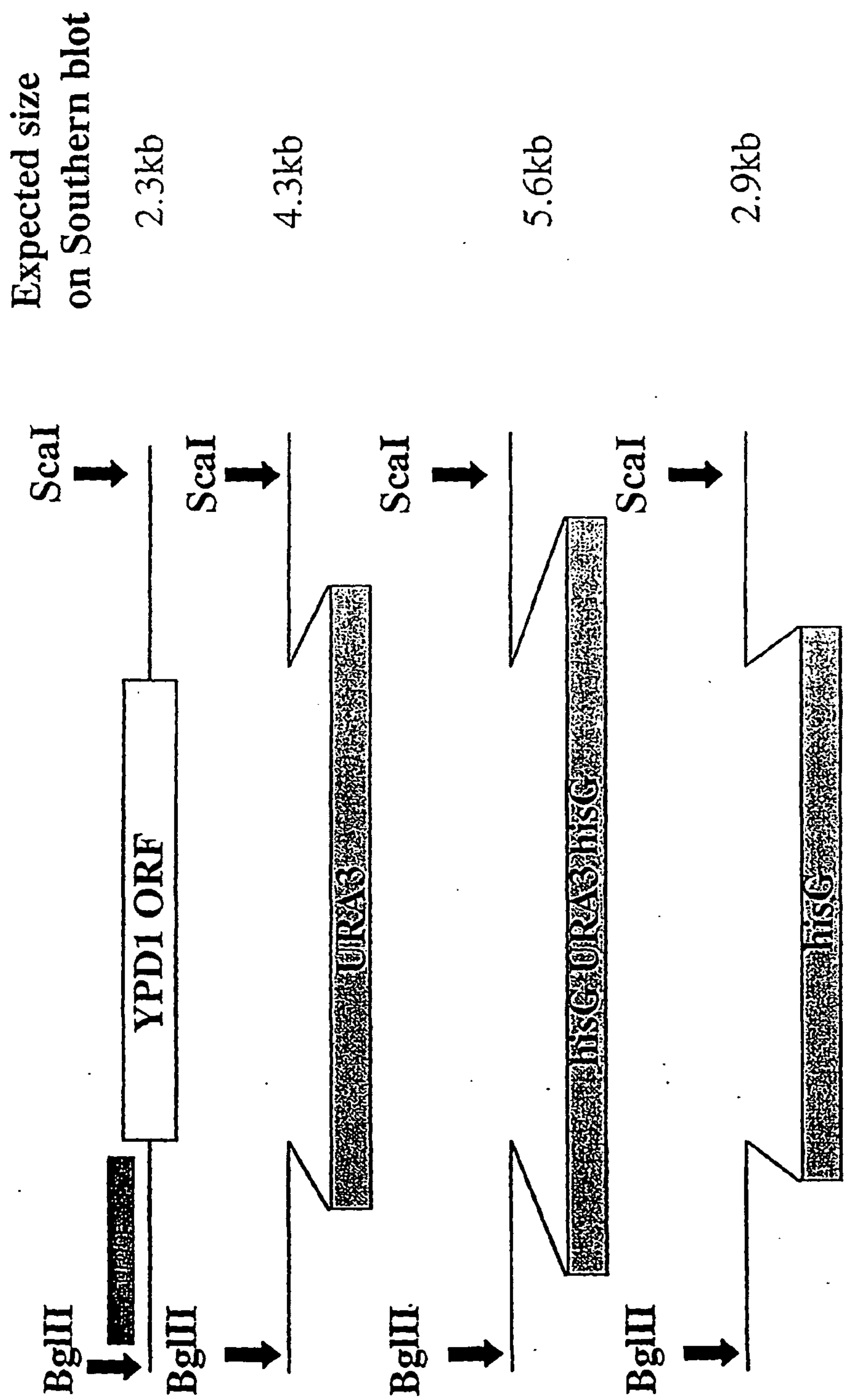
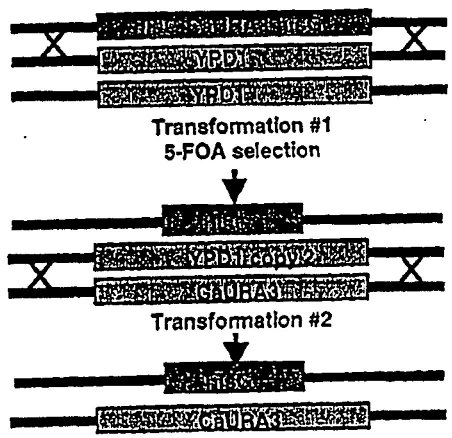


Figure 76A

C. albicans YPD1 deletion analysis



CAI4
(Ura-)

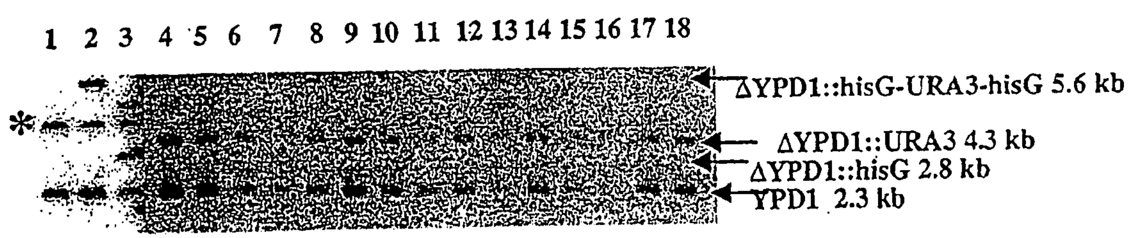
Transformation #1
5-FOA selection

Δypd1::hisG / YPD1
(Ura-)

Transformation #2

Δypd1::hisG / ΔYPD1::CaURA3???
(Ura+)

>20 Transformants examined
by Southern blot



*cross hybridizing background band

Lane	
1	YPD1/YPD1 (CAI4)
2	YPD1/ypd1::hisG-URA3-hisG
3	YPD1/ypd1::hisG
4	YPD1/ypd1::URA3
5-18	YPD1/ypd1::hisG, Ura+ =>YPD1/ypd1::URA3 (20/20 transformants)

<u>Unable to delete second copy of *CaYPD1*</u>

Figure 76B

C. albicans TIM10 deletion analysis

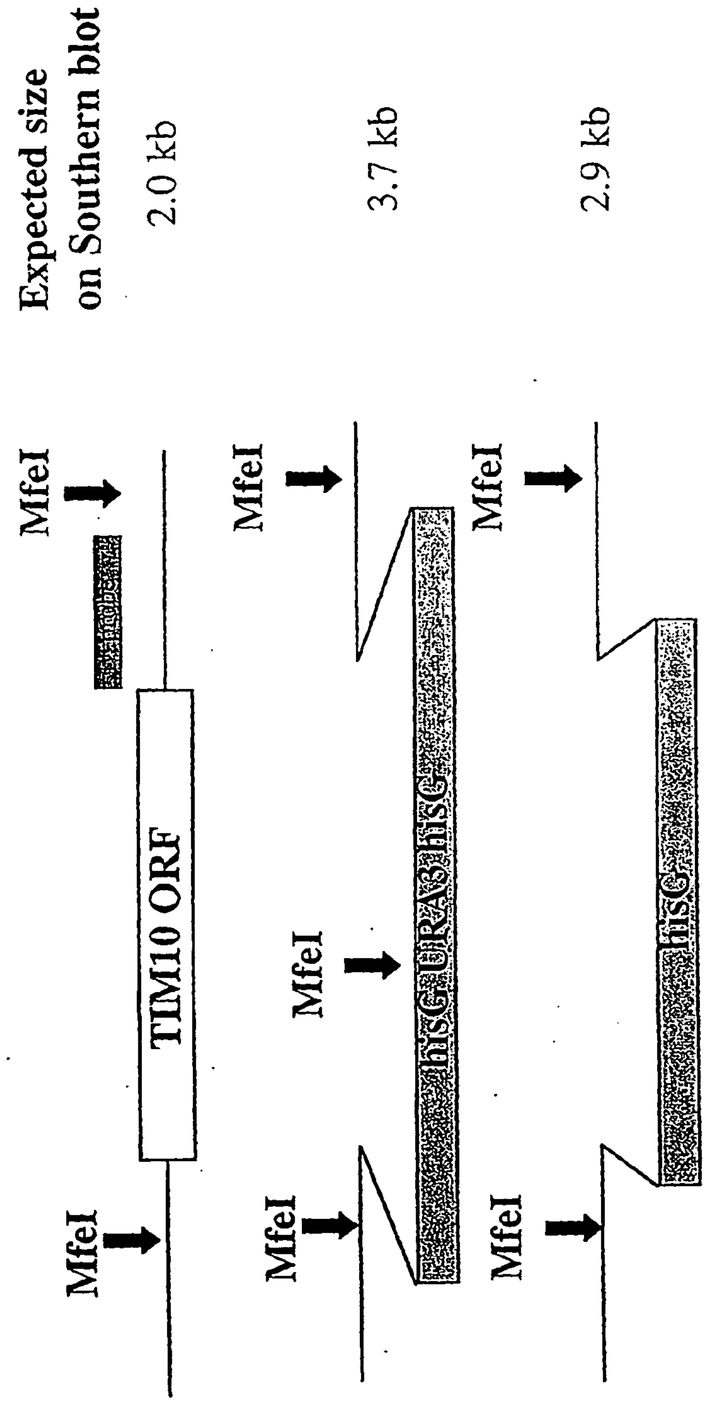
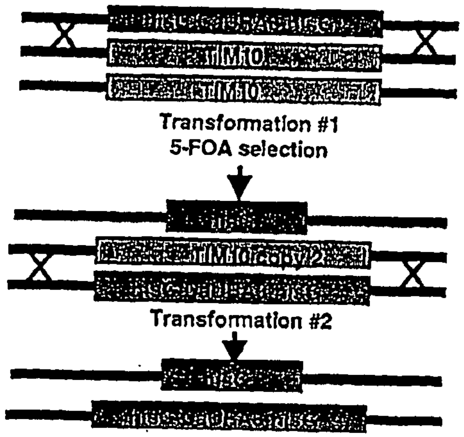


Figure 77A

C. albicans TIM10 deletion analysis

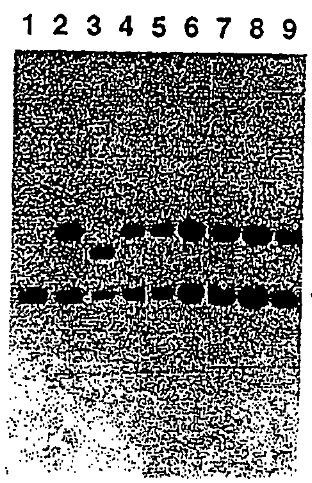


CAI4
(Ura-)

Δtim10::hisG / TIM10
(Ura-)

Δtim10::hisG / Δtim10::hisG-CaURA3-hisG ???
(Ura+)

24 transformants were examined
– all carried the TIM10+ locus



Δtim10::hisG-URA3-hisG 3.6 kb
Δtim10::hisG 2.9 kb
TIM10 2.0 kb

Lane	Genotype
1	TIM10/TIM10 (CAI4)
2	TIM10/Δtim10::hisG-URA3-hisG
3	TIM10/Δtim10::hisG
4 - 9	TIM10/Δtim10::hisG, Ura+ =>TIM10/Δtim10::hisG-URA3-hisG

Unable to delete both copies of *CaTIM10*

Figure 77B

C. albicans SRB4 deletion analysis

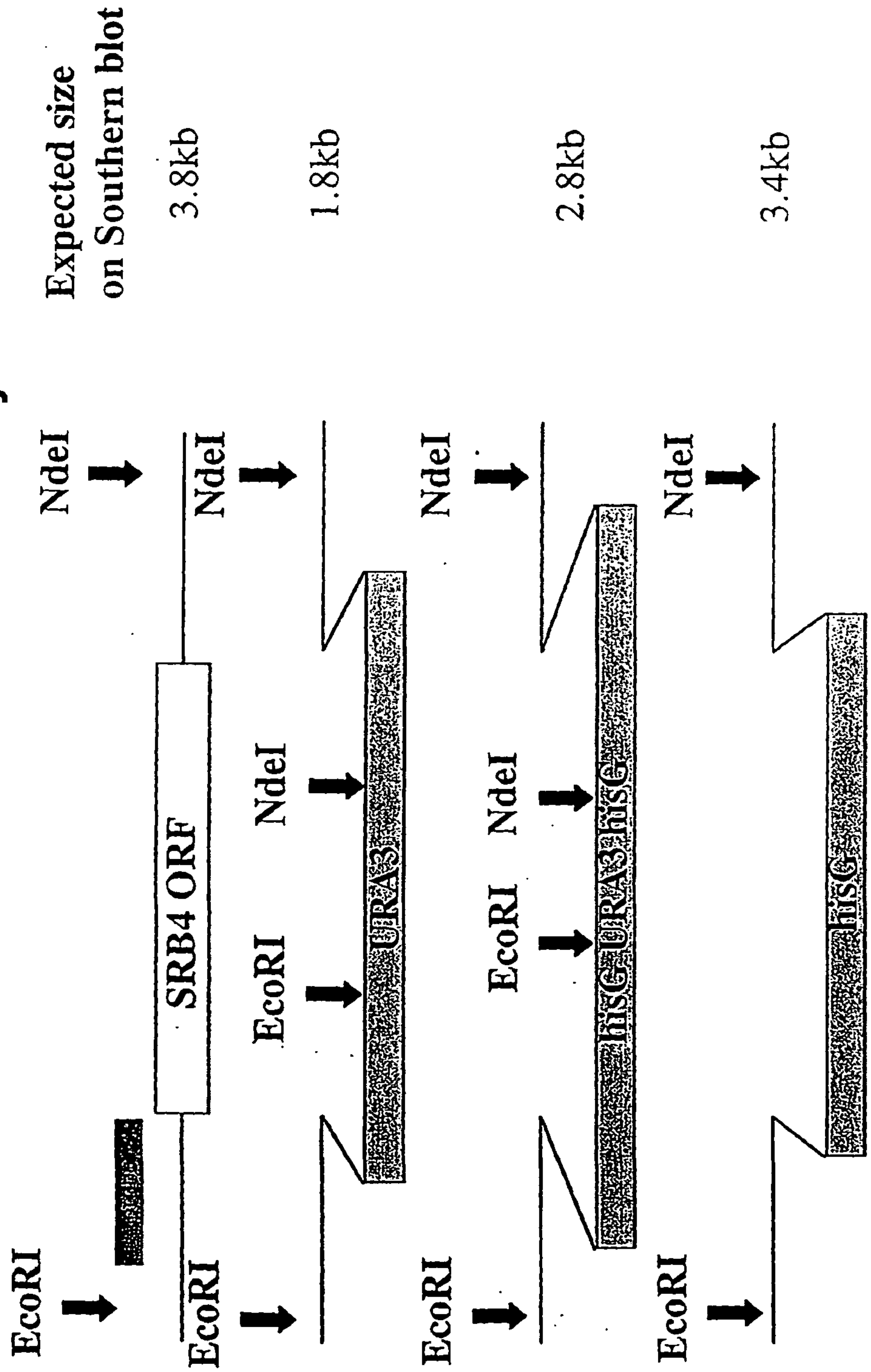
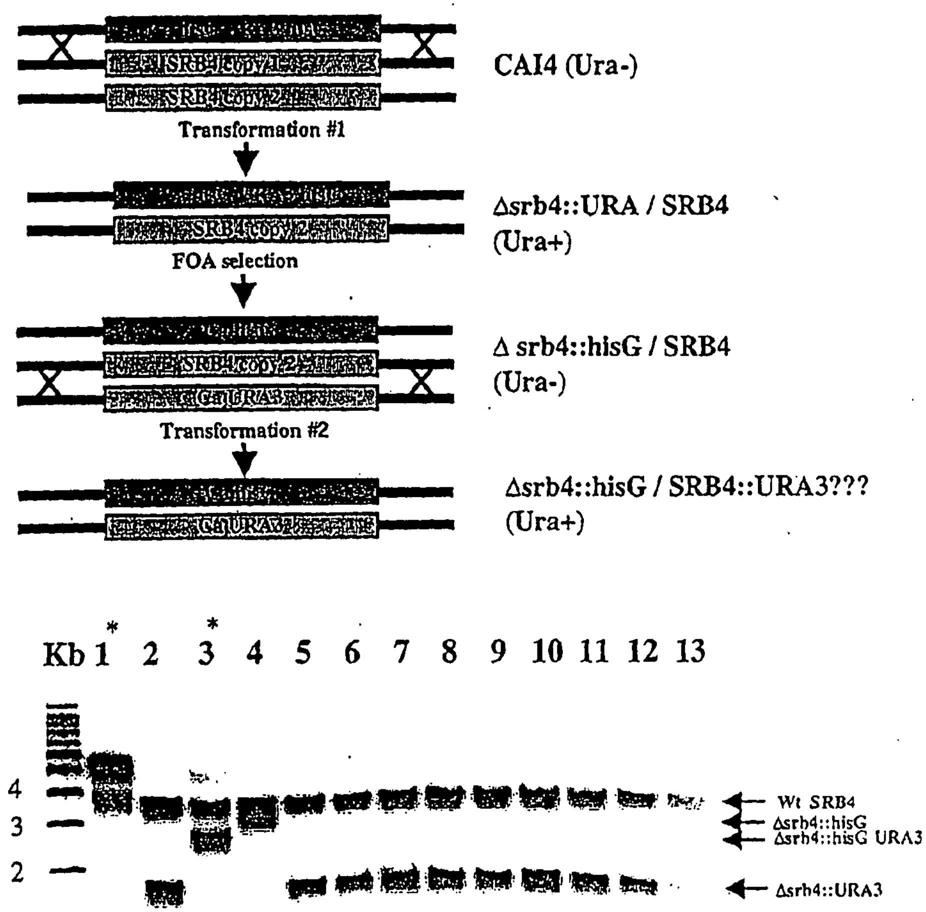


Figure 78A

C. albicans SRB4 deletion analysis



20 Transformants examined by Southern blot

Lane

1 SRB4/SRB4 (CAI4)
2 Δsrb4::URA3/SRB4
3 SRB4 / Δsrb4::hisG URA3 hisG
4 SRB4/ Δsrb4::hisG
5–13 Δsrb4::hisG / SRB4, Ura+

* Lanes 1 and 3 contain bands above wt band that are result of incomplete digestion

Unable to delete second copy of SRB4

Figure 78B

Figure 79

Saccharomyces cerevisiae orf name: YAL034W-A
Saccharomyces cerevisiae gene name: MTW1
Candida albicans protein: SEQ ID NO: 30
MSDKTLDERTTAILTEHLEFAPLTLIDDVINAVNEIMYKGTTAIETYLKEQKQLMKNGITK
VTEDEIEIGMGKLESLLESTIDKNFDKFELYCLRNIFNIPKDLIPYIQLSHQQGIEFKSDNVE
QKREFDQQIKNLQLKIMQELQLRKILKLQLVKVQKLIKVLIAIDNDFKKIDFASGGGGNEE
SIRILKNLQPIDETLYFLISQIKNLINQIEQLSNKVNTNLKTQKFIPNLRDKFIDGRTFRVLQQ
TGIWKDLEKNDIKILVQGNDNNNNNNNNNNNTLTDLQNQDDIDMIIPEQDDIDVDAIKNI
NAQIF
Saccharomyces cerevisiae protein:SEQ ID NO: 29
MSAPTMRSTSILTEHLGYPPISLVDDIINAVNEIMYKCTAAMEKYLLSKSKIGEEDYGEEI
KSGVAKLESLLENSVDKNFDKLELYVLRNVLRIPEEYLDANVFRLENQKDLVIVDENELK
KSEEKLREKVNDVELAFKKNEMLLKRVTKVKRLLFTIRGFKQKLNELLKCKDDVQLQKI
LESLKPIDDTMTLLTDSLRKLYVDSESTSSTEEVEALLQRLKTNGKQNNKDFRTRYIDIR

Saccharomyces cerevisiae orf name: YBR060C
Saccharomyces cerevisiae gene name: ORC2
Candida albicans protein:SEQ ID NO: 60
MSHSNALPNSPFRSPKKQRMEVIGPLNASRFSFSPVKTPPHGRAGLSSPEKRLVKDLDKA
RKRANNSLYNRLMDEYLDTDDYLDEQDRILADRIIKQSRGEPDEVNYGSDVELEIDLTQ
QRRTRRREKKVVYSSDSSNEYEDTGMPEESSSEEEEADDDDGNVEFVYGPPKERKTSLS
SSPPTVKPTVRRTKRGRPSKSELVLGQIKSIFHQDDVLFSTDRKTFTPTKPTAAKKPVSNY
LTSIFDQNFDRSKVPSLSGIPKSTNTHEEKKTFVPLPIPTLDADGNITDKEYISKYFDGVDP
AKFKEGRFVDEKVFYLEGPEGYFEQQTTRVKQSGNSLTALAPQIEYKDFARLVKLGDNL
SFQRKRHLFELHKYIYHQWCFEMSQGFNLNFYGVGSKIDLLRDFATNYFGIWWENVVH
ADLPKVLVVNGFNPSINIKKLILEIASILLPNELYPKHIAGTVPFVVDYLNNHRLPCGSIGFH
KPKILLIIHNLDGEVFRVDKTQTLLSQLMTLPEVWAMSSTDHINASLLWDLSKVKNLNFI
WHNLTTYATYQRETSFRDVISLGKSKKFVGGLGAKYVLRSLTDNHRNLYRELLIAQLDK
Saccharomyces cerevisiae protein:SEQ ID NO: 59
MLNGEDFVEHNDILSSPAKSRNVTPKRVDPHGERQLRRIHSSKKNLLERISLVGNERKNT
SPDPALKPKTPSKAPRKRGRPRKIQEELTDRIKKDEKDTISSKKKRKLDKDTSGNVNEES
KTSNNKQVMEKTGIKEKREREKIQVATTTYEDNVTPQTDDNFVSNSPEPPEPATPSKKSL
TTNHDFTSPLKQIIMNNLKEYKDSTSPGKLTLSRNFTPTPVPKNKKLYQTSETKSASSFLD
TFEGYFDQRKIVRTNAKSRHTMSMAPDVTREEFSLVSNFFNENFQKRPRQKLFEIQKKM
FPQYWFELTQGFSLLFYGVGSKRNFLEEFAIDYLSPKIAYSQLAYENELQQNKPVNSIPCLI
LNGYNPSCNYRDVFKEITDLLVPAELTRSETKYWGNHVILQIQKMIDFYKNQPLDIKLILV
VHNLDGPSIRKNTFQTMLSFLSVIRQIAIVASTDHIYAPLLWDNMKAQNYNFVFHDISNFE
PSTVESTFQDVMKMGKSDTSSGAEGAKYVLQSLTVNSKKMYKLLIETQMQNMGNLSA
NTGPKRGTQRTGVELKLFNHLCAADFIASNEIALRSMLREFIEHKMANITKNNSGMEIIW

Figure 79 (continued)

VPYTYAELEKLLKTVLNTL
human genbank accession #: Q13416
human protein:SEQ ID NO: 61
MSKPELKEDKMLEVHFVGDDDVLNHILDREGGAKLKKERAQLLVNPKKIIKKPEYDLEEDDQEVLKI
FLEKEEEEA

Saccharomyces cerevisiae orf name: YBR088C
Saccharomyces cerevisiae gene name: POL30
Candida albicans protein:SEQ ID NO: 18
MLEGKFEEAALLKKVVEAIKDCVKKCNFNCSEHGITVQAVDDSRVLLVSLLIGQTSFSER
CDRDVTLGIDLESFSKIIKSANNEDFLTLLAEDSPDQIMAILEEKQKEKISEYSLKLMDIDSE
FLQIDDMEYDAVVNMPSSDFAKLVRDLKNLSESLRVVVTKDSVKFTSEGDSGSGSVILK
PYTNLKNERESVTISLDDPVDLTFGLKYLNDIVKAATLSDVITIKLADKTPALFEFKMQSG
GYLRFYLAPKFDDDEY
Saccharomyces cerevisiae protein:SEQ ID NO: 17
MLEAKFEEASLFKRIIDGFKDCVQLVNFQCKEDGIIAQAVDDSRVLLVSLEIGVEAFQEYR
CDHPVTLGMDLTSLSKILRCGNNTDTLTLIADNTPDSIILLFEDTKKDRIAEYSLKLMDIDA
DFLKIEELQYDSTLSLPSSEFSKIVRDLSQLSDSINIMITKETIKFVADGDIGSGSVIIKPFVD
MEHPETSIKLEMDQPVDLTFGAKYLLDIIKGSSLSDRVGIRLSSEAPALFQFDLKSGFLQFF
LAPKFNDEE
human genbank accession #: P12004
human protein:SEQ ID NO: 19
MFEARLVQGSILKKVLEALKDLINEACWDISSSGVNLQSMDSSHVSLVQLTLRSEGFDTY
RCDRNLAMGVNLTSMSKILKCAGNEDIITLRAEDNADTLALVFEAPNQEKVSDYEMKL
MDLDVEQLGIPEQEYSCVVKMPSGEFARICRDLSHIGDAVVISCAKDGVKFSASGELGNG
NIKLSQTSNVDKEEEAVTIEMNEPVQLTFALRYLNFFTKATPLSSTVTLSMSADVPLVVE
YKIADMGHLKYYLAPKIEDEEGS

Saccharomyces cerevisiae orf name: YBR155W
Saccharomyces cerevisiae gene name: CNS1
Candida albicans protein:SEQ ID NO: 63
MSKIEPVTEKEEEYVSEWDRRRYVPKAGEPELPPQLSEFSNKTTDEVIEELNRLPFFMTLD
ETDGDGGENVNLEALKSLAYEGDPDEIASNFKNQGNNCYKFKKYKDAIIFYTKGLEVNC
DVDAINSALYLNRAACNLELKNYRRCIEDCKKVLMLDEKNIKACFRSGKAFFAIEKYDE
AIKVLEYGLNIEPENKDLQKLLQQVQKRQETLAQIKAKKAQEEEQERLKNIVLENSIKLR
HIEIVKSSSPPEVLKTAKIRLEDPKDYQSQLIFPAMILYPTTDEFDFIAEISELTTPLELL
Saccharomyces cerevisiae protein:SEQ ID NO: 62
MSSVNANGGYTKPQKYVPGPGDPELPPQLSEFKDKTSDEILKEMNRMPFFMTKLDETDG

Figure 79 (continued)

AGGENVELEALKALAYEGEPHEIAENFKKQGNELYKAKRFKDARELYSKGLAVECEDK
SINESLYANRAACELELKNYRRCIEDCSKALTINPKNVKCYYRTSKAFFQLNKLEEAKSA
ATFANQRIDPENKSILNMLSVIDRKEQELKAKEEKQQREAQERENKKIMLESAMTLRNIT
NIKTHSPVELLNEGKIRLEDPMDFESQLIYPALIMYPTQDEFDFVGEVSELTTVQELVDLV
LEGPQERFKKEGKENFTPKKVLVFMETKAGGLIKAGKKLTFHDILKKESPDVPLFDNALK
IYIVPKVESEGWISKWDKQKALERRSV
human genbank accession #: NP_004614
human protein:SEQ ID NO: 64
MEQPGQDPTSDDVMDSFLEKFQSQPYRGGFHEDQWEKEFEKVPLFMSRAPSEIDPRENP
DLACLQSIIFDEERSPEEQAKTYKDEGNDYFKEKDYKKAVISYTEGLKKKCADPDLNAV
LYTNRAAAQYYLGNFRSALNDVTAARKLKPCHLKAIIRGALCHLELIHFAEAVNWCDEG
LQIDAKEKKLLEMRAKADKLKRIEQRDVRKANLKEKKERNQNEALLQAIKARNIRLSEA
ACEDEDSASEGLGELFLDGLSTENPHGARLSLDGQGRLSWPVLFLYPEYAQSDFISAFHE
DSRFIDHLMVMFGETPSWDLEQKYCLIIWRSTLRMRTGQNYTGCLPRAPCYRFYSTRGT
L
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Saccharomyces cerevisiae orf name: YDL235C
Saccharomyces cerevisiae gene name: YPD1
Candida albicans protein:SEQ ID NO: 66
MSEDKLQKLQDSGLVDWAVFSEIVTMDEDEEGFSKSLVEVFVSQVEETFEEIDKYLKEK
NLEKLSSSGHFLKGSAAALGLTKISNQCERIQNYGHKINFDNFQLEDIKTKGDSAVSAEN
VAVNDGETNPENGSNGNETSNNKTNTSNIPDESSDDFWIALIEDALAKARDGFDQSRRA
LDEYYE
Saccharomyces cerevisiae protein:SEQ ID NO: 65
MSTIPSEIINWTILNEIISMDDDDSDFSKGLIIQFIDQAQTTFAQMQRQLDGEKNLTELDNL
GHFLKGSSAALGLQRIAWVCERIQNLGRKMEHFFPNKTELVNTLSDKSIINGINIDEDDEEI
KIQVDDKDENSIYLILIAKALNQSRLEFKLARIELSKYYNTNL
human genbank accession #: CAA78727
human protein:SEQ ID NO: 67
TDKLSNMQKDLENSNAKLQEKIQELKANEHQLITLKKDVNETQKKVSEMEQLKKQIKD
QSLTLSKLEIENLNLAQELHENLEEMKSVMKERDNLRRVEETLKLERDQLKESLQETKA
RDLEIQQELKTARMLSKEHKETVDKLREKISEKTIQISDIQKDLDKSKDELQKKIQELQKK
ELQLLRVKEDVNMSHKKINEMEQLKKQFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAK
ERD--

Saccharomyces cerevisiae orf name: YDR299W
Saccharomyces cerevisiae gene name: BFR2
Candida albicans protein:SEQ ID NO: 38
MSFFGLHFQLNSLTLNISNMAKKSLSEQISSLYTPKTDYDIEDHDLDVSKDNGIFQHHDG
GSENESEDEDTGLRNEHYVESSKSKLRQQNEGVNLGEKYVGNVTSRSKLYDDEDDKQP

Figure 79 (continued)

TEASSGEELDAESAEEEEDEESEDVADDDEDDQESDRSSSSDAENDEDENISHKRELLKQ
LMSKERSHIVNRLSQSATNDALKGYSIQQQNKTFEKIIDVRLKFQKSVTSSNMLPINTSTY
SETKSEDSDELVTKAKKQLYSLLDHLFTLRNELDESTSVKTPKKRSFAKYSEVTSAADAQ
LNSRRNQILTKWSAKVANSSGRNAMNANKFKTINQSFEQQVNNNLSDMDRLIKRTKLN
RRNVTPIGYTTKEEDDHENGNKNKSIDEDDDDIPEDTSVRKKTQGLENDYIFDDEDFYRV
LLNDLVDKKVQTSDPTSGITISLRAAQKSNKLKNNVDTKASKGRKLRYHVQEPIANFETS
RGS
Saccharomyces cerevisiae protein:SEQ ID NO: 37
MEKSLADQISDIAIKPVNKDFDIEDEENASLFQHNEKNGESDLSDYGNSNTEETKKAHYL
EVEKSKLRAEKGLELNDPKYTGVKGSRQALYEEVSENEDEEEEEEEEEEKEEDALSFRT
DSEDEEVEIDEEESDADGGETEEAQQKRHALSKLIQQETKQAINKLSQSVQRDASKGYSI
LQQTKLFDNIIDLRIKLQKAVIAANKLPLTTESWEEAKMDDSEETKRLLKENEKLFNNLF
NRLINFRIKFQLGDHITQNEEVAKHKLSKKRSLKELYQETNSLDSELKEYRTAVLNKWST
KVSSASGNAALSSNKFKAINLPADVQVENQLSDMSRLMKRTKLNRRNITPLYFQKDCAN
GRLPELISPVVKDSVDDNENSDDGLDIPKNYDPRRKDNNAIDITENPYVFDDEDFYRVLL
NDLIDKKISNAHNSESAAITITSTNARSNNKLKKNIDTKASKGRKLNYSVQDPIANYEAPI
TSGYKWSDDQIDEFFAGLLGQRVNFNENEDEEQHARIENDEELEAVKNDDIQIFG
human genbank accession #: NM_000055
human protein:SEQ ID NO: 39
MGRPLALQLEQLLNPRPSEADPEADPEEATAARVIDRFDEGEDGEGDFLVVGSIRKLASA
SLLDTDKRYCGKTTSRKAWNEDHWEQTLPGSSDEEISDEEGSGDEDSEGLGLEEYDEDD
LGAAEEQECGDHRESKKTRSHSAKTPGFSVQSISDFEKFTKGMDDLGSSEEEEDEESGME
EGDDAEDSQGESEEDRAGDRNSEDDGVVMTFSSVKVSEEVEKGRAVKNQIALWDQLLE
GRIKLQKALLTTNQLPQPDVFPVFKDKGGPEFASALKNSHKALKALLRSLVGLQEELLFQ
YPDTRYVVDGTKPNAGSEEISSEDDELVEEKKQQRRRVPAKRKLEMEDYPSFMAKALPT
LQSTGTTLQKWHDKTKLASGKLGKGFGAFERSILTQIDHILMCKERLLRRTQTKRSVYR
VLGKPEPAAQPVPESLPGEPEILPQAPANAHLKDLDEEIFDDDDFYHQLLRELIERKTSSL
DPNDQVAHGKAVACNPEVTEAKSTKKVDRKASKGRKLRFHVLSKLLSFMAPIDHTTMN
DDARTELYRSLFGQLHPPDEGHGD
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Saccharomyces cerevisiae orf name: YDR311W
Saccharomyces cerevisiae gene name: TFB1
Candida albicans protein:SEQ ID NO: 32
MDIIRGACSVDKIGGMVYIREDLAPLMLEWKPIDEQEEDRAISIPLNSLTTLQSTKETSPK
MILKIVYKLTSGPPNTNADGTDNGGGGGGEQKSFKLTFTNRPTMNTIKDSLQTIVARSRT
KGGLKVPVLQLQLQHQLQHLGSAPQADSTRDSTSSSTPIPPTTSGTSTSSSLLSLAASQSLS
DANLLKNFELQQKLLLEDRQLRDVFTKSVMQFKLSPQVFWSSRLNQLRTFALTISQHKG
PYNVLSTIKPVATSDNQVNVNVTRDTINEIFTIYPIIKKAFDDLVPNKFNEGEFWSRFFNSK
LFRRLRGDKISISNSRGDVVLDKYLYIDQNYQEKLQKSSTLENNGSGGGGGAGGGSGN
SEQGIQTLESPHVKKFLDLMGNQQDNSQKLGNRPDFTMRYDEDNVDDDNKKPTLGNEN
EMIILMKNMNRLSSKMMSMSSTNGPEKPSETTIDGLSAAELNEYEEELDLHDLNDSENLQ

Figure 79 (continued)

YIKLNINTDIAKGTKLDSYEGSNTNNKISQDELHKYLQSQTFQGQIELTETYTCKSEEIEKT
SMEIAMLIKQNFRTFKLINKENDIAGTNIVPNSLIQEIITYNITIVEFLSHFWKIFLHGNNPGQ
LKKIFTSLKNCQSGLIELENKAIDQFKSMDILQKNQKLQDKVLKDFASCLQPMKIALDKA
CNE
Saccharomyces cerevisiae protein:SEQ ID NO: 31
MSHSGAAIFEKVSGIIAINEDVSPAELTWRSTDGDKVHTVVLSTIDKLQATPASSEKMML
RLIGKVDESKKRKDNEGNEVVPKPQRHMFSFNNRTVMDNIKMTLQQIISRYKDADIYEE
KRRREESAQHTETPMSSSSVTAGTPTPHLDTPQLNNGAPLINTAKLDDSLSKEKLLTNLK
LQQSLLKGNKVLMKVFQETVINAGLPPSEFWSTRIPLLRAFALSTSQKVGPYNVLSTIKPV
ASSENKVNVNLSREKILNIFENYPIVKKAYTDNVPKNFKEPEFWARFFSSKLFRKLRGEKI
MQNDRGDVIIDRYLTLDQEFDRKDDDMLLHPVKKIIDLDGNIQDDPVVRGNRPDFTMQP
GVDINGNSDGTVDILKGMNRLSEKMIMALKNEYSRTNLQNKSNITNDEEDEDNDERNEL
KIDDLNESYKTNYAIIHLKRNAHEKTTDNDAKSSADSIKNADLKVSNQQMLQQLSLVMD
NLINKLDLNQVVPNNEVSNKINKRVITAIKINAKQAKHNNVNSALGSFVDNTSQANELEV
KSTLPIDLLESCRMLHTTCCEFLKHFYIHFQSGEQKQASTVKKLYNHLKDCIEKLNELFQD
V
human genbank accession #: W19128
human protein:SEQ ID NO: 33
MATSSEEVLLIVKKVRQKKQDGALYLMAERIAWAPEGKDRFTISHMYADIKCQKISPEG
KAKIQLQLVLHAGDTTNFHFSNESTAVKERDAVKDLLQQLLPFKRANKELEKNRCCKIL
FCFSFIKLRTGEEQMLEDPVLFQLYKDVSQVISAEEFWNRLNVNATDSSTSNHKQDVGIS
AAFLADVRPQTDGCNGLRYNLTSDIIESIFRTYPAVKMKYAENVPHNMTEKEFWTRFFQ
SHYFHRDRLNTGSKDLFAECAKIDEKGLKTMVSLGVKNPLLDLTALEDKPLDEGYGISSV
PSSNSKSIKENSNAAIIKRFNHHSAMVLAAGLRKQEAQNEQTSEPSNMDGNSGDADCFQ
PAVKRAKLQESIEYEDLGKNNSVKTIALNLKKSDRYYHGPTPIQSLQYATSQDIINSFQSIR
QEMEAYTPKLTQVLSSSAASSTITALSPGGALMQGGTQQAINQMVPNDIQTNLVSHIEEM
LQTAYNKLHTWQSRRLMKKT
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Saccharomyces cerevisiae orf name: YER022W
Saccharomyces cerevisiae gene name: SRB4
Candida albicans protein:SEQ ID NO: 72
MVEKQFNIDLELNDTGHIDPFLQDEYVCFLTLLVFLVLFFSLLTLPRDKLKLEELIPRIFER
KSFLNVTEDSLRKEIDNSLKISEEDALDTEESREDTVEADQQEVFNKHKFELSKNINNAL
NETQLSLDFVSLLISSVKPSLAKSTISPHLSKFVKPTSLNSDRLGQDSNDNQESKATDSFGQ
GWKLESLGKITDLFREASTNLNDQVIKERRYWNMINLVLANDEVLFRMRDPQNNARAIG
VKYGYGDSGSNFHDQGLALLRKDNQTGEISFHPISSINNAKIVEKVSRFIRVKILSQIDGDY
MLTGQSIFNFDFEKSKQSIINDIEKARFFLFEEDLFHQLIREAKLLVNYNVSIISNKIIIEINNII
IEIESIVYDELNEEELENYYQNVNEYSTLHNKKCQLILNYLKLMLCCYYKYNLKLKQKVP
TALTKWKQSNSHPLILRPLVGNMRHELNLLNMKSVLDRLMHAHESELSYSKLDVEKFIN
LATRSKKQNPFQKSIEKPISKFHLVLCNKTSNMLDVNIQLDNYELFVNLIINMTIIRFETEH
DFKNNVNGINVLQLGFSDFNEIEECLDWSIQNFVL

Figure 79 (continued)

Saccharomyces cerevisiae protein:SEQ ID NO: 71
MTTEDPDSNHLSSETGIKLALDPNLITLALSSNPNSSLHSPTSDEPVPESAGKADTSIRLEG
DELENKTKKDNDKNLKFLKNKDSLVSNPHEIYGSMPLEQLIPIILRQRGPGFKFVDLNEKE
LQNEIKQLGSDSSDGHNSEKKDTDGADENVQIGEDFMEVDYEDKDNPVDSRNETDHKT
NENGETDDNIETVMTQEQFVKRRRDMLEHINLAMNESSLALEFVSLLLSSVKESTGMSS
MSPFLRKVVKPSSLNSDKIPYVAPTKKEYIELDILNKGWKLQSLNESKDLLRASFNKLSSI
LQNEHDYWNKIMQSISNKDVIFKIRDRTSGQKLLAIKYGYEDSGSTYKHDRGIANIRNNIE
SQNLDLIPHSSSVFKGTDFVHSVKKFLRVRIFTKIESEDDYILSGESVMDRDSESEEAETKD
IRKQIQLLKKIIFEKELMYQIKKECALLISYGVSIENENKVIIELPNEKFEIELLSLDDDSIVN
HEQDLPKINDKRANLMLVMLRLLLVVIFKKTLRSRISSPHGLINLNVDDDILIIRPILGKVR
FANYKLLLKKIIKDYVLDIVPGSSITETEVEREQPQENKNIDDENITKLN
human genbank accession #: BAA88763
human protein:SEQ ID NO: 73
MYGSARSVGKVEPSSQSPGRSPRLPRSPRLGHRRTNSTGGSSGSSVGGGSGKTLSMENIQ
SLNAAYATSGPMYLSDHENVGSETPKSTMTLGRSGGRLPYGVRMTAMGSSPNIASSGV
ASDTIAFGEHHLPPVSMASTVPHSLRQARDNTIMDLQTQLKEVLRENDLLRKDVEVKES
KLSSSMNSIKTFWSPELKKERALRKDEASKITIWKEQYRVVQEENQHMQMTIQALQDEL
RIQRDLNQLFQQDSSSRTGEPCVAELTEENFQRLHAEHERQAKELFLLRKTLEEMELRIET
QKQTLNARDESIKKLLEMLQSKGLSAKATEEDHERTRRLAEAEMHVHHLESLLEQKEKE
NSMLREEMHRRFENAPDSAKTKALQTVIEMKDSKISSMERGLRDLEEEIQMLKSNGALS
TEEREEEMKQMEVYRSHSKFMKNKIGQVKQELSRKDTELLALQTKLETLTNQFSDSKQH
IEVLKESLTAKEQRAAILQTEVDALRLRLEEKETMLNKKTKQIQDMAEEKGTQAGEIHDL
KDMLDVKERKVNVLQKKIENLQEQLRDKEKQMSSLKERVKSLQADTTNTDTALTTLEE
ALAEKERTIERLKEQRDRDEREKQEEIDNYKKDLKDLKEKVSLLQGDLSEKEASLLDLKE
HASSLASSDESSKAQAEVDRLLEILKEVENEKNDKDKKIAELESLTSRQVKDQNKKVAN
LKHKEQVEKKKSAQMLEEARRREDNLNDSSQQLQVEELLMAMEKVKQELESMKAKLS
STQQSLAEKETHLTNLRAERRKHLEEVLEMKQEALLAAISEKDANIALLELSSSKKKTQE
EVAALKREKDRLVQQLKQQTQNRMKLMADNYEDDHFKSSHSNQTNHKPSPDQDEEEG
IWA
–

Saccharomyces cerevisiae orf name: YER127W
Saccharomyces cerevisiae gene name: LCP5
Candida albicans protein:SEQ ID NO: 53
MSKVDTVLKEIISSTKSTEASVKELIAFVKDSSSQHPELVRNLLAKSNSSLEGVSLLGLKN
ESLVSYINNIVLVVLSHLERLESDSETGSSAVERSIIQRVTLEKGVKPLEKKLSYQLDKMIR
AYGRMEQDEIKAEQKLNDRGSGENDENDENDSEEDSEEDSEDDSEDDELAYRPDASSFA
KLTSAKTKSKPTSSAVSTSNEKYRPPKISAMAPPTAVKSHDLDANTTSSKNRKLQSMEEY
LQEQSDMPMVEASVGSTIVEHGRGGVKTQHDRKKEREIQTYEEDNFVRLPTSQTKKSF
Saccharomyces cerevisiae protein:SEQ ID NO: 52
MSELNALLKDINGSLTATSESLERLSGIYSNSATDEIPESNQLHEHLFYDAKKPAEKVSLL
SLKNGSMLGYINSLLMLIGNRLDDECKDPSAMDARERSIQHRVVLERGVKPLEKKLAYQ

Figure 79 (continued)

LDKLTRAYVKMEKEYKDAEKRALEKSTLVNHSGNDDSEDDESSEDEIAYRPNTSGIINT
NKKSSAYRVEETAKQENGEENDDNETGVYKPPKITAVLPPQQTHFEDRFDAREHKDRSN
KSNKAEKRKQKQRERNARMNVIGGEDFGIFSSKRKLEDSTSRRGAKKTRSAWDRAQRR
L
human genbank accession #: AL050003
human protein:SEQ ID NO: 54
MAALGVLESDLPSAVTLLKNLQEQVMAVTAQVKSLTQKVQAGAYPTEKGLSFLEVKDQ
LLLMYLMDLTHLILDKASGGSLQGHDAVLRLVEIRTVLEKLRPLDQKLKYQIDKLIKTAV
TGSLSENDPLRFKPHPSNMMSKLSSEDEEEDEAEDDQSEASGKKSVKGVSKKYVPPRLV
PVHYDETEAEREKKRLERAKRRALSSSVIRELKEQYSDAPEEIRDARHPHVTRQSQEDQH
RINYEESMMVRLSVSKREKGRRKRANVMSSQLHSLTHFSDISALTGGTVHLDEDQNPIK
KRKKIPQKGRKKKGQ
Saccharomyces cerevisiae orf name: YFR027W
Saccharomyces cerevisiae gene name: ECO1
Candida albicans protein:SEQ ID NO: 58
MGSINSQKAQKIQSILALPSNFKKITCSTCDMTYNPHISQDKLLHNKYHTNFINGIPWNYK
TDNDVLIIENFTLVETPKLNSTGKSLKLTKTRQTFKGSIICINKSNKRHIQKVELLLNMVNQ
ELNASQDSGQWKKPEFDRSKAFVIIIDSKAIGLCTTDTIQPDQGRWMIHKTQSIVPNQINK
NVVIGISRIWISRKWRQYGLGKKLLNVVLKNSIYSVQLLKNQVAFSQPSFSGGMLAKSFN
GVKHKSGEMLLPVYIE
Saccharomyces cerevisiae protein:SEQ ID NO: 57
MKARKSQRKAGSKPNLIQSKLQVNNGSKSNKIVKCDKCEMSYSSTSIEDRAIHEKYHTL
QLHGRKWSPNWGSIVYTERNHSRTVHLSRSTGTITPLNSSPLKKSSPSITHQEEKIVYVRP
DKSNGEVRAMTEIMTLVNNELNAPHDENVIWNSTTEEKGKAFVYIRNDRAVGIIIIENLY
GGNGKTSSRGRWMVYDSRRLVQNVYPDFKIGISRIWVCRTARKLGIATKLIDVARENIV
YGEVIPRYQVAWSQPTDSGGKLASKYNGIMHKSGKLLLPVYI
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Saccharomyces cerevisiae orf name: YGL122C
Saccharomyces cerevisiae gene name: NAB2
Candida albicans protein:SEQ ID NO: 10
MQFAPDNQIGKELQQNLIQEIQRRFNKPADDAVDIADYIIYLIVAKKSEQEIVAEVKDIADI
SIDVGFIGDVYLEIRKLEVKYNQPPAAVEEASQPQQEQQQQSQASVVAPQIPIGPKKQLTE
EEKIALRSQRFGTTTRLSGRGGRGGITKTRTDFRNGHNNKNFLDPKKLDQIISGANNGAIK
FVPLPPKGRCPDFPYCKNQNCEKAHPTKNCFNYPDCPNPPGTCNFLHPDQDQELIAKLET
SKKEFEEKKKNQLMVKQGSCKYGLKCAKENCPFAHPTPANPESGKIETLEWCPQGKNC
QDRNCTKSHPPPPTANSEKLLSAADLALEQCKFGSQCTNLKCPRRHATSAVPCRAGAEC
RRVDCTFSHPLKEPCRFGTKCTNKVCMYQHPEGRTIASHTWTRDGSGNNNSTSNRSF
Saccharomyces cerevisiae protein:SEQ ID NO: 9
MSQEQYTENLKVIVAEKLAGIPNFNEDIKYVAEYIVLLIVNGGTVESVVDELASLFDSVSR
DTLANVVQTAFFALEALQQGESAENIVSKIRMMNAQSLGQSDIAQQQQQQQQQQPDIA
QQQPQQQPQLQPLQPQLGTQNAMQTDAPATPSPISAFSGVVNAAAPPQFAPVDNSQRFT

Figure 79 (continued)

QRGGGAVGKNRRGGRGGNRGGRNNNSTRFNPLAKALGMAGESNMNFTPTKKEGRCRL
FPHCPLGRSCPHAHPTKVCNEYPNCPKPPGTCEFLHPNEDEELMKEMERTREEFQKRKA
DLLAAKRKPVQTGIVLCKFGALCSNPSCPFGHPTPANEDAKVIDLMWCDKNLTCDNPEC
RKAHSSLSKIKEVKPISQKKAAPPPVEKSLEQCKFGTHCTNKRCKYRHARSHIMCREGAN
CTRIDCLFGHPINEDCRFGVNCKNIYCLFRHPPGRVLPEKKGAAPNSNVPTNERPFALPEN
AIIEN
human genbank accession #: AAD42873
human protein:SEQ ID NO: 11
PQQLHLLSRQLEDPNGSFSNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISP
CKAFPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIQLCRYFPACKKMECPFYHP
KHCRFNTQCTRPDCTFYHPTINVPPRHALKWIRPQTSE
--

Saccharomyces cerevisiae orf name: YGR195W
Saccharomyces cerevisiae gene name: SKI6
Candida albicans protein:SEQ ID NO: 47
MELYSPEGLRIDGRRWNELRRFECRINTHPNSSDGSSYVEQGNTKVMCTVQGPIEPALRS
QQHSERANIEVNLNIASFSTFERKKRSRNERRLVELKTTLEKTFEESVMINLYPRTNIVINV
QVLCQDGGMLAAVINSITLALIDAGISMYDYVSGVSCGLYDQTPLLDVNNLEEHDMSC
Saccharomyces cerevisiae protein:SEQ ID NO: 46
MSRLEIYSPEGLRLDGRRWNELRRFESSINTHPHAADGSSYMEQGNNKIITLVKGPKEPR
LKSQMDTSKALLNVSVNITKFSKFERSKSSHKNERRVLEIQTSLVRMFEKNVMLNIYPRT
VIDIEIHVLEQDGGIMGSLINGITLALIDAGISMFDYISGISVGLYDTTPLLDTNSLEENAMS
TVTLGVVGKSEKLSLLLVEDKIPLDRLENVLAIGIAGAHRVRDLMDEELRKHAQKRVSN
ASAR
human genbank accession #: BAA91279
human protein:SEQ ID NO: 48
MAGLELLSDQGYRVDGRRAGELRKIQARMGVFAQADGSAYIEQGNTKALAVVYGPHEI
RSRARALPDRALVNCQYSSATFSTGERKRRPHGDRKSCEMGLQLRQTFEAAILTQLHPR
SQIDIYVQVLQADGGTYAACVNAATLAVLDAGIPMRDFVCACSAGFVDGTALADLSHV
EEAAGGPQLALALLPASGQIALLEMDARLHEDHLERVLEAAAQAARDVHTLLDRVVRQ
HVREASILLGDG
--

Saccharomyces cerevisiae orf name: YHR005C-A
Saccharomyces cerevisiae gene name: TIM10
Candida albicans protein:SEQ ID NO: 69
MFGLGGTTPQISSQQKLQAAEAELDMVTGMFNALVSQCHTKCINKSYNEADISKQESLC
LDRCVAKYFETNVQVGENMQKLGQSGQFMGRR
Saccharomyces cerevisiae protein:SEQ ID NO: 68
MSFLGFGGGQPQLSSQQKIQAAEAELDLVTDMFNKLVNNCYKKCINTSYSEGELNKNES
SCLDRCVAKYFETNVQVGENMQKMGQSFNAAGKF

Figure 79 (continued)

human genbank accession #: NP_036588
human protein:SEQ ID NO: 70
MDPLRAQQLAAELEVEMMADMYNRMTSACHRKCVPPHYKEAELSKGESVCLDRCVSK
YLDIHERMGKKLTELSMQDEELMKRVQQSSGPA
--

Saccharomyces cerevisiae orf name: YIR012W
Saccharomyces cerevisiae gene name:SQT1
Candida albicans protein:SEQ ID NO: 27
MSHQQEDVVDDTQEEYINVNEVAEEVADDDQAPPDEEDEEMELDDEHETLEIDMSNNS
WTYFDKHTDSIFTIFSHPKLPMVLTEGGDNTAYLWTTHTQPPRFVGEITGHKESVISGGFT
ADGKFVVTADMNGLIQVFKATKGGEQWVKFGELDEVEEVLFVTVHPTLPFFAFGATDG
SIWVYQIDESSKLLVQIMSGFSHTLKCNGAVFIQGKDENDLTLVSISEDGTVVNWNCFTG
QVNYKLQPHDDFKGVESPWVTVKVHGNLVAIGGRDGQLSIVNNDTGKIVHTLKTLDNV
DDIAELSIEALSWCESKNINLLAVGLVSGDXLLFDTQQWRLRKNLKVDDAITKLQFVGET
PILVGNSMDGKXYKWEPRTGEKXFAGVGTNMGSYGLCYFKIEVKNWLLLVDERCFHW
SLFMK
Saccharomyces cerevisiae protein:SEQ ID NO: 26
MEPQEEFITTEEVEQEIVPTVEVEQDVPVDIEGENDDDEMMNDDEEALEVDMSNNSLT
YFDKHTDSVFAIGHHPNLPLVCTGGGDNLAHLWTSHSQPPKFAGTLTGYGESVISCSFTS
EGGFLVTADMSGKVLVHMGQKGGAQWKLASQMQEVEEIVWLKTHPTIARTFAFGATD
GSVWCYQINEQDGSLEQLMSGFVHQQDCSMGEFINTDKGENTLELVTCSLDSTIVAWNC
FTGQQLFKITQAEIKGLEAPWISLSLAPETLTKGNSGVVACGSNNGLLAVINCNNGGAILH
LSTVIELKPEQDELDASIESISWSSKFSLMAIGLVCGEILLYDTSAWRVRHKFVLEDSVTKL
MFDNDDLFASCINGKVYQFNARTGQEKFVCVGHNMGVLDFILLHPVANTGTEQKRKVI
TAGDEGVSLVFEVPN
human genbank accession #: NP_001078
human protein:SEQ ID NO: 28
MDSGRRLGPEKWIRRLRRMESESESGAAADTPPLETLSFHGDEEIIEVVELDPGPPDPDDL
AQEMEDVDFEEEEEEEGNEEGWVLEPQEGVVGSMEGPDDSEVTFALHSASVFCVSLDP
KTNTLAVTGGEDDKAFVWRLSDGELLFECAGHKDSVTCAGFSHDSTLVATGDMSGLLK
VWQVDTKEEVWSFEAGDLEWMEWHPRAPVLLAGTADGNTWMWKVPNGDCKTFQGP
NCPATCGRVLPDGKRAVVGYEDGTIRIWDLKQGSPIHVLKGTEGHQGPLTCVAANQDG
SLILTGSVDCQAKLVSATTGKVVGVFRPETVASQPSLGEGEESESNSVESLGFCSVMPLA
AVGYLDGTLAIYDLATQTLRHQCQHQSGIVQLLWEAGTAVVYTCSLDGIVRLWDARTG
RLLTDYRGHTAEILDFALSKDASLVVTTSGDHKAKVFCVQRPDRDFSPDGALLATASYD
TRVYIWDPHNGDILMEFGHLFPPPTPIFAGGANDRWVRSVSFSHDGLHVASLADDKMVR
FWRIDEDYPVQVAPLSNGLCCAFSTDGSVLAAGTHDGSVYFWATPRQVPSLQHLCRMSI
RRVMPTQEVQELPIPSKLLEFLSYRI
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Saccharomyces cerevisiae orf name: YKL186C

Figure 79 (continued)

Saccharomyces cerevisiae gene name: MTR2
Candida albicans protein:SEQ ID NO:16
MNQDPTQQLEPFLKRFLASLDLLYTQPTSQPFPNVESYATQLGSNLKRSSAIIVNGQPIIPS
PQEDCKLQFQKKWLQTPLSSHQLTSYDGHLIPGTGTFVVHFSAKVRFDQSGRNRLGESA
DLFQENNSIVSKTNQRPIWGSWFGVDVNLVVDENVMQDGEIINSMDYRFTYVPNDSIIKV
Saccharomyces cerevisiae protein:SEQ ID NO:15
MNTNSNTMVMNDANQAQITATFTKKILAHLDDPDSNKLAQFVQLFNPNNCRIIFNATPF
AQATVFLQMWQNQVVQTQHALTGVDYHAIPGSGTLICNVNCKVRFDESGRDKMGQDA
TVPIQPNNTGNRNRPNDMNKPRPLWGPYFGISLQLIIDDRIFRNDFNGVISGFNYNMVYK
PEDSLLKI
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Saccharomyces cerevisiae orf name: YKR062W
Saccharomyces cerevisiae gene name: TFA2
Candida albicans protein:SEQ ID NO:7
MSDLSAQLSAFKNKIKSGPSVIVPRKATFTQSPSSPLSSSTTTTTSKNDANVKKRSTTDSV
TRVLKKQKANMGEMTGSHLSTQLHLAVEYIKEHDQPISVEKLQNYLSFDISHTLLPLLNEI
DRVKYDESKGTLEYVSLHNIRSSDDVLEFLRRQTTFKGTSVKELKDGWAGCVAAIDELE
SQGKILVLRNKKENAPRLVWANNGGELGYIDTEFKDMWDQVKLPEPDVLYQKLLDQGL
KPTGADPNLIKKQPQQKEKKQKKARRGKITNTHMKGILKDYSQLV
Saccharomyces cerevisiae protein:SEQ ID NO:6
MSKNRDPLLANLNAFKSKVKSAPVIAPAKVGQKKTNDTVITIDGNTRKRTASERAQENT
LNSAKNPVLVDIKKEAGSNSSNAISLDDDDDDEDFGSSPSKKVRPGSIAAAALQANQTDI
SKSHDSSKLLWATEYIQKKGKPVLVNELLDYLSMKKDDKVIELLKKLDRIEFDPKKGTF
KYLSTYDVHSPSELLKLLRSQVTFKGISCKDLKDGWPQCDETINQLEEDSKILVLRTKKD
KTPRYVWYNSGGNLKCIDEEFVKMWENVQLPQFAELPRKLQDLGLKPASVDPATIKRQ
TKRVEVKKKRQRKGKITNTHMTGILKDYSHRV
human genbank accession #: NP_002086
human protein:SEQ ID NO:8
MDPSLLRERELFKKRALSTPVVEKRSASSESSSSSSKKKKTKVEHGGSSGSKQNSDHSNG
SFNLKALSGSSGYKFGVLAKIVNYMKTRHQRGDTHPLTLDEILDETQHLDIGLKQKQWL
MTEALVNNPKIEVIDGKYAFKPKYNVRDKKALLRLLDQHDQRGLGGILLEDIEEALPNSQ
KAVKALGDQILFVNRPDKKKILFFNDKSCQFSVDEEFQKLWRSVTVDSMDEEKIEEYLK
RQGISSMQESGPKKVAPIQRRKKPASQKKRRFKTHNEHLAGVLKDYSDITSSK
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Saccharomyces cerevisiae orf name: YLR078C
Saccharomyces cerevisiae gene name: BOS1
Candida albicans protein:SEQ ID NO:18
MNSIYNHGLKQTQTITKDLTQFEKNLSTSPLSLQGAITTSLTAFRKTIKEYSDLLEKNVND
TSYTKHENRLNKFNQDLNEFTLKFDTLKKQRDIQVQEANKQELLGRRHISTTATAALGST
SSDNPYESSSNPSQQQQQQLQDEQNTMSYREGLYHEKNSLERGSEQLDRILEMGQQAFE

Figure 79 (continued)

DIVEQNEILRKVQTKFEESLITLGVSQGTIRSVERRAKQDKWLFWFCVVVMLVVFYYI
Saccharomyces cerevisiae protein:SEQ ID NO:17
MNALYNHAVKQKNQLQQELARFEKNSVTAPISLQGSISATLVSLEKTVKQYAEHLNRYK
EDTNAEEIDPKFANRLATLTQDLHDFTAKFKDLKQSYNENNSRTQLFGSGASHVMDSDN
PFSTSETIMNKRNVGGASANGKEGSSNGGGLPLYQGLQKEQSVFERGNAQLDYILEMGQ
QSFENIVEQNKILSKVQDRMSNGLRTLGVSEQTITSINKRVFKDKLVFWIALILLIIGIYYVL
KWLR
human genbank accession #: NP_003560
human protein:SEQ ID NO:19
MSYTPGVGGDPTQLAQRISSNIQKITQCSVEIQRTLNQLGTPQDSPELRQQLQQKQQYTN
QLAKETDKYIKEFGSLPTTPSEQRQRKIQKDRLVAEFTTSLTNFQKVQRQAAEREKEFVA
RVRASSRVSGSFPEDSSKERNLVSWESQTQPQVQVQDEEITEDDLRLIHERESSIRQLEAD
IMDINEIFKDLGMMIHEQGDVIDSIEANVENAEVHVQQANQQLSRAADYQRKSRKTLCIII
LILVIGVAIISLIIWGLNH
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Saccharomyces cerevisiae orf name: YLR291C
Saccharomyces cerevisiae gene name: GCD7
Candida albicans protein:SEQ ID NO:44
MSKLLTPEILALIDPVVSSLKRHQLVDDKEIALTIAQLLMKVISAARWSNTYDLIELIRQVG
VIFTEAYPRKVIPGNIVRRVLALIRDETETETETETEQTDNIPMMSSMFSLLATHNKNETIK
EQTQLQLKKQTSDMRAIIIQGIRDLVDEISNVNDGIETMAVDLIHDDEILLTPTPNSETVQH
FLIKARLKRKFTVVVTENYPNDIKAAHKFVKTLAEHNIETILIPDTTIYAVMSRVGKVIIGT
NAVFANGGCLSNSGVANVVECAKEHRTPVFAVAGLFKLSPLYPFTRNDLIEVGNSGKVL
NYDDFELVQNVDVVTNPLEDYIPPQHIDIFMTNIGGFSPSFIYRIVLDNYKAEDNKLE
Saccharomyces cerevisiae protein:SEQ ID NO:43
MSSQAFTSVHPNAATSDVNVTIDTFVAKLKRRQVQGSYAIALETLQLLMRFISAARWNH
VNDLIEQIRDLGNSLEKAHPTAFSCGNVIRRILAVLRDEVEEDTMSTTVTSTSVAEPLISSM
FNLLQKPEQPHQNRKNSSGSSSMKTKTDYRQVAIQGIKDLIDEIKNIDEGIQQIAIDLIHDH
EILLTPTPDSKTVLKFLITARERSNRTFTVLVTEGFPNNTKNAHEFAKKLAQHNIETLVVP
DSAVFALMSRVGKVIIGTKAVFVNGGTISSNSGVSSVCECAREFRTPVFAVAGLYKLSPL
YPFDVEKFVEFGGSQRILPRMDPRKRLDTVNQITDYVPPENIDIYITNVGGFNPSFIYRIAW
DNYKQIDVHLDKNKA
human genbank accession #: AAC42002
human protein:SEQ ID NO:45
MPGSAAKGSELSERIESFVETLKRGGGPRSSEEMARETLGLLRQIITDHRWSNAGELMELI
RREGRRMTAAQPSETTVGNMVRRVLKIIREEYGRLHGRSDEDQQESLHKLLTSGGLNED
FSFHYAQLQSNIIEAINELLVELEGTMENIAAQALEHIHSNEVIMTIGFSRTVEAFLKEAAR
KRKFHVIVAECAPFCQGHEMAVNLSKAGIETTVMTAAIFAVMSRVNKVIIGTKTILANGA
LRAVTGTHTLALAAKHHSTPLIVCAPMFKLSPQFPNEEDSFHKFVAPEEVLPFTEGDILEK
VSVHCPVFDYVPPELITLFISNIGGNAPSYIYRLMSELYHPDDHVL
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Figure 79 (continued)

Saccharomyces cerevisiae orf name: YMR005W
Saccharomyces cerevisiae gene name: MPT1
Candida albicans protein:SEQ ID NO:13
MSHKSMTSTPQESSNLKRQLENSEDSSSPNKRSKTETTTENQSSWESDFNSLPVELLQTE
TNGTSPAPAPATPIDTTNASSTKERDQDTSKLNDAIAAAGVDIQQEEEILLQQQLNRKSAE
GMASNLKSVIRSSKLPPFLHNYHLAAFIDKVAKQNGIQQNFLMDGEMLELISAACETWLS
NLATKTIILSRHRRRGIPVINKKSGSSSVPRSEISKELRSLALKQKEMEEKRVNKRVMLGL
EKSTKDASKNDENGESKAGAEETLHRAANATAAMMTMNPGRKKYSWMTSSATAGGG
SDFGKSSGGSSKDSGKHQSPIISVRGDNGLRFREIRSGNSIIMKDLLGAIEDEKMGTRNA
Saccharomyces cerevisiae protein:SEQ ID NO:12
MANSPKKPSDGTGVSASDTPKYQHTVPETKPAFNLSPGKASELSHSLPSPSQIKSTAHVSS
THNDAAGNTDDSVLPKNVSPTTNLRVESNGDTNNMFSSPAGLALPKKDDKKKNKGTSK
ADSKDGKASNSSGQNAQQQSDPNKMQDVLFSAGIDVREEEALLNSSINASKSQVQTNN
VKIPNHLPFLHPEQVSNYMRKVGKEQNFNLTPTKNPEILDMMSSACENYMRDILTNAIVI
SRHRRKAVKINSGRRSEVSAALRAIALIQKKEEERRVKKRIALGLEKEDYENKIDSEETLH
RASNVTAGLRAGSKKQYGWLTSSVNKPTSLGAKSSGKVASDITARGESGLKFREAREEP
GIV
human genbank accession #: CAA72189
human protein:SEQ ID NO:14
MAAGSDLLDEVFFNSEVDEKVVSDLVGSLESQLAASAAHHHHLAPRTPEVRAAAAGAL
GNHVVSGSPAGAAGAGPAAPAEGAPGAAPEPPPAGRARPGGGGPQRPGPPSPRRPLVPA
GPAPPAAKLRPPPEGSAGACAPVPAAAAVAAGPEPAPAGPAKPAGPAALAARAGPGPGP
GPGPGPGPGKPAGPGAAQTLNGSAALLNSHHAAAPAVSLVNNGPAALLPLPKPAAPGTV
IQTPPFVGAAAPPAPAAPSPPAAPAPAAPAAAPPPPPPAPATLARPPGHPAGPPTAAPAVP
PPAAAQNGGSAGAAPAPAPAAGGPAGVSGQPGPGAAAAAPAPGVKAESPKRVVQAAP
PAAQTLAASGPASTAASMVIGPTMQGALPSPAAVPPPAPGTPTGLPKGAAGAVTQSLSR
TPTATTSGIRATLTPTVLAPRLPQPPQNPTNIQNFQLPPGMVLVRSENGQLLMIPQQALAQ
MQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIARQVTPTTIIKQVSQAQTTVQP
SATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQRTVPGATTTSSAATETMENVK
KCKNFLSTLIKLASSGKQSTETAANVKELVQNLLDGKIEAEDFTSRLYRELNSSPQPYLVP
FLKRSLPALRQLTPDSAAFIQQSQQQPPPPTSQATTALTAVVLSSSVQRTAGKTAATVTS
ALQPPVLSLTQPTQVGVGKQGQPTPLVIQQPPKPGALIRPPQVTLTQTPMVALRQPHNRI
MLTTPQQVNLSEESARILATNSELVGTLTRSCKDETFLLQAPLQRRILEIGKKHGITELHPD
VVSYVSHATQQRLQNLVEKISETAQQKNFSYKDDDRYEQASDVRAQLKFFEQLDQIEKQ
RKDEQEREILMRAAKSRSRQEDPEQLRLKQKAKEMQQQELAQMRQRDANLTALAAIGP
RKKRKVDCPGPGSGAEGSGPGSVVPGSSGVGTPRQFTRQRITRVNLRDLIFCLENERETS
HSLLLYKAFLK
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Saccharomyces cerevisiae orf name: YMR131C
Saccharomyces cerevisiae gene name: RSA2
Candida albicans protein:SEQ ID NO:24

Figure 79 (continued)

MSKRSAEDDLSGNGSTSHTAVKTNKDSLPTTTNGKEEEPDNMDIGEFEDPYGDEFESDEI
IELDDNNDEEDDEMIDENSTQAKIEELEAKEQEQEQQSSIYLPHKSKPLGPDEVLEADPTV
YEMLHNINLPWPCLTVDILPDSLGNERRSYPATVYLATATQAAKAKDNELLAMKASSLA
KTLVKDENEEDEEDEDDDDDVDSDPILDSESIPLRHTTNRIRVSPHAQQTGEYLTASMSE
NGEVYIFDLLAQYKAFDTPGYMIPKSSKRPIHTIRAHGNVEGYGLDWSPLVNTGALLSGD
MSGRIYLTNRTTSSWTTDKTPFFASQSSIEDIQWSTGETTVFATGGCDGYICIWDTRSKKH
KPALSVIASKSDVNVISWSSKINHLLASGHDDGSWGVWDLRNFTNNTTSNPSPVANYDF
Saccharomyces cerevisiae protein:SEQ ID NO:23
MSKRSIEVNEEQDRVVSAKTESHSVPAIPASEEQDAPKNDLEEQLSDEFDSDGEIIEIDGD
DEINDEDDLRKKQEEAETLVQKDQSEGNKEKIQELYLPHMSRPLGPDEVLEADPTVYEM
LHNVNMPWPCLTLDVIPDTLGSERRNYPQSILLTTATQSSRKKENELMVLALSNLAKTLL
KDDNEGEDDEEDDEDDVDPVIENENIPLRDTTNRLKVSPFAISNQEVLTATMSENGDVYI
YNLAPQSKAFSTPGYQIPKSAKRPIHTVKNHGNVEGYGLDWSPLIKTGALLSGDCSGQIY
FTQRHTSRWVTDKQPFTVSNNKSIEDIQWSRTESTVFATAGCDGYIRIWDTRSKKHKPAI
SVKASNTDVNVISWSDKIGYLLASGDDNGTWGVWDLRQFTPSNADAVQPVAQYDFHK
GAITSIAFNPLDESIVAVGSEDNTVTLWDLSVEADDEEIKQQAAETKELQEIPPQLLFVHW
QKEVKDVKWHKQIPGCLVSTGTDGLNVWKTISV
human genbank accession #: NP_005601
human protein:SEQ ID NO:25
MADKEAAFDDAVEERVINEEYKIWKKNTPFLYDLVMTHALEWPSLTAQWLPDVTRPEG
KDFSIHRLVLGTHTSDEQNHLVIASVQLPNDDAQFDASHYDSEKGEFGGFGSVSGKIEIEI
KINHEGEVNRARYMPQNPCIIATKTPSSDVLVFDYTKHPSKPDPSGECNPDLRLRGHQKE
GYGLSWNPNLSGHLLSASDDHTICLWDISAVPKEGKVVDAKTIFTGHTAVVEDVSWHLL
HESLFGSVADDQKLMIWDTRSNNTSKPSHSVDAHTAEVNCLSFNPYSEFILATGSADKT
VALWDLRNLKLKLHSFESHKDEIFQVQWSPHNETILASSGTDRRLNVWDLSKIGEEQSPE
DAEDGPPELLFIHGGHTAKISDFSWNPNEPWVICSVSEDNIMQVWQMAENIYNDEDPEG
SVDPEGQGS

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Saccharomyces cerevisiae orf name: YMR235C
Saccharomyces cerevisiae gene name: RNA1
Candida albicans protein:SEQ ID NO:41
MASVEVELGVTPETTYSISGKQLKFDSESDIAPYIKELTEKENVKKVDFSGNTIGIEASKA
LSEALLKHKDTIVEINFSDLYTGRLNTEIPQSLEYLLPALSKLPNLKLINLSDNAFGLQTIDP
IEAYLAKAVSIEHLILSNNGMGPFAGSRIGGSLFKLAKAKKAEGKESLKTFICGRNRLENG
SVNYLSVGLRNHKDLEVVRLYQNGIRPAGISKLVEQGLSNNKKLKVLDLQDNTITTRGAI
HIAESLSNWPLLVELNLNDSLLKNKGSLKLVEAFHAGDEKPQLITLKLQYNELETDSLRV
LADAIASKLPQLKFLELNGNRFEEDSEHIDKINGIFEERGYGEIDELDELEELDSEEEEDDE
DDEGEDDTLEEDLDLTQLEEELAGVSLEDKDGNVDEIAEELSKTHIKZ
Saccharomyces cerevisiae protein:SEQ ID NO:40
MATLHFVPQHEEEQVYSISGKALKLTTSDDIKPYLEELAALKTCTKLDLSGNTIGTEASEA
LAKCIAENTQVRESLVEVNFADLYTSRLVDEVVDSLKFLLPVLLKCPHLEIVNLSDNAFG

Figure 79 (continued)

LRTIELLEDYIAHAVNIKHLILSNNGMGPFAGERIGKALFHLAQNKKAASKPFLETFICNTF
TKHASLILAKALPTWKDSLFELNLNDCLLKTAGSDEVFKVFTEVKFPNLHVLKFEYNEM
AQETIEVSFLPAMEKGNLPELEKLEINGNRLDEDSDALDLLQSKFDDLEVDDFEEVDS
human genbank accession #: CAA57714
human protein:SEQ ID NO:42
MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNT
VGVEAARVIAKALEKKSELKRCHWSDMFTGRLRTEIPPALISLGEGLITAGAQLVELDLS
DNAFGPDGVQGFEALLKSSACFTLQELKLNNCGMGIGGGKILAAALTECHRKSSAQGKP
LALKVFVAGRNRLENDGATALAEAFRVIGTLEEVHMPQNGINHPGITALAQAFAVNPLL
RVINLNDNTFTEKGAVAMAETLKTLRQVEVINFGDCLVRSKGAVAIADAIRGGLPKLKE
LNLSFCEIKRDAALAVAEAMADKAELEKLDLNGNTLGEEGCEQLQEVLEGFNMAKVLA
SLSDDEDEEEEEEGEEEEEEAEEEEEEDEEEEEEEEEEEEEEPQQRGQGEKSATPSRKILDP
NTGEPAPVLSSPPPADVSTFLAFPSPEKLLRLGPKSSVLIAQQTDTSDPEKVVSAFLKVSSV
FKDEATVRMAVQDAVDALMQKAFNSSSFNSNTFLTRLLVHMGLLKSEDKVKAIANLYG
PLMALNHMVQQDYFPKALAPLLLAFVTKPNSALESCSFARHSLLQTLYKV
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Saccharomyces cerevisiae orf name: YMR309C
Saccharomyces cerevisiae gene name: NIP1
Candida albicans protein:SEQ ID NO:50
MSRFFVSGYTSDSSSEEEDLLSTSEEELLSSSDEGEDNESDSSFFGEDDDESEESSSDDED
GRPSGPAYFLKKSFLKGAGGDDSDSDSDDEGRKVVKSAKDKLLDDMKSSIEIINSNKYN
NNWSIVLGEFDKFGRFLIRCNQTNLGTPKFYIKLLTSLDNSITETSNNERDDKTLKADEAR
AFNTLRQRIKKQIREFQVYYDLYKENPEEFDENEDEPLESVQAGLNDNVKNEADNSNVG
ALASNRVLSPIFHTLKTISESRGKKNIDKLEQIATLEKLLEANVSKSSPFELISIYQMLLSVR
FDASSNQAFMPLEQWQKNEHDLGKLLDLLEANVDTYQVSELGSTTDDIDIEPVANAQGV
KVIFGSITSSIDRLDDELTKSLQHTDPHSIEYVERLKDESTIYNLIVRGQAYVESITPEDVKY
NSEQLARIVLRRLEHIYYKPKQLIKANEEEAWRNIEYNSSIVSKGSSVDEVIDQLTEFLQK
QQKNKTYGKHAILFSIYYYAVNSQYEKAKELFLRSQFYSNINSAESSLQVQYNRALVQL
GLSAFRAGSIEESHKILNEIVNSQRSKELLGQGFNSKFPNQATVLERQKLLPFHQHINLELL
ECVFMTCSLLIEIPTLAAIANNHKDSKRKNASLKSFKSKLDFHDRQFFTGPPESIKDHIVHA
SIALQKGDWLKSYNLLSSIKIWKLFPDNDKLLAMMKNQLQIEGLRTYIFTYKSVFKKLSIE
KLQQIFQLSKDEVVSILEKMITTGNVSGGEIIDNKFISFTSTTEPQRSKLQELAIVLNEKIQL
LTEKNEKTQSNGYGKKQQNKDQQNQQQQNQNQNQQQQQNQQQQQQQQSSQQQSNNI
LSEESANKFRYANVNSNNDEFQATA
Saccharomyces cerevisiae protein:SEQ ID NO:49
MSRFFSSNYEYDVASSSSEEDLLSSSEEDLLSSSSSESELDQESDDSFFNESESESEADVDS
DDSDAKPYGPDWFKKSEFRKQGGGSNKFLKSSNYDSSDEESDEEDGKKVVKSAKEKLL
DEMQDVYNKISQAENSDDWLTISNEFDLISRLLVRAQQQNWGTPNIFIKVVAQVEDAVN
NTQQADLKNKAVARAYNTTKQRVKKVSRENEDSMAKFRNDPESFDKEPTADLDISANG
FTISSSQGNDQAVQEDFFTRLQTIIDSRGKKTVNQQSLISTLEELLTVAEKPYEFIMAYLTLI
PSRFDASANLSYQPIDQWKSSFNDISKLLSILDQTIDTYQVNEFADPIDFIEDEPKEDSDGV

Figure 79 (continued)

KRILGSIFSFVERLDDEFMKSLLNIDPHSSDYLIRLRDEQSIYNLILRTQLYFEATLKDEHDL
ERALTRPFVKRLDHIYYKSENLIKIMETAAWNIIPAQFKSKFTSKDQLDSADYVDNLIDGL
STILSKQNNIAVQKRAILYNIYYTALNKDFQTAKDMLLTSQVQTNINQFDSSLQILFNRVV
VQLGLSAFKLCLIEECHQILNDLLSSSHLREILGQQSLHRISLNSSNNASADERARQCLPYH
QHINLDLIDVVFLTCSLLIEIPRMTAFYSGIKVKRIPYSPKSIRRSLEHYDSLKTYFFSFKRFY
SSFSVAKLAELFDLPENKVVEVLQSVIAELEIPAKLNDEKTIFVVEK
human genbank accession #: AAD03462
human protein:SEQ ID NO:51
MSRFFTTGSDSESESSLSGEELVTKPVGGNYGKQPLLLSEDEEDTKRVVRSAKDKRFEEL
TNLIRTIRNAMKIRDVTKCLEEFELLGKAYGKAKSIVDKEGVPRFYIRILADLEDYLNELW
EDKEGKKKMNKNNAKALSTLRQKIRKYNRDFESHITSYKQNPEQSADEDAEKNEEDSE
GSSDEDEDEDGVSAATFLKKKSEAPSGESRKFLKKMDDEDEDSEDSEDDEDWDTGSTSS
DSDSEEEEGKQTALASRFLKKAPTTDEDKKAAEKKREDKAKKKHDRKSKRLDEEEEDN
EGGEAAENNLGEGVIVKIKFNIIASLYDYNPNLATYMKPEMWGKCLDCINELMDILFANP
NIFVGENILEESENLHNADQPLRVRGCILTLVERMDEEFTKIMQNTDPHSQEYVEHLKDE
AQVCAIIERVQRYLEEKGTTEEVCRIYLLRILHTYYKFDYKAHQRQLTPPEGSSKSEQDQ
AENEGEDSAVLMERLCKYIYAKDRTDRIRTCAILCHIYHHALHSRWYQARDLMLMSHL
QDNIQHADPPVQILYNRTMVQLGICAFRQGLTKDAHNALLDIQSSGRAKELLGQGLLLRS
LQERNQEQEKVERRRQVPFHLHINLELLECVYLVSAMLLEIPYMAAHESDARRRMISKQ
FHHQLRVGERQPLLGPPESMREHVVAASKAMKMGDWKTCHSFIINEKMNGKVWDLFP
EADKVRTMLVRKIQEESLRTYLFTYSSVYDSISMETLSDMFELDLPTVHSIISKMIINEELM
ASLDQPTQTVVMHRTEPTAQQNLALQLAEKLGSLVENNERVFDHKQGTYGGYFRDQK
DGYRKNEGYMRRGGYRQQQSQTAY
--

Saccharomyces cerevisiae orf name: YNL036W
Saccharomyces cerevisiae gene name: NCE103
Candida albicans protein:SEQ ID NO:56
MGRENILKYQLEHDHESDLVTEKDQSLLLDNNNNLNGMNNTIKTHPVRVSSGNHNNFPF
TLSSESTLQDFLNNNKFFVDSIKHNHGNQIFDLNGQGQSPHTLWIGCSDSRAGDQCLATL
PGEIFVHRNIANIVNANDISSQGVIQFAIDVLKVKKIIVCGHTDCGGIWASLSKKKIGGVLD
LWLNPVRHIRAANLKLLEEYNQDPKLKAKKLAELNVISSVTALKRHPSASVALKKNEIEV
WGMLYDVATGYLSQVEIPQDEFEDLFHVHDEHDEEEYNPH
Saccharomyces cerevisiae protein:SEQ ID NO:55
MSATESSSIFTLSHNSNLQDILAANAKWASQMNNIQPTLFPDHNAKGQSPHTLFIGCSDSR
YNENCLGVLPGEVFTWKNVANICHSEDLTLKATLEFAIICLKVNKVIICGHTDCGGIKTCL
TNQREALPKVNCSHLYKYLDDIDTMYHEESQNLIHLKTQREKSHYLSHCNVKRQFNRIIE
NPTVQTAVQNGELQVYGLLYNVEDGLLQTVSTYTKVTPK
--

Saccharomyces cerevisiae orf name: YNL126W
Saccharomyces cerevisiae gene name: SPC98

Figure 79 (continued)

Candida albicans protein:SEQ ID NO:35
MALNKVQLIKLYSNRLVKSLVPVEFGEAFIQSIINDLQTTLLNTSSEEQNLSIIINKLKMQF
LSNNLKNEWVEFQNIVNSLSKFKSLDQICNYLAFLDALRDEKPEDILSTSTASLSPGKQNV
MINTVNTALTLSQLIEPYYDTLSEQTILTYLPYTMLGLDSKIFTFSNNYTRLEIPKDINNSFS
SLLREVFEFAILYKQLAIVVDRYKGTLVLAIKTAYIAILEAQLNKYVNDINNIFNNKPNSIL
VVYNSIFPWISILRFLYRVSNRLNRLDGYEFLTFIYSFTNHGDPKIRGIAVTAFTEVVKPYY
NIVEHWIVKGELIDNNNEFFIIFDQEQNEFNSIIKLLPKKIPAFIKSSDKIFQIGTTLIFLNKYC
RELKWVNQYNVKYSAILFNNHQGLASMTTNEMIKLIDLQYNEILTFLTQIIQGNNKLLTH
VYNIKRYYFMETNDFIDAIMVKGKDVFNESSVNISSTYLRKVLQDAIQISSVKNFEYVDR
LDSRVLNPQHGNLGWESFTIEYKIDDLPMSYLFEGHQHLQYLKMFHFLWKLRQLNNLLN
WHFEMFNELNHNVVTKLSSRNRRPLAKSLSIITSIRFHFTQFLNELIAYLSYDVIEENFQQH
IVRKLFYNKNDQDLLLNKLFMNLLEIDPNNDLPKFNVNLLTIDELVELHGTYIDSIINSSLL
NEKLKGNETNISYIDQIFDILQTIFNFIIQVRNS
Saccharomyces cerevisiae protein:SEQ ID NO:34
MELEPTLFGIIEALAPQLLSQSHLQTFVSDVVNLLRSSTKSATQLGPLIDFYKLQSLDSPET
TIMWHKIEKFLDALFGIQNTDDMVKYLSVFQSLLPSNYRAKIVQKSSGLNMENLANHEH
LLSPVRAPSIYTEASFENMDRFSERRSMVSSPNRYVPSSTYSSVTLRQLSNPYYVNTIPEE
DILKYVSYTLLATTSALFPFDHEQIQIPSKIPNFESGLLHLIFEAGLLYQSLGYKVEKFRML
NISPMKKALIIEISEELQNYTAFVNNLVSSGTVVSLKSLYREIYENIIRLRIYCRFTEHLEELS
GDTFLIELNIFKSHGDLTIRKIATNLFNSMISLYYEYLMNWLTKGLLRATYGEFFIAENTDT
NGTDDDFIYHIPIEFNQERVPAFIPKELAYKIFMIGKSYIFLEKYCKEVQWTNEFSKKYHVL
YQSNSYRGISTNFFEIINDQYSEIVNHTNQILNQKFHYRDVVFALKNILLMGKSDFMDALI
EKANDILATPSDSLPNYKLTRVLQEAVQLSSLRHLMNSPRNSSVINGLDARVLDLGHGSV
GWDVFTLDYILYPPLSLVLNVNRPFGRKEYLRIFNFLWRFKKNNYFYQKEMLKSNDIIRS
FKKIRGYNPLIRDIINKLSRISILRTQFQQFNSKMESYYLNCIIEENFKEMTRKLQRTENKSQ
NQFDLIRLNNGTIELNGILTPKAEVLTKSSSSKPQKHAIEKTLNIDELESVHNTFLTNILSHK
LFATNTSEISVGDYSGQPYPTSLVLLLNSVYEFVKVYCNLNDIGYEIFIKMNLNDHEASNG
LLGKFNTNLKEIVSQYKNFKDRLYIFRADLKNDGDEELFLLSKSLR
human genbank accession #: AAC39727
human protein:SEQ ID NO:36
MATPDQKSPNVLLQNLCCRILGRSEADVAQQFQYAVRVIGSNFAPTVERDEFLVAEKIK
KELIRQRREADAALFSELHRKLHSQGVLKNKWSILYLLLSLSEDPRRQPSKVSSYATLFA
QALPRDAHSTPYYYARPQTLPLSYQDRSAQSAQSSGSVGSSGISSIGLCALSGPAPAPQSL
LPGQSNQAPGVGDCLRQQLGSRLAWTLTANQPSSQATTSKGVPSAVSRNMTRSRREGD
TGGTMEITEAALVRDILYVFQGIDGKNIKMNNTENCYKVEGKANLSRSLRDTAVRLSEL
GWLHNKIRRYTDQRSLDRSFGLVGQSFCAALHQELREYYRLLSVLHSQLQLEDDQGVNL
GLESSLTLRRLLVWTYDPKIRLKTLAALVDHCQGRKGGELASAVHAYTKTGDPYMRSL
VQHILSLVSHPVLSFLYRWIYDGELEDTYHEFFVASDPTVKTDRLWHDKYTLRKSMIPSF
MTMDQSRKVLLIGKSINFLHQVCHDQTPTTKMIAVTKSAESPQDAADLFTDLENAFQGKI
DAAYFETSKYLLDVLNKKYSLLDHMQAMRRYLLLGQGDFIRHLMDLLKPELVRPATTL
YQHNLTGILETAVRATNAQFDSPEILRRLDVRLLEVSPGDTGWDVFSLDYHVDGPIATVF
TRECMSHYLRVFNFLWRAKRMEYILTDIRKGHMCNAKLLRNMPEFSGVLHQCHILASE

Figure 79 (continued)

MVHFIHQMQYYITFEVLECSWDELWNKVQQAQDLDHIIAAHEVFLDTIISRCLLDSDSRA
LLNQLRAVFDQIIELQNAQDAIYRAALEELQRRLQFEEKKKQREIEGQWGVTAAEEEEEN
KRIGEFKESIPKMCSQLRILTHFYQGIVQQFLVLLTTSSDESLRFLSFRL--

Saccharomyces cerevisiae orf name: YNL282W
Saccharomyces cerevisiae gene name: POP3
Candida albicans protein:SEQ ID NO:5
MNKSNKVKKPSVAKVSTKAASSSLKSQEAKRQVFRPILDNSFTQSNQWPFIEPTIANDIV
DLLEVLLKMQDSTFKYRGFNPTVSALEKQAAANRGIHKNACVQIKYVFVCKYDISPATL
TNVFPTLCFTASKSAEDRVKLIQLPRGSLERLSKALGVDRVGIFGLTKDTEGAQPLFDLIN
ENVKDIEAPWLDCIFREEMVFNQPNTKHVASTVGRKKNKK
Saccharomyces cerevisiae protein:SEQ ID NO:4
MSGSLKSLDKKIAKRRQVYKPVLDNPFTNEAHMWPRVHDQPLIWQLLQSSIINKLIHIQS
KENYPWELYTDFNEIVQYLSGAHGNSDPVCLFVCNKDPDVPLVLLQQIPLLCYMAPMTV
KLVQLPKSAMDTFKSVSKYGMLLLRCDDRVDKKFVSQIQKNVDLLQFPWLNAIKYRPTS
VKLLKTTVPIVSKKRQK
--

Saccharomyces cerevisiae orf name: YNR003C
Saccharomyces cerevisiae gene name: RPC34
Candida albicans protein:SEQ ID NO:2
MSEMLVSDKARHLYTKMREYPTSKLFDQDELQTLFDIKKGSELMEYLQELVNGKYVKIS
KMGDQLKFQTVAEEEAKKVSSMSDDEAMIYSYIEASGREGIWTKTIKAKTNLHQHIVQK
CLKNLENNRYIKSIKSVKHPTRKIYMLYNLQPSIDVTGGPWFTDSELDTEFIETLLEVCWR
FIVGKTMYIKDEEADNEDINPLQTTYHNHHPGVNLDQLVEFINNSNITSVELGINDIRSLC
DVLIYDDRIEEVGGNQENSGIFKATWQSIIDKGNTILQNNYQDLKNVVSEDCFNYLQQNQ
SDFSVFQYKSTIQDLQDESDLVYLDSWMNE
Saccharomyces cerevisiae protein:SEQ ID NO:1
MGEVKVKVQPPDADPVEIENRIIELCHQFPHGITDQVIQNEMPHIEAQQRAVAINRLLSM
GQLDLLRSNTGLLYRIKDSQNAGKMKGSDNQEKLVYQIIEDAGNKGIWSRDIRYKSNLP
LTEINKILKNLESKKLIKAVKSVAASKKKVYMLYNLQPDRSVTGGAWYSDQDFESEFVE
VLNQQCFKFLQSKAETARESKQNPMIQRNSSFASSHEVWKYICELGISKVELSMEDIETIL
NTLIYDGKVEMTIIAAKEGTVGSVDGHMKLYRAVNPIIPPTGLVRAPCGLCPVFDDCHEG
GEISPSNCIYMTEWLEF
human genbank accession #: U93869
human protein:SEQ ID NO:3
MSGMIENGLQLSDNAKTLHSQMMSKGIGALFTQQELQKQMGIGSLTDLMSIVQELLDKN
LIKLVKQNDELKFQGVLESEAQKKATMSAEEALVYSYIEASGREGIWSKTIKARTNLHQ
HVVLKCLKSLESQRYVKSVKSVKFPTRKIYMLYSLQPSVDITGGPWFTDGELDIEFINSLL
TIVWRFISENTFPNGFKNFENGPKKNVFYAPNVKNYSTTQEILEFITAAQVANVELTPSNI
RSLCEVLVYDDKLEKVTHDCYRVTLESILQMNQGEGEPEAGNKALEDEEEFSIFNYFKM
FPASKHDKEVVYFDEWTI

FIGURE 80

Saccharomyces cerevisiae orf name: YAL034W-A
Saccharomyces cerevisiae gene name: MTW1
GENBANK Accession Number: BAA77792.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 102
ATGTCTGCTCCCACTATGAGATCCACCTCAATATTGACAGAGCATTTGGGATATCCGCCC
ATCTCGCTTGTTGATGATATCATTAATGCTGTAAATGAAATTATGTACAAGTGCACTGCT
GCCATGGAAAAATATCTGCTATCCAAGAGCAAAATCGGCGAGGAAGATTATGGAGA
AGAGATCAAAAGTGGAGTTGCTAAGTTGGAATCACTTTTGGAAAACTCCGTGGATAA
GAATTTTGACAAACTAGAACTATATGTTTTGAGGAACGTCCTTCGAATCCCTGAAGA
GTATTTGGACGCCAATGTTTTTAGATTGGAGAACCAAAAGGATCTGGTCATTGTAGA
TGAGAATGAGTTGAAGAAAAGTGAGGAGAAACTTCGAGAGAAAGTGAACGACGTGG
AGTTAGCGTTCAAAAAGAATGAAATGCTATTGAAAAGAGTTACAAAAGTGAAAAGAC
TGTTGTTTACGATAAGAGGATTCAAACAAAAGCTAAACGAGTTACTGAAATGCAAAG
ACGATGTACAATTGCAGAAAATTTTGGAGTCGTTAAAACCTATAGATGACACAATGA
CTCTACTGACTGATTCATTACGTAAACTATATGTTGATAGTGAAAGTACCAGTTCAAC
AGAGGAGGTAGAGGCACTACTGCAGAGATTGAAGACCAACGGGAAGCAAAATAATA
AGGATTTCAGAACACGATATATCGATATAAGGACGAATAATGTCCTACGAAAATTGG
GGCTACTAGGTGATAAAGAGGACGAAAAACAGTCTGCCAAGCCGGATGCGAGGACG
CAAGCAGGGGATATAGTTAGTATAGATATTGAAGAGCCT

Candida albicans nucleic acid: SEQ ID NO: 103
ATGTCAGATAAAACTTTAGACGAACGTACTACAGCAATTCTTACTGAACATTTAGAAT
TTGCTCCCTTGACACTTATTGATGACGTGATCAATGCGGTGAATGAAATCATGTACAA
GGGAACAACAGCTATTGAAACATATTTAAAAGAACAAAAACAATTAATGAAAAATGG
GATATTTACCAAAGTTACTGAAGATGAAATAGAAATTGGTATGGGGAAATTAGAATC
ATTATTAGAATCGACTATAGATAAGAATTTTGATAAATTTGAATTATATTGTTTAAGA
AATATTTTCAATATACCTAAAGATCTAATACCATATATACAGTTAAGCCATCAACAAG
GAATTGAATTTAAAAGTGATAATGTTGAACAAAAACGTGAATTTGATCAACAAATTA
AAAATTTACAATTGAAAATCATGCAAGAATTACAACTTCGAAAAATCTTAAAATTAC
AACTTGTCAAAGTCCAAAAATTAATTAAAGTATTAATAGCCATTGATAATGATTTCAA
GAAAATAGATTTTGCTAGTGGTGGTGGTGGTAATGAAGAATCAATAAGAATTTTGAA
AAATCTTCAACCTATTGATGAAACATTATATTTTTTAATTAGTCAAATTAAAAATCTA
ATAAATCAAATTGAACAATTATCAAATAAAGTTAATACCAATTTGAAAACTCAAAAA
TTTATACCCAATTTGCGTGATAAATTCATTGATGGTAGAACATTTAGAGTTTTACAAC
AAACGGGGATTTGGAAAGATTTGGAAAAAAATGATATCAAGATTCTGGTGCAGGGA
AATGACAATAATAATAATAATAATAATAATAATAATAATACCTTAACAGATTTACAA
AATCAAGACGACATTGATATGATAATACCAGAACAAGACGATATAGATGTGGATGCA
ATAAAGAATATAAATGCTCAAATTTAA

FIGURE 80 (CONT'D)

Saccharomyces cerevisiae orf name: YBR060C
Saccharomyces cerevisiae gene name: ORC2
GENBANK Accession Number: CAA85003.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 132
ATGCTAAATGGGGAAGACTTTGTAGAGCATAATGATATCCTATCGTCTCCGGCAAAA
AGCAGGAATGTAACCCCAAAAAGGGTTGACCCACATGGAGAAAGACAACTGAGAAG
AATTCATTCATCAAAGAAGAATTTGTTGGAAAGAATCTCGCTTGTAGGCAACGAAAG
GAAAAATACATCTCCAGATCCGGCACTCAAACCTAAAACGCCAAGTAAAGCTCCCCG
TAAACGTGGAAGACCAAGAAAGATACAGGAAGAATTAACTGATAGGATCAAGAAGG
ATGAGAAAGATACAATTTCCTCTAAGAAAAAGAGGAAATTGGACAAAGATACATCAG
GTAATGTCAATGAGGAAAGCAAGACTTCTAACAACAAGCAGGTGATGGAAAAGACG
GGGATAAAAGAGAAAAGAGAACGCGAAAAAATACAGGTAGCGACCACAACATATGA
AGATAATGTGACTCCACAAACTGATGATAATTTTGTATCAAATTCACCCGAGCCACCA
GAACCTGCAACACCATCTAAGAAGTCTTTAACCACTAATCATGATTTTACTTCGCCCC
TAAAGCAAATTATAATGAATAATTTAAAAGAATATAAAGACTCAACCTCCCCAGGTA
AATTAACCTTGAGTAGAAATTTTACTCCAACCCCTGTACCGAAAAATAAAAAGCTCTA
CCAAACTTCGGAAACCAAGTCAGCAAGCTCGTTTTTGGATACTTTTGAAGGATATTTC
GACCAAAGAAAAATTGTCAGAACTAATGCGAAGTCAAGGCACACCATGTCAATGGCA
CCTGACGTTACCAGAGAAGAGTTTTCCCTAGTATCAAACTTTTTCAACGAAAATTTTC
AAAAACGTCCCAGGCAAAAGTTATTTGAAATTCAGAAAAAAATGTTTCCCCAGTATT
GGTTTGAATTGACTCAAGGATTCTCCTTATTATTTTATGGTGTAGGTTCGAAACGTAA
TTTTTTGGAAGAGTTTGCCATTGACTACTTGTCTCCGAAAATCGCGTACTCGCAACTG
GCTTATGAGAATGAATTACAACAAAACAAACCTGTAAATTCCATCCCATGCCTTATTT
TAAATGGTTACAACCCTAGCTGTAACTATCGTGACGTCTTCAAAGAGATTACCGATCT
TTTGGTCCCCGCTGAGTTGACAAGAAGCGAAACTAAGTACTGGGGCAATCATGTGAT
TTTGCAGATCCAAAAGATGATTGATTTCTACAAAAATCAACCTTTAGATATCAAATTA
ATACTTGTAGTGCATAATCTGGATGGTCCTAGCATAAGGAAAAACACTTTTCAGACGATG
CTAAGCTTCCTCTCCGTCATCAGACAAATCGCCATAGTCGCCTCTACAGACCACATTTAC
GCTCCGCTCCTCTGGGACAACATGAAGGCCCAAAACTACAACTTTGTCTTTCATGATATT
TCGAATTTTGAACCGTCGACAGTCGAGTCTACGTTCCAAGATGTGATGAAGATGGGT
AAAAGCGATACCAGCAGTGGTGCTGAAGGTGCGAAATACGTCTTACAATCACTTACT
GTGAACTCCAAGAAGATGTATAAGTTGCTTATTGAAACACAAATGCAGAATATGGGG
AATCTATCCGCTAACACAGGTCCTAAGCGTGGTACTCAAAGAACTGGAGTAGAACTT
AAACTTTTCAACCATCTCTGTGCCGCTGATTTTATTGCTTCTAATGAGATAGCTCTAA
GGTCGATGCTTAGAGAATTCATAGAACATAAAATGGCCAACATAACTAAGAACAATT
CTGGAATGGAAATTATT

Candida albicans nucleic acid: SEQ ID NO: 133
ATGTCACACTCAAATGCTCTACCAAATAGTCCATTCCGGTCACCTAAAAAACAACGTA
TGGAGGTCATAGGACCACTCAATGCGTCTCGTTTTTCCTTTTCGCCGGTAAAGACACC
TCCTCATGGGAGAGCTGGTCTATCATCTCCAGAGAAAAGATTAGTCAAAGACCTTGA

FIGURE 80 (CONT'D)

CAAGTCGGCGAGAAAAAGAGCCAACAATAGCTTATATAACCGATTAATGGATGAGTA
TCTGGACACAGATGATTATTTGGATGAACAAGATAGGATATTGGCCGACAGAATTAT
CAAACAGTCGAGGGGAGAACCCGACGAAGTCAATTATGGCAGCGACGTGGAATTGG
AAATTGATCTAACTCAGCAGAGACGAACCCGAAGAAGAGAAAAGAAAGTTGTTTACT
CGAGCGATAGTAGCAACGAATATGAGGATACAGGAATGCCAGAAGAATCTTCAAGC
GAGGAAGAAGAGGCAGATGATGATGATGGCAATGTGGAGTTTGTTTATGGACCACCC
AAAGAAAGAAAAACGTCGTTATCAAGCTCACCACCCACAGTCAAGCCTACTGTGCGC
CGAACCAAGCGAGGTAGACCAAGCAAGAGTGAGCTTGTTCTGGGTCAAATCAAAAGT
ATATTCCATCAAGATGACGTGTTGTTCAGTACAGATAGAAAAACGTTCACACCGACT
AAACCAACCGCAGCGAAAAAACCAGTCAGCAATTATTTGACATCTATTTTTGATCAA
AATTTCGATAGAAGCAAGGTGCCAAGTCTAAGTGGAATTCCCAAATCAACCAACACG
CATGAAGAGAAGAAAACGTTTGTGCCGCTTCCTATTCCCACCCTCGATGCTGACGGA
AATATCACTGACAAGGAGTACATCTCCAAATACTTTGATGGAGTTGACCCTGCAAAG
TTCAAAGAAGGCAGGTTTGTGGACGAAAAAGTATTTTACTTAGAAGGGCCAGAAGGA
TACTTTGAACAGCAAACTACCAGAGTTAAACAAAGTGGCAACTCTTTAACAGCATTG
GCACCCCAGATTGAGTACAAAGATTTTGCCAGGTTAGTAAAGTTGGGCGACAACCTC
AGTTTCCAACGCAAACGCCACCTTTTCGAATTGCACAAGTATATCTATCACCAGTGGT
GTTTTGAAATGTCACAAGGGTTCAATTTGAATTTCTACGGAGTCGGATCCAAAATCGATC
TACTCCGAGATTTTGCCACAAACTATTTTGGCATCTGGTGGAAAATGTGGTACACGCCG
ATTTGCCAAAGGTTTTGGTGGTTAACGGTTTTAACCCTAGCATCAATATCAAAAAACTAA
TTCTCGAAATCGCTTCCATCCTTTTGCCAAACGAACTGTACCCAAAACATATAGCTGGAA
CGGTTCCCTTTGTGGTTGATTATCTAAACAACCATAGACTGCCCTGTGGAAGTATCGGTT
TCCATAAACCCAAAATCTTGTTGATTATTCACAATCTTGATGGGGAAGTTTTTAGAGTAG
ACAAGACACAGACGCTTTTGTCGCAATTAATGACACTACCAGAAGTATGGGCCATGT
CATCTACCGACCACATCAATGCATCATTGTTATGGGACCTGTCCAAAGTTAAAAACTT
GAATTTCATCTGGCATAATCTCACAACATATGCCACTTACCAACGAGAAACATCTTTC
CGAGACGTGATAAGTTTAGGCAAATCCAAAAAATTTGTGGGTGGCCTTGGTGCCAAG
TATGTCTTGCGCTCGCTTACCGACAATCACCGAAACCTCTACCGCGAGCTATTGATTG
CACAATTGGATAAAATGGAGAAAGCTGTCCCATCTGCTTCTGGAAGAGTGGGTTTGA
AAGGTAATGCCAAGGTTGCTGTTGACCTAAAAAGCCTATACAATACATGTTTGGACG
AGTTCATTACTTCCAACGAGATGAACTTTAGAACATTCTTAAAAGAGTATGTTGAGCA
TAAAATGTGTCAGCTAGTAAAAGATCCTTCAGGAGTTGAGAAGGTATTCATTCCGTT
CACATACGAAGAGATACAAAACATATATAAGCAAGAATTTGATGTATAGTGGGTACC
CTACACGTATGCGGAACTTGAAAAACTTCTGAAAACCGTTTTAAATACTCTATAA

Human GENBANK Accession Number: GI:4433811
Human nucleic acid sequence: SEQ ID NO: 134
GGCGCGAATTACTGGAAATTGGCTTTTCCCGTTGGGGCCGAAGGTACCTTCCCTGCG
GCGGCGACTCAGCGGGGTGTCGTTCGGCCGGCGTGACGCAGCCGGATCGGCGCCAG
ACGGAAACCTAGCGGTGACTGTATCTGAATTTTGCAGCTGCAGAATGTGTAGTACCT
TAAAAGGTTGGCAACAATGAGTAAACCAGAATTAAAGGAAGACAAGATGCTGGAGG

FIGURE 80 (CONT'D)

TTCACTTTGTGGGAGATGATGATGTTCTTAATCACATTCTAGATAGAGAAGGAGGAG
CTAAATTGAAGAAGGAGCGAGCGCAGCTTTTGGTCAACCCCAAAAAAATAATAAAGA
AGCCAGAATATGATTTGGAGGAAGATGACCAGGAGGTCTTAAAAGATCAGAACTATG
TGGAAATTATGGGAAGAGATGTTCAAGAATCATTGAAAAATGGCTCTGCTACAGGTG
GTGGAAATAAAGTTTATTCTTTTCAGAATAGAAAACACTCTGAAAAGATGGCTAAAT
TAGCTTCAGAACTAGCAAAAACACCACAAAAAAGTGTTTCATTCAGTTTGAAGAATG
ATCCTGAGATTACGATAAACGTTCCTCAAAGTAGCAAGGGCCATTCTGCTTCAGACA
AGGTTCAACCGAAGAACAATGACAAAAGTGAATTTCTGTCAACAGCACCTCGTAGTC
TAAGAAAAAGATTAATAGTTCCAAGGTCTCATTCTGACAGTGAAAGCGAATATTCTG
CTTCCAACTCAGAGGATGATGAAGGGGTTGCACAGGAACATGAAGAGGACACTAAT
GCAGTCATATTCAGCCAAAAGATTCAAGCTCAGAATAGAGTAGTTTCAGCTCCTGTT
GGCAAAGAAACACCTTCTAAGAGAATGAAAAGAGATAAAACAAGTGACTTAGTAGA
AGAATATTTTGAAGCTCACAGCAGTTCAAAAGTTTTAACCTCTGATAGAACACTGCA
GAAGCTAAAGAGAGCTAAACTGGATCAGCAAACTTTGCGTAACTTATTGAGCAAGGT
TTCCCCTTCCTTTTCTGCCGAACTTAAACAACTAAATCAACAGTATGAAAAATTATTT
CATAAATGGATGCTGCAATTACACCTTGGGTTCAACATTGTGCTTTATGGTTTGGGTTCT
AAGAGAGATTTACTAGAAAGGTTTCGAACCACTATGCTGCAAGATTCCATTCACGTTGTC
ATCAATGGCTTCTTTCCTGGAATCAGTGTGAAATCAGTCCTGAATTCTATAACAGAAGAA
GTCCTCGATCATATGGGTACTTTCCGCAGTATACTGGATCAGCTAGACTGGATAGTAAAC
AAATTTAAAGAAGATTCTTCTTTAGAACTCTTCCTTCTCATCCACAATTTGGATAGCCAG
ATGTTGAGAGGAGAGAAGAGCCAGCAAATCATTGGTCAGTTGTCATCTTTGCATAAC
ATTTACCTTATAGCATCCATTGACCACCTCAATGCTCCTCTCATGTGGGATCATGCAA
AGCAGAGTCTTTTTAACTGGCTCTGGTATGAAACTACTACATACAGTCCTTATACTGA
AGAAACCTCCTATGAGAACTCTCTTCTGGTAAAGCAGTCTGGATCCCTGCCACTTAGC
TCCCTTACTCATGTCTTACGAAGCCTTACCCCTAATGCAAGGGGAATTTTCAGGCTAC
TAATAAAATACCAGCTGGACAACCAGGATAACCCTTCTTACATTGGCCTTTCTTTTCA
AGATTTTTACCAGCAGTGTCGGGAGGCATTCCTCGTCAATAGTGATCTGACACTCCG
GGCCCAGTTAACTGAATTTAGGGACCACAAGCTTATAAGAACAAAGAAGGGAACTGA
TGGAGTAGAGTATTTATTAATTCCTGTTGATAATGGAACATTGACTGATTTCTTGGAA
AAGGAAGAAGAGGAGGCTTGAAGCTTTCCTTTATTCTTGAATCTCCCATGGAAGGGT
TGTACCCCAGCTGCCACTCCTCTAGTTGAAAGTGTTGTGTTTACATCTGACATTAAAT
TATTTTTCCAGCATACAAGATTTAAATTTGGGAAGGGGGGGATGTCCTCAATTAGAA
CTTTTTGATCAGCCTGGCTGGTACCGTCTAGTACTATGCAGCGGTCCTCAAGTTGGAG
AAAATGTGCCTTTCATTCATTACCTCTCTGGAGACTTCTTGCTGGAATGAACAGTGTG
CTCAGGGACTATTTGGAACTGGATGTTTTTGAATTATTTTATACTTAGAGATATTCTG
AATTTTTTGAGGGCCTTTTAACACTCCCCGAGCTGATTGTTTGCAAGTGTGTTTGTTC
CAGAGTGTGGAAGTATAAAGACATGGGCATCACGTAAATTGGTTTTGTTTGCTATTC
TGTGTGTCAGAACCAACGAGTGTAATGGAGAGGGCAGGTCATCTCTTATTGTTTCTA
AAACAACTTAAAAGGTGTAGATTGGGAAGAGGTGAGTGATCCAGCTTTCTCCTTTTG
GATTGAGGCTATGTACTTGGTGGGGGCAGGGGAGGGAATATATTATAATACTATTCA
GTTGGGATAATGGGAAAAACAGAGTATATAGGGTATCTACCCAGCCTAGAAAGCACA
GGAACAATACGTCATATATTTGGAACAGTTATTGTCTGTGCCATGACCTTCA

FIGURE 80 (CONT'D)

Saccharomyces cerevisiae orf name: YBR088C
Saccharomyces cerevisiae gene name: POL30
GENBANK Accession Number: CAA85038.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 93
ATGTTAGAAGCAAAATTTGAAGAAGCATCCCTTTTCAAGAGAATAATTGATGGTTTCAAA
GATTGTGTCCAGTTGGTCAATTTCCAATGTAAAGAAGATGGTATCATTGCACAAGCTGTC
GATGACTCAAGAGTTCTATTGGTCTCCTTGGAAATAGGTGTCGAAGCCTTCCAAGAATAT
AGATGTGACCATCCTGTTACGTTAGGTATGGATCTAACCTCACTAAGTAAAATCCTACGT
TGTGGTAACAACACCGATACATTAACACTAATTGCTGACAACACACCGGATTCCATCATC
TTATTATTTGAGGATACCAAGAAAGACCGTATAGCCGAATACTCTCTGAAATTGATGGAT
ATCGATGCTGATTTCTTAAAGATTGAAGAATTACAGTACGACTCCACCCTGTCATTGCCA
TCTTCCGAATTCTCTAAAATTGTTCGTGACTTGTCCCAATTGAGTGATTCTATTAATATC
ATGATCACCAAAGAAACAATAAAGTTTGTAGCTGACGGTGATATCGGATCAGGTTCA
GTCATAATAAAACCATTCGTGGATATGGAACATCCTGAAACAAGCATCAAACTTGAA
ATGGATCAACCTGTCGACTTGACGTTCGGAGCTAAATATTTATTGGACATCATTAAG
GGCTCCTCCCTTTCTGATAGAGTTGGTATCAGGCTCTCCAGCGAAGCTCCTGCTTTAT
TCCAATTTGAT

Candida albicans nucleic acid: SEQ ID NO: 94
ATGTTAGAAGGTAAATTTGAAGAAGCTGCTTTATTAAAAAAAGTTGTTGAAGCCATT
AAAGATTGTGTTAAAAAATGTAACTTCAATTGTTCAGAGCATGGGATTACTGTACAA
GCAGTGGATGATTCTCGTGTATTATTAGTTTCATTATTAATTGGTCAAACTTCTTTCA
GTGAATATAGATGTGACAGAGACGTTACATTAGGTATTGACTTGGAAAGTTTCAGTA
AGATTATCAAATCTGCTAACAATGAAGATTTCTTGACCCTTTTAGCTGAAGATTCACC
AGATCAAATAATGGCTATTCTTGAAGAAAAACAAAAAGAGAAAATCAGTGAATATTC
TTTAAAATTAATGGATATTGATTCTGAATTTTTACAAATTGATGATATGGAATACGAT
GCTGTTGTGAATATGCCAAGTAGTGATTTTGCTAAACTTGTGAGGGATTTGAAAAAT
TTAAGTGAATCTTTACGTGTTGTTGTTACTAAAGATTCCGTCAAGTTTACATCTGAAG
GTGATTCTGGTTCCGGAAGTGTTATCTTGAAACCTTACACCAACTTGAAAAATGAAA
GAGAAAGTGTCACTATTAGTTTAGATGACCCAGTTGATTTGACTTTTGGTTTGAAATA
CTTGAATGATATTGTGAAGGCAGCTACATTATCCGATGTCATCACCATCAAATTGGCC
GATAAAACTCCTGCATTGTTTGAATTTAAAATGCAATCTGGAGGTTATTTGAGATTCT
ACTTGGCACCAAAATTCGATGATGATGAGTAG

Human GENBANK Accession Number: GI:181271
Human nucleic acid sequence: SEQ ID NO: 95
AGGTCTCAGCCGGTCGTCGCGACGTTCGCCCGCTCGCTCTGAGGCTCCTGAAGCCGA
AACTAGCTAGACTTTCCTCCTTCCCGCCTGCCTGTAGCGGCGTTGTTGCCACTCCGCC
ACCATGTTCGAGGCGCGCCTGGTCCAGGGCTCCATCCTCAAGAAGGTGTTGGAGGCA
CTCAAGGACCTCATCAACGAGGCCTGCTGGGATATTAGCTCCAGCGGTGTAAACCTG

FIGURE 80 (CONT'D)

CAGAGCATGGACTCGTCCCACGTCTCTTTGGTGCAGCTCACCCTGCGGTCTGAGGGC
TTCGACACCTACCGCTGCGACCGCAACCTGGCCATGGGCGTGAACCTCACCAGTATG
TCCAAAATACTAAAATGCGCCGGCAATGAAGATATCATTACACTAAGGGCCGAAGAT
AACGCGGATACCTTGGCGCTAGTATTTGAAGCACCAAACCAGGAGAAAGTTTCAGAC
TATGAAATGAAGTTGATGGATTTAGATGTTGAACAACTTGGAATTCCAGAACAGGAG
TACAGCTGTGTAGTAAAGATGCCTTCTGGTGAATTTGCACGTATATGCCGAGATCTCA
GCCATATTGGAGATGCTGTTGTAATTTCCTGTGCAAAAGACGGAGTGAAATTTTCTG
CAAGTGGAGAACTTGGAAATGGAAACATTAAATTGTCACAGACAAGTAATGTCGATA
AAGAGGAGGAAGCTGTTACCATAGAGATGAATGAACCAGTTCAACTAACTTTTGCAC
TGAGGTACCTGAACTTCTTTACAAAAGCCACTCCACTCTCTTCAACGGTGACACTCAG
TATGTCTGCAGATGTACCCCTTGTTGTAGAGTATAAAATTGCGGATATGGGACACTTA
AAATACTACTTGGCTCCCAAGATCGAGGATGAAGAAGGATCTTAGGCATTCTTAAAA
TTCAAGAAAATAAAACTAAGCTCTTTGAGAACTGCTTCTAAGATGCCAGCATATACT
GAAGTCTTTTCTGTCACCAAATTTGTACCTCTAAGTACATATGTAGATATTGTTTTCT
GTAAATAACCTATTTTTTTTCTCTATTCTCTCCAATTTGTTTAAAGAATAAAGTCCAAA
GTCTGATCTGGTCTAGTTAACCTAGAAGTATTTTTGTCTCTTAGAAATACTTGTGATT
TTTATAATACAAAAGGGTCTTGACTCTAAATGCAGTTTTAAGAAGTGTTTTT

Saccharomyces cerevisiae orf name: YBR155W
Saccharomyces cerevisiae gene name: CNS1
GENBANK Accession Number: CAA85114.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 35
CCAATCAAAGGATTGACCCAGAGAACAAATCAATTTTGAATATGTTATCAGTGATTG
ATAGAAAAGAACAAGAATTGAAAGCAAAAGAAGAAAAACAGCAAAGAGAAGCTCAG
GAACGTGAAAACAAGAAAATTATGTTAGAGAGCGCAATGACGCTGAGAAACATAAC
TAACATCAAAACTCACTCTCCAGTAGAGTTACTTAATGAGGGTAAAATAAGGCTAGA
AGACCCAATGGATTTTGAATCTCAATTGATCTATCCCGCATTAATTATGTACCCCACG
CAAGATGAATTTGATTTTGTAGGTGAAGTAAGTGAGTTAACTACTGTGCAAGAACTT
GTTGACCTAGTTTTGGAAGGGCCGCAAGAACGCTTCAAAAAAGAAGGTAAGGAAAA
CTTCACACCAAAGAAAGTGTTGGTGTTCATGGAAACAAAGGCAGGTGGTTTGATTAA
AGCTGGTAAGAAACTGACATTTCACGATATCTTGAAGAAAGAGTCGCCAGATGTACC
ATTGTTCGATAACGCTTTGAAAATATATATTGTGCCAAAGGTAGAAAGTGAAGGGTG
GATTTCCAAGTGGGATAAGCAAAAAGCCTTAGAAAGAAGATCTGTGTGA

Candida albicans nucleic acid: SEQ ID NO: 36
ATGTCCAAAATAGAGCCAGTCACTGAAAAAGAAGAAGAATACGTTTCCGAATGGGAT
AGAAGAAGATATGTTCCCAAAGCAGGTGAACCTGAATTACCTCCCCAATTATCAGAA
TTCTCTAACAAGACCACAGACGAGGTTATTGAGGAATTGAATAGATTGCCATTTTTTA
TGACAAAGTTAGATGAAACTGATGGAGATGGCGGAGAAAATGTAAACTTGGAAGCA
CTTAAAAGTTTGGCATATGAAGGTGATCCTGACGAAATTGCCTCAAATTTCAAAAAT

FIGURE 80 (CONT'D)

CAGGGGAATAATTGTTACAAATTTAAAAAATACAAAGATGCAATTATATTTTATACG
AAAGGTCTTGAAGTAAACTGTGACGTGGACGCAATCAATTCAGCATTATACTTGAAT
CGTGCTGCTTGTAACTTGGAGTTGAAAAATTACCGTCGGTGCATTGAAGATTGTAAG
AAAGTATTAATGCTTGATGAGAAGAATATTAAGGCTTGTTTCCGTTCAGGAAAGGCA
TTCTTTGCAATTGAAAAATACGATGAAGCAATCAAAGTGCTTGAATACGGTCTAAAT
ATAGAACCAGAAAACAAAGATTTACAGAAATTATTACAGCAAGTTCAAAAGAGGCAA
GAAACTTTAGCTCAAATAAAAGCTAAAAAGGCACAAGAAGAGGAACAAGAGCGGTT
GAAAAATATCGTGTTGGAGAATTCTATAAAATTAAGACACATTGAAATAGTGAAGTC
CTCATCTCCTCCAGAAGTCTTGAAGACTGCCAAGATACGATTGGAAGACCCCAAAGA
TTATCAGTCACAATTAATATTCCCTGCTATGATACTATACCCCACCACCGATGAATTT
GACTTTATTGCAGAAATAAGCGAATTAACTACTCCTTTGGAATTGCTAGAGATGGTAT
TAAATAGACCTAGGGAATGGTTTGATGATCCAAAACACAAGGATTTCAATGTCAAAA
AATTGGAATGCTTTATGGAAACTGAATCTGGTGGGTTGATTAAAGTGGGCAAGAAAA
TTGAAGTTAACAATGCTTTGATGAATGAAAAACCTAAGGCACCATTGTTTGATAACG
CTTTAAGACTTTATGTCGTTCCAAAATTAGACGTCGCCAAATGGACATCTGAATGGA
ATAAAGAAACCGCCTTGGCAGCTCGTAAATAG

Human GENBANK Accession Number: NM_004623.1
Human nucleic acid sequence: SEQ ID NO: 37
CTGGGACCCGGGCTGGAAGGCAGGGCATCAGCTATGGAACAACCTGGGCAGGATCC
CACCTCAGACGACGTCATGGACTCGTTCCTGGAAAAGTTCCAGAGCCAGCCTTACCG
TGGCGGCTTTCATGAGGACCAGTGGGAGAAGGAATTTGAAAAGGTCCCCCTATTTAT
GTCGAGAGCGCCATCAGAAATTGATCCCAGGGAGAATCCTGACTTGGCTTGTCTCCA
GTCAATTATTTTTGATGAGGAGCGTTCTCCAGAAGAACAGGCCAAGACCTATAAAGA
TGAGGGCAATGATTACTTTAAAGAAAAAGACTACAAGAAAGCTGTAATTTCATACAC
TGAAGGCTTAAAGAAGAAATGTGCAGATCCTGATTTGAATGCTGTCCTTTATACCAA
CCGGGCAGCAGCACAGTACTATCTGGGCAATTTTCGTTCTGCTCTCAATGATGTGACA
GCTGCCAGAAAGCTAAAACCCTGCCACCTCAAAGCAATAATAAGAGGTGCCTTATGC
CATCTGGAACTGATACACTTTGCCGAGGCCGTGAACTGGTGTGATGAGGGACTGCAA
ATAGATGCCAAAGAGAAGAAGCTTCTGGAAATGAGGGCTAAAGCAGACAAGCTGAA
GCGAATTGAACAGAGGGATGTGAGGAAAGCCAACTTGAAAGAAAAGAAGGAGAGGA
ATCAGAATGAGGCTTTACTCCAGGCCATCAAGGCTAGGAATATCAGGCTCTCAGAAG
CTGCCTGTGAGGATGAAGATTCAGCCTCAGAAGGTCTAGGTGAGCTTTTCCTGGATG
GACTCAGCACTGAGAACCCCCATGGAGCCAGGCTGAGTCTAGATGGCCAGGGCAGG
CTGAGCTGGCCTGTGCTCTTTCTGTACCCAGAGTATGCCCAGTCGGACTTCATCTCTG
CTTTTCATGAGGACTCCAGGTTTATTGATCATCTAATGGTGATGTTTGGTGAAACACC
TTCTTGGGACCTAGAGCAAAAATATTGCCTGATAATTTGGAGGTCTACTTTGAGGAT
GAGGACAGGGCAGAACTATACCGGGTGCCTGCCAAGAGCACCTTGCTACAGGTTCTA
CAGCACCAGAGGTACTTTGTAAAAGCCCTGACACCAGCATTTTTGGTCTGTGTAGGAT
CCTCTCCTTTTTGCAAGAATTTTCTCCGGGGGAGAAAGGTGTACCAGATACGATGACTAA
GCCAGGGCCCCTGGATCTCCTCCCTTACCCTCCTCTGCTGGGAACCTAGCACACCTGAAT

FIGURE 80 (CONT'D)

CAGCTGGACATACTGCTGGAGTCCAGTGCTTTCTTTCCGTCACCCTGGGGATAGTCCTTC
CTGGCATCGTGGTGGGGGAGGAGCCTCTGGCTTCCCTAAACTGCAGCTCTCTGGCTG
GTCTTCACTTTCCTCAGTTGATATAAAACTCTGGTCTTGGCCATGATGTCCTTGGATT
CCATCGCTAAAGGGACCATCTGCTGCAGTTACCACAGCAACTGACTTGAGCGGCACC
TGGTCTGTGGAGATGGACTCAGGATCCAGTGACATGATTCTGAACTTTTGTGGAGTT
TGACACCTTAGAGAAGCTACCCCTCAAACTGCACATCTACACACAAACAAACAATGC
ATAGGATTCCAAGGCTTTAAAGCTGAGAGACCCTGGCCTCAAGTTATTTCATGCGCA
CAGAGGGAAGCCATGTGGGGTTGCTGAAGATGCCTTGAGGTGAAATGGGGGCAGGA
AAGCCACATCTTGCTCTGCATTTATAAAGACCGTACAAACTCAGATCCTTGGTACCCC
TAAAAAGATTGCCAATTTTCTTCATCTTTGCCATATGGAGGACTGTGACAGACTTTGG
ACAGTGGCCTCTTGAGTTCCTCTGCAGTTTTGACATTTAGGATTTTGTGTCTTTTAAA
CTGGAAAATCTTCTAGCATGTTGGGTTGTTACAGAGTATATTTTTGTCTGCAGCTGTT
TGTTGCCCCATTCCTAAGAGGAGTTTATCCATCCTGAAAAAAAAAAAAAAAAAA

Saccharomyces cerevisiae orf name: YDL235C
Saccharomyces cerevisiae gene name: YPD1
GENBANK Accession Number: CAA98815.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 138
ATGTCTACTATTCCCTCAGAAATCATCAATTGGACCATCTTAAATGAAATTATATCTATG
GATGACGATGATTCCGATTTTTCTAAAGGTCTAATTATTCAATTTATCGACCAGGCACAA
ACAACTTTTGCTCAAATGCAACGACAGCTGGACGGTGAAAAAAATCTTACCGAATTA
GACAATCTGGGCCATTTTTTAAAGGGTTCTTCTGCTGCATTAGGCTTACAAAGAATTG
CCTGGGTTTGTGAAAGAATTCAAAACTTGGGAAGAAAAATGGAACATTTCTTCCCCA
ACAAGACCGAATTGGTCAACACTCTGAGCGATAAATCGATTATTAATGGAATCAATA
TTGATGAAGATGACGAGGAAATAAAGATACAAGTGGACGATAAAGACGAAAATTCC
ATATATCTCATCTTGATAGCAAAAGCTTTGAACCAGTCTAGGTTGGAGTTCAAACTGG
CGAGAATTGAGTTATCTAAATATTACAACACAAACCTATAA

Candida albicans nucleic acid: SEQ ID NO: 139
ATGTCAGAAGATAAATTACAAAAATTACAAGACTCAGGACTTGTCGACTGGGCAGTG
TTTAGTGAAATAGTGACCATGGACGAGGATGAAGAAGGGTTTTCCAAATCACTAGTA
GAAGTCTTTGTTAGCCAAGTGGAAGAAACATTTGAAGAAATTGATAAAATATTTAAAG
GAAAAGAATTTGGAGAAATTGTCATCGTCGGGTCATTTTTTTGAAAGGATCTGCTGCT
GCTTTGGGGTTGACCAAAATTTCAAATCAATGCGAACGAATTCAAAACTATGGCCAT
AAGATCAACTTTGACAATTTTCAATTGGAAGATATAAAAACTAAAGGCGATTCGGCC
GTAAGTGCGGAAAATGTGGCCGTTAATGATGGTGAAACTAATCCAGAAAATGGATCC
AATGGCAACGAAACAAGTAATAACAAAACAAATACTAGCAATATACCGGATGAATCA
AGCGATGACTTTTGGATAGCATTAATTGAGGATGCATTAGCCAAGGCGAGAGATGGA
TTCGACCAATCTAGAAGAGCATTGGACGAATATTACGAATAG

FIGURE 80 (CONT'D)

Human GENBANK Accession Number: Z15005.1
Human nucleic acid sequence: SEQ ID NO: 140
ATGGCGGAGGAAGGAGCCGTGGCCGTCTGCGTGCGAGTGCGGCCGCTGAACAGCAG
AGAAGAATCACTTGGAGAAACTGCCCAAGTTTACTGGAAAACTGACAATAATGTCAT
TTATCAAGTTGATGGAAGTAAATCCTTCAATTTTGATCGTGTCTTTCATGGTAATGAA
ACTACCAAAAATGTGTATGAAGAAATAGCAGCACCAATCATCGATTCTGCCATACAA
GGCTACAATGGTACTATATTTGCCTATGGACAGACTGCTTCAGGAAAAACATATACC
ATGATGGGTTCAGAAGATCATTTGGGAGTTATACCCAGGGCAATTCATGACATTTTC
CAAAAAATTAAGAAGTTTCCTGATAGGGAATTTCTCTTACGTGTATCTTACATGGAAA
TATACAATGAAACCATTACAGATTTACTCTGTGGCACTCAAAAAATGAAACCTTTAAT
TATTCGAGAAGATGTCAATAGGAATGTGTATGTTGCTGATCTCACAGAAGAAGTTGT
ATATACATCAGAAATGGCTTTGAAATGGATTACAAAGGGAGAAAAGAGCAGGCATTA
TGGAGAAACAAAAATGAATCAAAGAAGCAGTCGTTCTCATACCATCTTTAGGATGAT
TTTGGAAAGCAGAGAGAAGGGTGAACCTTCTAATTGTGAAGGATCTGTTAAGGTATC
CCATTTGAATTTGGTTGATCTTGCAGGCAGTGAAAGAGCTGCTCAAACAGGCGCTGC
AGGTGTGCGGCTCAAGGAAGGCTGTAATATAAATCGAAGCTTATTTATTTTGGGACA
AGTGATCAAGAAACTTAGTGATGGACAAGTTGGTGGTTTCATAAATTATCGAGATAG
CAAGTTAACACGAATTCTTCAGAATTCCTTGGGAGGAAATCCAAAGACACGTATTAT
CTGCACAATTACTCCAGTATCTTTTGATGAAACTCTTACTGCTCTCCAGTTTGCCAGT
ACTGCTAAATATATGAAGAATACTCCTTATGTTAATGAGGTATCAACTGATGAAGCTC
TCCTGAAAAGGTATAGAAAAGAAATAATGGATCTTAAAAAACAATTAGAGGAGGTTT
CTTTAGAGACGCGGGCTCAGGCAATGGAAAAAGACCAATTGGCCCAACTTTTGGAAG
AAAAAGATTTGCTTCAGAAAGTACAGAATGAGAAAATTGAAAACTTAACACGGATG
CTGGTGACCTCTTCTTCCCTCACGTTGCAACAGGAATTAAAGGCTAAAAGAAAACGA
AGAGTTACTTGGTGCCTTGGCAAAATTAACAAAATGAAGAACTCAAACTATGCAGAT
CAATTTAATATACCAACAAATATAACAACAAAAACACATAAGCTTTCTATAAATTTAT
TACGAGAAATTGATGAATCTGTCTGTTCAGAGTCTGATGTTTTCAGTAACACTCTTGA
TACATTAAGTGAGATAGAATGGAATCCAGCAACAAAGCTACTAAATCAGGAGAATAT
AGAAAGTGAGTTGAACTCACTTCGTGCTGACTATGATAATCTGGTATTAGACTATGA
ACAACTACGAACAGAAAAAGAAGAAATGGAATTGAAATTAAAAGAAAAGAATGATT
TGGATGAATTTGAGGCTCTAGAAAGAAAAACTAAAAAAGATCAAGAGATGCAACTA
ATTCATGAAATTTCGAACTTAAAGAATTTAGTTAAGCATCGAGAAGTATATAATCAA
GATCTTGAGAATGAACTCAGTTCAAAAGTAGAGCTGCTTAGAGAAAAGGAAGACCAG
ATTAAGAAGCTACAGGAATACATAGACTCTCAAAAGCTAGAAAATATAAAAATGGAC
TTGTCATACTCATTGGAAAGCATTGAAGACCCAAAACAAATGAAGCAGACTCTGTTT
GATGCTGAAACTGTAGCCCTTGATGCCAAGAGAGAATCAGCCTTTCTTAGAAGTGAA
AATCTGGAGTTGAAGGAGAAAATGAAAGAACTTGCAACTACATACAAGCAAATGGA
AAATGATATTCAGTTATATCAAAGCCAATTGGAGGCAAAAAAGAAAATGCAAGTTGA
TCTGGAGAAAGAATTACAATCTGCTTTTAATGAGATAACAAAACTCACCTCCCTTATA
GATGGCAAAGTTCCAAAAGATTTGCTCTGTAATTTGGAATTGGAAGGAAAGATTACT
GATCTTCAGAAAGAACTAAATAAAGAAGTTGAAGAAAATGAAGCTTTGCGGGAAGA

FIGURE 80 (CONT'D)

AGTCATTTTGCTTTCAGAATTGAAATCTTTACCTTCTGAAGTAGAAAGGCTGAGGAAA
GAGATACAAGACAAATCTGAAGAGCTCCATATAATAACATCAGAAAAAGATAAATTG
TTTTCTGAAGTAGTTCATAAGGAGAGTAGAGTTCAAGGTTTACTTGAAGAAATTGGG
AAAACAAAAGATGACCTAGCAACTACACAGTCGAATTATAAAAGCACTGATCAAGAA
TTCCAAAATTTCAAAACCCTTCATATGGACTTTGAGCAAAAGTATAAGATGGTCCTTG
AGGAGAATGAGAGAATGAATCAGGAAATAGTTAATCTCTCTAAAGAAGCCCAAAAAT
TTGATTCGAGTTTGGGTGCTTTGAAGACCGAGCTTTCTTACAAGACCCAAGAACTTCA
GGAGAAAACACGTGAGGTTCAAGAAAGACTAAATGAGATGGAACAGCTGAAGGAAC
AATTAGAAAATAGAGATTCTCCGCTGCAAACTGTAGAAAGGGAGAAAACACTGATTA
CTGAGAAACTGCAGCAAACTTTAGAAGAAGTAAAAACTTTAACTCAAGAAAAAGATG
ATCTAAAACAACTCCAAGAAAGCTTGCAAATTGAGAGGGACCAACTCAAAAGTGATA
TTCACGATACTGTTAACATGAATATAGATACTCAAGAACAATTACGAAATGCTCTTGA
GTCTCTGAAACAACATCAAGAAACAATTAATACACTAAAATCGAAAATTTCTGAGGA
AGTTTCCAGGAATTTGCATATGGAGGAAAATACAGGAGAAACTAAAGATGAATTTCA
GCAAAAGATGGTTGGCATAGATAAAAAACAGGATTTGGAAGCTAAAAATACCCAAA
CACTAACTGCAGATGTTAAGGATAATGAGATAATTGAGCAACAAAGGAAGATATTTT
CTTTAATACAGGAGAAAAATGAACTCCAACAAATGTTAGAGAGTGTTATAGCAGAAA
AGGAACAATTGAAGACTGACCTAAAGGAAAATATTGAAATGACCATTGAAAACCAG
GAAGAATTAAGACTTCTTGGGGATGAACTTAAAAAGCAACAAGAGATAGTTGCACAA
GAAAAGAACCATGCCATAAAGAAAGAAGGAGAGCTTTCTAGGACCTGTGACAGACT
GGCAGAAGTTGAAGAAAAACTAAAGGAAAAGAGCCAGCAACTCCAAGAAAAACAGC
AACAACTTCTTAATGTACAAGAAGAGATGAGTGAGATGCAGAAAAAGATTAATGAAATA
GAGAATTTAAAGAATGAATTAAAGAACAAAGAATTGACATTGGAACATATGGAAACA
GAGAGGCTTGAGTTGGCTCAGAAACTTAATGAAAATTATGAGGAAGTGAAATCTATA
ACCAAAGAAAGAAAAGTTCTAAAGGAATTACAGAAGTCATTTGAAACAGAGAGAGA
CCACCTTAGAGGATATATAAGAGAAATTGAAGCTACAGGCCTACAAACCAAAGAAGA
ACTAAAAATTGCTCATATTCACCTAAAAGAACACCAAGAAACTATTGATGAACTAAG
AAGAAGCGTATCTGAGAAGACAGCTCAAATAATAAATACTCAGGACTTAGAAAAATC
CCATACCAAATTACAAGAAGAGATCCCAGTGCTTCATGAGGAACAAGAGTTACTGCC
TAATGTGAAAAAAGTCAGTGAGACTCAGGAAACAATGAATGAACTGGAGTTATTAAC
AGAACAGTCCACAACCAAGGACTCAACAACACTGGCAAGAATAGAAATGGAAAGGC
TCAGGTTGAATGAAAAATTTCAAGAAAGTCAGGAAGAGATAAAATCTCTAACCAAGG
AAAGAGACAACCTTAAAACGATAAAAGAAGCCCTTGAAGTTAAACATGACCAGCTGA
AAGAACATATTAGAGAAACTTTGGCTAAAATCCAGGAGTCTCAAAGCAAACAAGAAC
AGTCCTTAAATATGAAAGAAAAAGACAATGAAACTACCAAAATCGTGAGTGAGATGG
AGCAATTCAAACCCAAAGATTCAGCACTACTAAGGATAGAAATAGAAATGCTCGGAT
TGTCCAAAAGACTTCAAGAAAGTCATGATGAAATGAAATCTGTAGCTAAGGAGAAAG
ATGACCTACAGAGGCTGCAAGAAGTTCTTCAATCTGAAAGTGACCAGCTCAAAGAAA
ACATAAAAGAAATTGTAGCTAAACACCTGGAAACTGAAGAGGAACTTAAAGTTGCTC
ATTGTTGCCTGAAAGAACAAGAGGAAACTATTAATGAGTTAAGAGTGAATCTTTCAG
AGAAGGAAACTGAAATATCAACCATTCAAAAGCAGTTAGAAGCAATCAATGATAAAT
TACAGAACAAGATCCAAGAGATTTATGAGAAAGAGGAACAACTTAATATAAAACAAATT

FIGURE 80 (CONT'D)

AGTGAGGTTCAGGAAAACGTGAATGAACTGAAACAATTCAAGGAGCATCGCAAAGC
CAAGGATTCAGCACTACAAAGTATAGAAAGTAAGATGCTCGAGTTGACCAACAGACT
TCAAGAAAGTCAAGAAGAAATACAAATTATGATTAAGGAAAAAGAGGAAATGAAAA
GAGTACAGGAGGCCCTTCAGATAGAGAGAGACCAACTGAAAGAAAACACTAAAGAA
ATTGTAGCTAAAATGAAAGAATCTCAAGAAAAAGAATATCAGTTTCTTAAGATGACA
GCTGTCAATGAGACTCAGGAGAAAATGTGTGAAATAGAACACTTGAAGGAGCAATTT
GAGACCCAGAAGTTAAACCTGGAAAACATAGAAACGGAGAATATAAGGTTGACTCA
GATACTACATGAAAACCTTGAAGAAATGAGATCTGTAACAAAAGAAAGAGATGACCT
TAGGAGTGTGGAGGAGACTCTCAAAGTAGAGAGAGACCAGCTCAAGGAAAACCTTA
GAGAAACTATAACTAGAGACCTAGAAAAACAAGAGGAGCTAAAAATTGTTCACATGC
ATCTGAAGGAGCACCAAGAAACTATTGATAAACTAAGAGGGATTGTTTCAGAGAAAA
CAAATGAAATATCAAATATGCAAAAGGACTTAGAACACTCAAATGATGCCTTAAAAG
CACAGGATCTGAAAATACAAGAGGAACTAAGAATTGCTCACATGCATCTGAAAGAGC
AGCAGGAAACTATTGACAAACTCAGAGGAATTGTTTCTGAGAAGACAGATAAACTAT
CAAATATGCAAAAAGATTTAGAAAATTCAAATGCTAAATTACAAGAAAAGATTCAAG
AACTTAAGGCAAATGAACATCAACTTATTACGTTAAAAAAAGATGTCAATGAGACAC
AGAAAAAAGTGTCTGAAATGGAGCAACTAAAGAAACAAATAAAAGACCAAAGCTTA
ACTCTGAGTAAATTAGAAATAGAGAATTTAAATTTGGCTCAAGAACTTCATGAAAAC
CTTGAAGAAATGAAATCTGTAATGAAAGAAAGAGATAATCTAAGAAGAGTAGAGGA
GACACTCAAACTGGAGAGAGACCAACTCAAGGAAAGCCTGCAAGAAACCAAAGCTA
GAGATCTGGAAATACAACAGGAACTAAAAACTGCTCGTATGCTATCAAAAGAACACA
AAGAAACTGTTGATAAACTTAGAGAAAAAATTTCAGAAAAGACAATTCAAATTTCAG
ACATTCAAAAGGATTTAGATAAATCAAAAGATGAATTACAGAAAAAGATCCAAGAAC
TTCAGAAAAAAGAACTTCAACTGCTTAGAGTGAAAGAAGATGTCAATATGAGTCATA
AAAAAATTAATGAAATGGAACAGTTGAAGAAGCAATTTGAGCCAAACTATCTATGCA
AGTGTGAGATGGATAACTTCCAGTTGACTAAGAAACTTCATGAAAGCCTTGAAGAAA
TAAGAATTGTAGCTAAAGAAAGAGATGAGCTAAGGAGGATAAAAGAATCTCTCAAA
ATGGAAAGGGACCAATTCATAGCAACCTTAAGGGAAATGATAGCTAGAGACCGACA
GAACCACCAAGTAAAACCTGAAAAAAGGTTACTAAGTGATGGACAACAGCACCTTAT
GGAAAGCCTGAGAGAAAAGTGCTCTAGAATAAAAGAGCTTTTGAAGAGATACTCAG
AGATGGATGATCATTATGAGTGCTTGAATAGATTGTCTCTTGACTTGGAGAAGGAAA
TTGAATTCCACAGAATCATGAAGAAACTGAAGTATGTGTTAAGCTATGTTACAAAAA
TAAAAGAAGAACAACATGAATGCATCAATAAATTTGAAATGGATTTTATTGATGAAG
TGGAAAAGCAAAAGGAATTGCTAATTAAAATACAGCACCTTCAACAAGATTGTGATG
TACCATCCAGAGAATTAAGGGATCTCAAATTGAACCAGAATATGGATCTACATATTG
AGGAAATTCTCAAAGATTTCTCAGAAAGTGAGTTCCCTAGCATAAAGACTGAATTTC
AACAAGTACTAAGTAATAGGAAAGAAATGACACAGTTTTTGGAAGAGTGGTTAAATACT
CGTTTTGATATAGAAAAGCTTAAAAATGGCATCCAGAAAGAAAATGATAGGATTTGT
CAAGTGAATAACTTCTTTAATAACAGAATAATTGCCATAATGAATGAATCAACAGAG
TTTGAGGAAAGAAGTGCTACCATATCCAAAGAGTGGGAACAGGACCTGAAATCACTG
AAAGAGAAAAATGAAAAACTATTTAAAAACTACCAAACATTGAAGACTTCCTTGGCA
TCTGGTGCCCAGGTTAATCCTACCACACAAGACAATAAGAATCCTCATGTTACATCAA

FIGURE 80 (CONT'D)

GAGCTACACAGTTAACCACAGAGAAAATTCGAGAGCTGGAAAATTCACTGCATGAAG
CTAAAGAAAGTGCTATGCATAAGGAAAGCAAGATTATAAAGATGCAGAAAGAACTT
GAGGTGACTAATGACATAATAGCAAAACTTCAAGCCAAAGTTCATGAATCAAATAAA
TGCCTTGAAAAAACAAAAGAGACAATTCAAGTACTTCAGGACAAAGTTGCTTTAGGA
GCTAAGCCATATAAAGAAGAAATTGAAGATCTCAAAATGAAGCTTGTGAAAATAGAC
CTAGAGAAAATGAAAAATGCCAAAGAATTTGAAAAGGAAATCAGTGCTACAAAAGC
CACTGTAGAATATCAAAAGGAAGTTATAAGGCTATTGAGAGAAAATCTCAGAAGAAG
TCAACAGGCCCAAGATACCTCAGTGATATCAGAACATACTGATCCTCAGCCTTCAAA
TAAACCCTTAACTTGTGGAGGTGGCAGCGGCATTGTACAAAACACAAAAGCTCTTAT
TTTGAAAAGTGAACATATAAGGCTAGAAAAAGAAATTTCTAAGTTAAAGCAGCAAAA
TGAACAGCTAATAAAACAAAAGAATGAATTGTTAAGCAATAATCAGCATCTTTCCAA
TGAGGTCAAAACTTGGAAGGAAAGAACCCTTAAAAGAGAGGCTCACAAACAAGTAA
CTTGTGAGAATTCTCCAAAGTCTCCTAAAGTGACTGGAACAGCTTCTAAAAAGAAAC
AAATTACACCCTCTCAATGCAAGGAACGGAATTTACAAGATCCTGTGCCAAAGGAAT
CACCAAAATCTTGTTTTTTGATAGCCGATCAAAGTCTTTACCATCACCTCATCCAGTT
CGCTATTTTGATAACTCAAGTTTAGGCCTTTGTCCAGAGGTGCAAAATGCAGGAGCA
GAGAGTGTGGATTCTCAGCCAGGTCCTTGGCACGCCTCCTCAGGCAAGGATGTGCCT
GAGTGCAAAACTCAGTAG

Saccharomyces cerevisiae orf name: YDR299W
Saccharomyces cerevisiae gene name: BFR2
GENBANK Accession Number:AAB64735.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 110
ATGGAAAAATCACTAGCGGATCAAATTTCCGATATCGCCATTAAACCGGTCAATAAA
GACTTCGATATTGAAGATGAGGAAAATGCATCTTTATTTCAACACAATGAAAAAAAT
GGAGAAAGTGATTTAAGCGACTATGGAAATAGCAACACAGAAGAAACCAAGAAGGC
GCACTATTTGGAGGTGGAAAAGTCTAAGTTAAGAGCAGAAAAAGGTTTAGAACTAAA
CGATCCAAAATATACAGGTGTTAAAGGTTCAAGACAAGCATTATATGAAGAAGTTTC
CGAGAATGAGGACGAAGAAGAAGAAGAAGAAGAGGAAGAAGAAAAAGAGGAAGAT
GCTCTTTCATTCAGGACAGATTCTGAAGATGAAGAAGTAGAGATTGATGAAGAAGAA
TCAGACGCGGACGGCGGTGAAACGGAGGAGGCTCAACAGAAAAGGCATGCACTATC
GAAACTAATTCAACAAGAGACTAAACAAGCTATTAACAAACTGTCTCAATCAGTTCA
AAGAGATGCTTCGAAGGGTTATTCCATTTTACAACAGACAAAATTATTTGACAACAT
CATTGATTTGAGAATAAAACTACAAAAAGCTGTAATTGCAGCAAATAAGCTCCCATT
AACTACAGAGTCCTGGGAAGAGGCTAAAATGGATGATTCAGAGGAAACAAAGCGTT
TGCTGAAGGAAAACGAAAAACTGTTCAATAATTTATTCAATCGGTTGATAAATTTCA
GAATAAAATTCCAACTTGGCGATCATATCACTCAAAATGAAGAGGTGGCGAAGCATA
AATTGTCCAAAAAAAGATCTCTCAAAGAGCTTTACCAAGAAACTAATAGCTTAGACT
CAGAACTAAAAGAGTACAGGACTGCCGTATTAAACAAGTGGTCTACCAAAGTTTCTT
CTGCATCAGGTAACGCTGCTTTATCATCTAACAAATTCAAAGCTATCAACTTACCTGC

FIGURE 80 (CONT'D)

AGATGTACAAGTCGAAAACCAATTATCCGATATGTCCCGTTTGATGAAAAGAACAAA
GTTGAACAGGAGAAACATAACGCCTTTGTATTTCCAAAAAGACTGTGCTAATGGCAGG
CTACCAGAATTGATTTCTCCCGTTGTCAAAGATAGTGTTGATGACAATGAGAATTCGGAT
GATGGGCTTGATATCCCGAAAAACTATGACCCAAGAAGAAAGGATAACAATGCCATT
GACATTACCGAAAACCCATATGTTTTTGATGACGAAGATTTTTACCGTGTTTTACTAA
ACGATTTAATTGACAAAAAGATTTCCAACGCTCACAATTCTGAAAGTGCAGCAATTA
CAATCACCTCAACTAATGCTCGTTCGAACAACAAGCTAAAGAAGAATATCGATACTA
AGGCTTCCAAGGGTAGGAAATTGAACTACTCAGTTCAAGATCCAATTGCGAATTATG
AAGCCCCCATCACATCCGGATACAAATGGTCAGACGACCAAATCGATGAATTCTTTG
CGGGATTGTTAGGTCAACGAGTGAACTTTAATGAAAATGAGGATGAGGAACAACATG
CCAGAATAGAAAATGACGAA

Candida albicans nucleic acid: SEQ ID NO: 111
ATGAGCTTCTTCGGCTTACACTTTCAACTTAATTCATTGACATTGAACATTTCAAATA
TGGCAAAAAAGTCTTTATCAGAGCAAATTTCTAGTTTATATACACCAAAGACTGATTA
TGATATTGAGGATCATGATTTAGATGTATCTAAAGACAATGGCATTTTTCAGCATCAT
GACGGTGGTTCTGAAAACGAATCTGAAGACGAGGATACTGGCTTAAGAAATGAGCAT
TATGTTGAATCTTCAAAATCAAAGTTGAGACAACAGAATGAAGGTGTGAACTTGGGG
GAAAAATACGTGGGCAATGTCACAAGCAGAAGCAAATTGTATGACGATGAGGATGA
CAAACAACCAACAGAAGCTAGCTCCGGAGAGGAGTTAGATGCTGAATCAGCGGAAG
AAGAAGAGGATGAAGAATCTGAAGATGTAGCAGATGATGATGAAGATGACCAAGAG
TCAGATCGCAGTAGCTCAAGTGATGCAGAGAATGACGAGGACGAGAACATTTCACAC
AAAAGGGAATTATTAAAACAATTAATGAGCAAAGAGAGAAGTCACATCGTTAACAGA
TTATCCCAATCAGCAACAAATGATGCATTAAAAGGTTATTCAATACAACAGCAAAAC
AAAACTTTTGAAAAAATCATTGATGTGAGGTTGAAATTTCAGAAATCGGTAACTTCA
AGTAATATGTTACCTATAAATACAAGTACATATTCAGAAACCAAATCTGAAGATAGC
GATGAATTAGTGACTAAAGCCAAGAAACAATTGTATAGTTTGTTGGATCATTTATTCAC
ACTTAGAAACGAACTAGACGAAAGTACCTCAGTCAAGACCCCCAAAAAACGATCATT
TGCTAAATATTCGGAGGTTACATCTGCTGCAGATGCACAATTGAATTCCCGTCGTAAC
CAAATATTAACCAAGTGGTCAGCTAAAGTTGCCAATTCATCCGGTAGAAATGCCATG
AATGCTAATAAATTCAAAACTATAAACCAATCTTTTGAACAACAGGTTAACAACAAC
TTGTCTGACATGGATAGATTAATCAAAAGAACAAAATTGAACCGAAGAAACGTAACT
CCCATTGGTTATACCACCAAAGAGGAGGATGATCATGAAAATGGCAATAAAAACAAA
TCTATCGACGAGGACGACGACGATATTCCCGAAGATACTTCTGTTCGTAAGAAAACC
CAAGGCTTGGAAAATGATTATATATTTGATGACGAAGATTTCTATAGAGTATTGTTG
AATGATTTAGTCGACAAGAAAGTGCAAACAAGTGATCCAACATCAGGTATAACTATC
AGTTTAAGAGCTGCTCAAAAGTCCAATAAATTGAAAAATAATGTTGATACAAAAGCA
TCTAAAGGTAGGAAATTGAGATATCACGTGCAAGAACCAATTGCTAATTTTGAAACT
TCAAGAGGCAGCTGGAGATGGAATGATGATCAAATTGACGAGTTTTTCGCATCTTTA
TTGGGCCAAAAGGTCAATATGAATGAGATAGATGATGAACAAGAAGAAGAACAAGA
GAATGATGATAATGATATTATTCCAGAGGATAACGGAATCCAGTTGTTTGGTTAA

FIGURE 80 (CONT'D)

Human GENBANK Accession Number: NM_000055
Human nucleic acid sequence: SEQ ID NO: 112
AGTAACAGTTGATTGTTACATTCAGTAACACTGAATGTCAGTGCAGTCCAATTTACAGGC
TGGAGCAGCAGCTGCATCCTGCATTTCCCCGAAGTATTACATGATTTCACTCCTTGCAA
ACTTTACCATCTTTGTTGCAGAGAATCGGAAATCAATATGCATAGCAAAGTCACAATCAT
ATGCATCAGATTTCTCTTTTGGTTTCTTTTGCTCTGCATGCTTATTGGGAAGTCACATAC
TGAAGATGACATCATAATTGCAACAAAGAATGGAAAAGTCAGAGGGATGAACTTGA
CAGTTTTTGGTGGCACGGTAACAGCCTTTCTTGGAATTCCCTATGCACAGCCACCTCT
TGGTAGACTTCGATTCAAAAAGCCACAGTCTCTGACCAAGTGGTCTGATATTTGGAA
TGCCACAAAATATGCAAATTCTTGCTGTCAGAACATAGATCAAAGTTTTCCAGGCTTC
CATGGATCAGAGATGTGGAACCCAAACACTGACCTCAGTGAAGACTGTTTATATCTA
AATGTATGGATTCCAGCACCTAAACCAAAAAATGCCACTGTATTGATATGGATTTAT
GGTGGTGGTTTTCAAACTGGAACATCATCTTTACATGTTTATGATGGCAAGTTTCTGG
CTCGGGTTGAAAGAGTTATTGTAGTGTCAATGAACTATAGGGTGGGTGCCCTAGGAT
TCTTAGCTTTGCCAGGAAATCCTGAGGCTCCAGGGAACATGGGTTTATTTGATCAAC
AGTTGGCTCTTCAGTGGGTTCAAAAAAATATAGCAGCCTTTGGTGGAAATCCTAAAA
GTGTAACTCTCTTTGGAGAAAGTGCAGGAGCAGCTTCAGTTAGCCTGCATTTGCTTTC
TCCTGGAAGCCATTCATTGTTCACCAGAGCCATTCTGCAAAGTGGATCCTTTAATGCT
CCTTGGGCGGTAACATCTCTTTATGAAGCTAGGAACAGAACGTTGAACTTAGCTAAA
TTGACTGGTTGCTCTAGAGAGAATGAGACTGAAATAATCAAGTGTCTTAGAAATAAA
GATCCCCAAGAAATTCTTCTGAATGAAGCATTTGTTGTCCCCTATGGGACTCCTTTGT
CAGTAAACTTTGGTCCGACCGTGGATGGTGATTTTCTCACTGACATGCCAGACATATT
ACTTGAACTTGGACAATTTAAAAAAACCCAGATTTTGGTGGGTGTTAATAAAGATGA
AGGGACAGCTTTTTTAGTCTATGGTGCTCCTGGCTTCAGCAAAGATAACAATAGTATC
ATAACTAGAAAAGAATTTCAGGAAGGTTTAAAAATATTTTTTCCAGGAGTGAGTGAG
TTTGGAAAGGAATCCATCCTTTTTCATTACACAGACTGGGTAGATGATCAGAGACCT
GAAAACTACCGTGAGGCCTTGGGTGATGTTGTTGGGGATTATAATTTCATATGCCCT
GCCTTGGAGTTCACCAAGAAGTTCTCAGAATGGGGAAATAATGCCTTTTTCTACTATT
TTGAACACCGATCCTCCAAACTTCCGTGGCCAGAATGGATGGGAGTGATGCATGGCTA
TGAAATTGAATTTGTCTTTGGTTTACCTCTGGAAAGAAGAGATAATTACACAAAAGCCGA
GGAAATTTTGAGTAGATCCATAGTGAAACGGTGGGCAAATTTTGCAAAATATGGGAA
TCCAAATGAGACTCAGAACAATAGCACAAGCTGGCCTGTCTTCAAAAGCACTGAACA
AAAATATCTAACCTTGAATACAGAGTCAACAAGAATAATGACGAAACTACGTGCTCA
ACAATGTCGATTCTGGACATCATTTTTTCCAAAAGTCTTGGAAATGACAGGAAATATT
GATGAAGCAGAATGGGAGTGGAAAGCAGGATTCCATCGCTGGAACAATTACATGAT
GGACTGGAAAAATCAATTTAACGATTACACTAGCAAGAAAGAAAGTTGTGTGGGTCT
CTAATTAATAGATTTACCCTTTATAGAACATATTTCCTTTAGATCAAGGCAAAAATA
TCAGGAGCTTTTTTACACACCTACTAAAAAAGTTATTATGTAGCTGAAACAAAAATGC
CAGAAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTTACCTAGCATTTCAA
AACCCAAATGGCTAGAACATGTTTAATTAAATTTCACAATATAAAGTTCTACAGTTAA
TTATGTGCATATTAAAACAATGGCCTGGTTCAATTTCTTTCTTTCCTTAATAAATTTAA
GTTTTTTCCCCCCAAAATTATCAGTGCTCTGCTTTTAGTCACGTGTATTTTCATTACCA

FIGURE 80 (CONT'D)

CTCGTAAAAAGGTATCTTTTTAAATGAATTAAATATTGAAACACTGTACACCATAGT
TTACAATATTATGTTTCCTAATTAAAATAAGAATTGAATGTCAATATGAGATATTAAA
ATAAGCACAGAAAATC

Saccharomyces cerevisiae orf name: YDR311W
Saccharomyces cerevisiae gene name: TFB1
GENBANK Accession Number: AAB64747.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 104
ATGTCACATTCCGGAGCTGCCATTTTTGAGAAAGTTTCTGGGATAATTGCCATAAATGAG
GATGTTTCACCCGCAGAATTGACATGGAGGTCTACGGACGGTGACAAGGTTCACACA
GTTGTCTTATCCACTATTGACAAGTTACAAGCTACCCCTGCTTCCAGTGAAAAAATGA
TGTTGAGGCTAATCGGGAAAGTGGATGAGTCAAAAAAGAGAAAAGACAACGAAGGA
AATGAGGTTGTGCCCAAACCGCAACGTCATATGTTTTCGTTTAACAATAGAACAGTT
ATGGATAATATCAAGATGACCCTTCAACAAATCATCTCACGGTATAAAGATGCAGAT
ATCTACGAAGAAAAGAGAAGAAGAGAGGAGTCTGCGCAACACACAGAAACACCAAT
GAGCTCTTCTTCTGTTACTGCAGGGACTCCCACACCACATCTCGATACACCACAATTG
AATAATGGGGCTCCGTTGATTAATACAGCCAAACTAGATGATTCTCTCTCTAAAGAA
AAATTGTTGACCAATTTAAAGCTACAGCAATCTTTACTGAAAGGAAACAAAGTTCTA
ATGAAGGTTTTTCAGGAAACAGTCATTAACGCCGGTTTGCCTCCATCTGAATTTTGGT
CAACTAGAATTCCGTTATTGAGGGCTTTTGCCTTATCTACTTCTCAAAAAGTTGGGCC
TTACAACGTTTTGTCAACTATCAAGCCGGTGGCTTCATCGGAAAACAAAGTCAATGTT
AATTTGTCAAGAGAAAAAAATTTTGAATATTTTTGAGAACTATCCAATTGTAAAGAAA
GCTTACACTGATAATGTGCCCAAAAATTTCAAAGAACCAGAGTTCTGGGCAAGGTTC
TTCTCTTCGAAGTTATTCAGAAAATTAAGGGGTGAAAAGATCATGCAAAATGATAGA
GGTGACGTAATCATTGACAGGTACTTGACATTGGATCAAGAGTTCGACAGAAAAGAT
GATGACATGCTATTGCATCCTGTGAAAAAAATTATAGATTTAGATGGTAACATACAG
GACGACCCAGTTGTACGAGGCAACAGGCCCGACTTCACTATGCAGCCAGGTGTGGAT
ATTAATGGTAATAGCGATGGTACCGTGGACATCTTAAAGGGTATGAATAGATTGAGT
GAAAAAATGATTATGGCTTTGAAGAATGAGTATTCAAGGACAAATCTACAGAAC
AAATCTAATATTACAAACGATGAGGAAGATGAAGATAATGATGAAAGAAATGAACT
GAAAATCGATGACTTAAACGAAAGCTACAAGACAAACTATGCAATCATACATCTGAA
AAGGAACGCACATGAAAAGACAACCGACAACGATGCGAAAAGCTCGGCAGACTCGA
TAAAGAATGCAGATTTGAAGGTTTCTAATCAACAAATGTTACAACAGTTGTCATTGG
TCATGGATAATTTAATTAATAAGCTAGACTTGAACCAAGTAGTTCCTAACAACGAAG
TCAGCAACAAGATCAATAAAAGAGTCATAACTGCAATCAAGATTAACGCCAAACAGG
CTAAGCATAACAATGTTAATTCAGCACTCGGCTCTTTTGTCGACAACACTTCTCAAGC
AAATGAATTAGAGGTGAAAAGTACCCTACCAATAGACCTATTAGAAAGTTGTAGAAT
GCTACACACAACGTGCTGTGAATTTCTAAAGCACTTTTATATTCATTTTCAGAGCGGT
GAACAAAAGCAAGCCAGTACCGTCAAAAAACTTTATAATCATTTGAAGGACTGTATT
GAAAAGCTGAATGAGCTATTTCAAGACGTCCTTAATGGTGATGGTGAATCTATGTCA
AACACATGTACCGCCTATTTGAAGCCAGTTTTGAACTCCATTACTTTGGCTACTCATA

FIGURE 80 (CONT'D)

AGTACGATGAGTACTTCAACGAATATAACAACAATTCGAACTAGGATGTTTCACCCG
CAGAATTGACATGGAGGTCTACGGACGGTGACAAGGTTCACACAGTTGTCTTATCCA
CTATTGACAAGTTACAAGCTACCCCTGCTTCCAGTGAAAAAATGATGTTGAGGCTAA
TCGGGAAAGTGGATGAGTCAAAAAAGAGAAAAGACAACGAAGGAAATGAGGTTGTG
CCCAAACCGCAACGTCATATGTTTTCGTTTAACAATAGAACAGTTATGGATAATATCA
AGATGACCCTTCAACAAATCATCTCACGGTATAAAGATGCAGATATCTACGAAGAAAAG
AGAAGAAGAGAGGAGTCTGCGCAACACACAGAAACACCAATGAGCTCTTCTTCTGTT
ACTGCAGGGACTCCCACACCACATCTCGATACACCACAATTGAATAATGGGGCTCCG
TTGATTAATACAGCCAAACTAGATGATTCTCTCTCTAAAGAAAAATTGTTGACCAATT
TAAAGCTACAGCAATCTTTACTGAAAGGAAACAAAGTTCTAATGAAGGTTTTTCAGG
AAACAGTCATTAACGCCGGTTTGCCTCCATCTGAATTTTGGTCAACTAGAATTCCGTT
ATTGAGGGCTTTTGCCTTATCTACTTCTCAAAAAGTTGGGCCTTACAACGTTTTGTCA
ACTATCAAGCCGGTGGCTTCATCGGAAAACAAAGTCAATGTTAATTTGTCAAGAGAA
AAAATTTTGAATATTTTTGAGAACTATCCAATTGTAAAGAAAGCTTACACTGATAATG
TGCCCAAAAATTTCAAAGAACCAGAGTTCTGGGCAAGGTTCTTCTCTTCGAAGTTATT
CAGAAAATTAAGGGGTGAAAAGATCATGCAAAATGATAGAGGTGACGTAATCATTG
ACAGGTACTTGACATTGGATCAAGAGTTCGACAGAAAAGATGATGACATGCTATTGC
ATCCTGTGAAAAAAATTATAGATTTAGATGGTAACATACAGGACGACCCAGTTGTAC
GAGGCAACAGGCCCGACTTCACTATGCAGCCAGGTGTGGATATTAATGGTAATAGCG
ATGGTACCGTGGACATCTTAAAGGGTATGAATAGATTGAGTGAAAAAATGATTATGG
CTTTGAAGAATGAGTATTCAAGGACAAATCTACAGAACAAATCTAATATTACAAACG
ATGAGGAAGATGAAGATAATGATGAAAGAAATGAACTGAAAATCGATGACTTAAAC
GAAAGCTACAAGACAAACTATGCAATCATACATCTGAAAAGGAACGCACATGAAAA
GACAACCGACAACGATGCGAAAAGCTCGGCAGACTCGATAAAGAATGCAGATTTGA
AGGTTTCTAATCAACAAATGTTACAACAGTTGTCATTGGTCATGGATAATTTAATTAA
TAAGCTAGACTTGAACCAAGTAGTTCCTAACAACGAAGTCAGCAACAAGATCAATAA
AAGAGTCATAACTGCAATCAAGATTAACGCCAAACAGGCTAAGCATAACAATGTTAAT
TCAGCACTCGGCTCTTTTGTCGACAACACTTCTCAAGCAAATGAATTAGAGGTGAAAAGT
ACCCTACCAATAGACCTATTAGAAAGTTGTAGAATGCTACACACAACGTGCTGTGAATTT
CTAAAGCACTTTTATATTCATTTTCAGAGCGGTGAACAAAAGCAAGCCAGTACCGTCAAA
AAACTTTATAATCATTTGAAGGACTGTATTGAAAAGCTGAATGAGCTATTTCAAGACGTC
CTTAATGGTGATGGTGAATCTATGTCAAACACATGTACCGCCTATTTGAAGCCAGTTTTG
AACTCCATTACTTTGGCTACTCATAAGTACGATGAGTACTTCAACGAATATAACAACAAT
TCGAACTAGATGGAACTAGAGCCCACTCTTTTTGGTATAATAGAGGCATTGGCTCCTC
AATTATTGTCGCAGAGTCATTTGCAGACATTTGTATCTGATGTAGTCAATTTACTGCG
ATCATCCACCAAATCGGCAACTCAATTAGGCCCTTTAATTGATTTTTACAAATTACAA
TCACTAGATTCGCCTGAAACAACAATTATGTGGCATAAAATTGAGAAATTTCTCGAT
GCTTTATTTGGAATCCAGAACACCGATGATATGGTAAAGTACCTCTCTGTCTTTCAAT
CTTTGCTTCCATCAAATTACAGAGCAAAAATTGTCCAAAAATCATCTGGGCTCAATAT
GGAGAACCTTGCTAACCATGAACATTTACTTAGCCCAGTGCGGGCTCCAAGTATATA
TACAGAAGCTTCATTTGAAAACATGGACCGATTTTCTGAAAGAAGGTCCATGGTATC
TTCGCCTAATCGTTACGTTCCCTCTTCAACCTACAGTTCTGTTACTTTGAGACAGTTGT

FIGURE 80 (CONT'D)

CAAATCCTTATTATGTGAACACTATACCCGAGGAAGATATCCTAAAATACGTATCATA
TACATTATTAGCTACGACATCGGCACTATTTCCGTTTGATCATGAGCAAATACAAATT
CCGTCTAAGATACCCAATTTTGAGAGTGGACTTTTACATTTAATATTTGAAGCGGGTT
TATTATATCAAAGTTTGGGTTATAAAGTGGAGAAGTTTAGGATGTTGAATATATCTCC
AATGAAAAAAGCATTGATTATAGAAATTTCAGAAGAATTACAAAACTACACAGCATT
TGTGAACAATCTGGTCTCTTCAGGGACAGTAGTGTCATTGAAATCGTTATATCGTGAA
ATATATGAAAATATAATAAGGCTTCGAATATACTGTAGGTTTACAGAACACCTTGAA
GAATTGAGCGGAGATACATTCTTGATTGAATTAAATATTTTCAAATCCCACGGAGAT
CTTACTATAAGAAAAATAGCAACGAATTTGTTTAATTCAATGATTTCTCTTTATTATG
AGTATTTAATGAATTGGTTGACTAAAGGTCTACTCCGAGCTACTTATGGAGAATTCTT
CATTGCTGAAAACACTGATACAAATGGTACAGACGATGATTTTATTTACCACATTCCT
ATAGAGTTCAACCAAGAAAGAGTTCCGGCCTTCATACCGAAAGAGTTGGCATATAAA
ATATTCATGATCGGCAAATCGTATATCTTCCTAGAAAAGTACTGTAAAGAGGTTCAAT
GGACAAACGAATTTTCTAAAAAGTATCATGTCCTGTACCAGAGCAATTCTTATCGGGGA
ATATCAACGAACTTTTTTGAAATTATAAATGATCAATATTCTGAAATTGTTAATCATACT
AATCAAATTCTAAATCAGAAGTTTCATTACAGAGACGTGGTATTTGCGTTAAAGAATATT
CTTCTCATGGGTAAATCTGATTTTATGGATGCTCTTATAGAAAAGGCCAATGATATTCTC
GCGACACCATCGGATTCATTGCCAAATTATAAGTTAACAAGGGTTTTACAGGAAGCC
GTGCAGCTTTCTTCCTTAAGACATTTAATGAATAGTCCCCGTAATAGTTCTGTCATTA
ATGGATTGGATGCGAGGGTACTCGATCTTGGACATGGATCCGTGGGTTGGGATGTTT
TTACTTTAGATTACATCCTCTACCCCCCTTTGAGTTTAGTATTAAACGTAAATCGTCCT
TTTGGCAGGAAAGAGTATCTACGAATTTTCAATTTTTTATGGAGATTTAAAAAGAAC
AATTATTTCTATCAAAAGGAAATGTTGAAGAGTAATGATATAATCAGATCATTCAAG
AAAATCAGAGGTTACAACCCGCTCATCCGTGATATTATCAATAAACTTTCTAGAATCA
GTATACTTAGAACTCAA

Candida albicans nucleic acid: SEQ ID NO: 105
ATGGATATAATTAGAGGTGCATGTTCAGTTGATAAAATTGGGGGGATGGTGTATATT
AGAGAAGATTTAGCACCGCTGATGTTGGAATGGAAACCAATTGATGAACAAGAAGA
AGATAGAGCAATTTCAATCCCATTGAATTCTTTAACTACATTACAAAGTACCAAAGAA
ACCTCACCGAAAATGATACTAAAAATTGTATACAAACTAACATCTGGTCCACCTAAT
ACAAATGCAGATGGAACTGACAATGGTGGTGGTGGTGGTGGTGAACAAAAATCATTT
AAATTGACATTTACTAATAGACCAACCATGAACACTATTAAAGATTCTCTACAAACAA
TTGTTGCTAGATCAAGAACTAAGGGTTTGAAGGTACCAGTACTCCAACTCCAGCTCC
AGCACCAGCTTCAACATTTGGGGTCAGCACCACAAGCTGATTCTACCAGAGATTCGA
CATCATCATCAACACCAATACCACCTACAACATCTGGAACTTCTACTAGTTCATCATT
ATTATCATTAGCAGCATCACAATCATTATCTGATGCAAATTTATTGAAAAATTTCGAA
CTACAGCAAAAACTTTTATTAGAAGATCGTCAATTACGTGATGTTTTCACTAAATCAG
TCATGCAATTTAAATTATCTCCTCAAGTATTTTGGTCATCAAGATTAAATCAATTACG
AACATTTGCTTTGACAATATCTCAACATAAAGGTCCATATAATGTATTGAGTACAATT
AAACCGGTGGCCACTTCTGATAATCAAGTGAATGTTAATGTTACGCGTGATACCATT

FIGURE 80 (CONT'D)

AATGAAATATTTACTATTTACCCCATCATAAAGAAAGCATTTGATGATTTGGTTCCTA
ACAAGTTTAATGAAGGAGAATTTTGGTCGAGATTTTTCAATTCTAAATTGTTTAGACG
CTTAAGAGGTGATAAAATCAGTATTAGTAATAGTCGAGGAGATGTTGTATTGGACAA
ATATTTGTATATAGATCAAAACTATCAAGAAAAATTACAAAAATCATCTACTTTGGAA
AACAACGGTTCTGGTGGTGGTGGTGGTGGCGCTGGTGGTGGTAGTGGTAATTCAGAA
CAAGGAATACAAACATTGGAATCTCCACATGTTAAAAAATTTCTTGATTTGATGGGA
AATCAACAAGATAATTCACAAAAATTGGGGAATAGACCAGATTTTACTATGAGATAT
GATGAAGACACCAATGTAGATGATGATAATAAAAAACCTACTTTAGGAAATGAAAAT
GAAATGATTATATTGATGAAAAATATGAATCGATTATCGTCGAAAATGATGAGTATG
AGTTCTACTAATGGACCAGAGAAACCTTCAGAAACTACAATTGATGGATTATCTGCT
GCTGAATTGAATGAATATGAAGAAGAATTAGATTTGCATGATTTAAATGATTCAGAA
AATTTACAATATATAAAATTAAACATTAATACTGATATTGCCAAGGGAACAAAACTT
GATTCATATGAAGGATCAAATACTAATAACAAGATTTCTCAAGATGAATTACATAAA
TATTTACAATCTCAAACTTTCCAAGGACAAATAGAATTAACAGAAACTTATACTTGTA
AAAGTGAAGAAATTGAAAAAACCTCCATGGAAATAGCCATGCTTATTAAACAAAATT
TCCGAACATTTAAATTAATTAATAAAGAAAATGATATTGCGGGGACAAACATTGTTC
CTAATTCATTAATACAAGAAATCATTACTTATAATATTACGATAGTTGAATTTTTATC
TCATTTTTGGAAGATTTTTTTACATGGGAATAATCCTGGTCAATTAAAGAAAATTTTC
ACCAGTTTGAAAAATTGTCAATCTGGTTTAATAGAATTAGAAAATAAAGCGATTGAT
CAATTCAAATCTATGGATATATTACAAAAAAATCAAAAATTACAAGATAAAGTTTTA
AAAGATTTTGCATCATGTCTTCAACCCATGAAAATAGCATTAGATAAAGCATGTAAT
GAATATGTTGAAGCAGTAAAGAAAGCTAAACCTGAATTAAATGAAAATGGTAAACGT
CCTCTACCAGAGGAGTGA

Human GENBANK Accession Number: W19128
Human nucleic acid sequence: SEQ ID NO: 106
NGNCACATTCTGCNNAGAGATCCTTTGACCCTGNATNCAGCCGATCCCTGTGAAAAT
AATGGGANTGGAAAAAAACGTGTCCAGNATTCCTTCTCTGTCATGTNGTGGGNAACAT
TTTCTGCATATTTCATTTTNACTGCTGGATAGGTCCTNAATATGGACTCAATGATANC
AGAAGTTAAATTATATCTTAGACCGTTANAGCCATCAGTTTGGGGCCGGACATCAGC
NAGAAATGCAGCAGANATGCCAANATCCTGCTTATGATTGGATNTGGAAGAACTATC
TGTTGCATTCACATTTAAACCGATTGGNCCAGAATTCCTCAGCACTGATCACTTGACT
CACGAACAAGGTCTTTATAAAGCTGAAACAAAACCAGGATCTTCTTGCAGCATTCTG
TTCATNCCCTCCAGTNCCTGNATTTGCNTTCCNCTTGAATTTGGGCAGCANCTGCTGA
NGAAGGT

FIGURE 80 (CONT'D)

Saccharomyces cerevisiae orf name: YER022W
Saccharomyces cerevisiae gene name: SRB4
GENBANK Accession Number: AAB64555.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 144
ATGACAACGGAAGATCCAGATTCAAATCACTTAAGTTCCGAAACTGGCATTAAATTG
GCATTGGACCCGAACTTAATTACATTGGCACTAAGTTCTAATCCAAACTCTAGCCTTC
ATTCACCAACGTCTGATGAACCCGTACCTGAATCTGCAGGAAAAGCAGATACTAGTA
TTCGACTAGAAGGTGATGAGTTAGAGAATAAAACTAAGAAAGACAATGATAAGAACT
TAAAATTTTTGAAGAATAAAGATTCTCTAGTCAGTAATCCACACGAAATTTATGGCTC
CATGCCGTTGGAGCAATTGATCCCAATCATCTTAAGACAGCGTGGTCCAGGCTTTAA
ATTCGTTGATTTAAATGAAAAAGAATTGCAAAATGAGATTAAGCAGCTTGGTAGTGA
TAGTAGTGACGGTCATAACAGCGAGAAGAAGGACACTGATGGCGCTGATGAGAATG
TACAAATTGGAGAAGATTTCATGGAAGTGGATTATGAAGATAAAGATAATCCAGTGG
ATTCACGAAATGAAACAGACCACAAAACGAATGAAAATGGCGAGACCGATGATAAT
ATTGAAACGGTAATGACACAGGAACAGTTTGTTAAAAGAAGGAGGGATATGCTAGA
GCATATAAATCTGGCCATGAACGAATCGTCTTTGGCTTTGGAATTCGTTTCTTTGCTA
CTGTCGAGTGTTAAAGAGTCTACAGGTATGTCATCAATGTCACCATTTCTTAGGAAA
GTTGTTAAACCTTCTAGTTTAAACAGTGATAAAATTCCATATGTTGCACCTACAAAAA
AAGAATATATCGAGTTGGATATATTGAATAAGGGATGGAAGTTACAAAGTTTAAACG
AATCTAAAGATCTCCTACGCGCAAGTTTTAATAAACTGAGTTCCATATTACAGAACGA
ACATGACTATTGGAATAAGATAATGCAGAGTATTAGCAACAAGGATGTTATTTTTAA
GATTAGGGACAGGACTAGTGGTCAAAAGCTGTTGGCAATTAAGTATGGTTACGAAGA
CTCTGGATCTACCTATAAGCATGACAGAGGTATTGCTAATATAAGGAATAATATAGA
ATCACAAAATTTGGATTTGATACCCCACAGTAGTTCAGTGTTCAAAGGCACTGATTTC
GTACATTCAGTAAAGAAATTCTTAAGGGTTCGTATCTTCACAAAAATCGAATCAGAA
GATGATTACATATTGAGTGGCGAAAGTGTGATGGATAGGGATAGTGAAAGTGAAGA
AGCTGAAACGAAAGATATCAGAAAGCAAATCCAACTTTTGAAAAAGATCATTTTTGA
AAAAGAACTGATGTACCAAATAAAGAAAGAATGCGCTTTGTTGATTTCCTATGGTGT
CAGTATTGAAAACGAAAACAAGGTAATAATTGAACTACCTAACGAAAAATTTGAAAT
CGAGTTGTTGTCCCTTGACGATGACTCCATTGTCAATCATGAACAAGACTTACCAAAA
ATCAACGACAAGAGAGCAAATTTAATGCTTGTTATGTTGAGACTATTATTAGTCGTTA
TATTCAAGAAAACATTACGATCGAGAATAAGCTCACCCCACGGACTGATCAATTTGA
ATGTTGACGATGATATCTTAATAATACGTCCCATTCTTGGTAAAGTTCGGTTTGCTAA
TTACAAACTGTTACTAAAAAAAATCATAAAGGATTACGTGCTCGATATAGTTCCTGG
CTCAAGTATAACAGAAACGGAAGTTGAGAGAGAACAACCTCAAGAAAATAAAAACA
TTGATGATGAAAATATAACTAAATTAAATAAAGAGATCCGTGCCTTCGATAAACTAT
TGAATATACCTAGACGTGAACTCAAAATAAATCTACCATTAACTGAGCACAAAAGCC
CTAATCTAAGTTTAATGCTCGAAAGTCCTAACTATTGTAACGCACTCATTCACATCAA
GTTTTCAGCTGGTACGGAAGCCAACGCAGTGTCCTTT

FIGURE 80 (CONT'D)

Candida albicans nucleic acid: SEQ ID NO: 145
ATGGTGGAAAAACAGTTTAACATAGACCTAGAGTTAAATGATACTGGTCATATAGAT
CCATTCTTACAAGATGAGTATGTTTGCTTTCTAACTTTATTGGTATTTTTGGTTCTGTT
TTTTAGTTTACTAACCTTGACCAAGAGATAAATTGAAACTTGAGGAACTAATTCCACG
AATTTTATTTGAACGTAAATCATTTTTGAATGTGACGGAGGATTCTTTGAGAAAAGAA
ATAGACAATTCATTGAAGATTTCCGAAGAGGATGCTTTAGACACTGAAGAAAGTAGA
GAGGACACAGTTGAAGCAGATCAACAAGAAGTGTTCAATAAACACAAGTTTGAATTA
TCGAAAAATATAAACAATGCACTTAATGAAACCCAACTTTCCTTAGATTTTGTATCCT
TATTAATATCTTCAGTGAAACCAAGTTTGGCAAAATCTACCATTTCACCACACTTGTC
AAAATTTGTCAAACCGACATCTTTAAATTCGGATAGATTGGGTCAAGATAGTAATGA
TAATCAAGAGAGTAAGGCTACTGATTCTTTTGGACAAGGATGGAAATTGGAGTCACT
TGGAAAGATAACCGATCTTTTCAGAGAAGCTAGTACTAATTTAAACGATCAAGTTAT
CAAAGAAAGACGATATTGGAATATGATAAATTTGGTGCTTGCCAACGACGAGGTTCT
ATTTCGAATGAGGGACCCCCAAAATAATGCTAGAGCAATAGGAGTGAAATATGGGTA
TGGAGATTCAGGATCAAATTTTCACGACCAAGGGTTGGCATTGTTACGCAAGGACAA
CCAAACAGGAGAAATCTCATTTCACCCCATATCGTCAATCAACAATGCTAAAATTGTA
GAAAAAGTTTCGAGATTTATTAGAGTGAAAATTTTGAGCCAAATAGATGGGGACTAT
ATGCTTACAGGACAGTCAATTTTTAATTTTGATTTTGAAAAAAGCAAGCAAAGCATA
ATTAATGACATCGAAAAGGCTAGATTCTTTTTATTTGAGGAGGACTTGTTTCATCAAT
TGATACGCGAGGCCAAATTGTTGGTAAACTACAATGTGTCAATCATATCGAATAAAA
TAATAATTGAAATCAACAACATTATTATTGAAATAGAGTCTATCGTGTATGATGAGTT
GAATGAGGAGGAACTAGAAAACTATTACCAGAATGTAAATGAATATTCCACCTTACA
CAATAAAAAGTGTCAGCTTATTTTAAACTACTTGAAACTTATGCTTTGTTGTTATTAC
AAATACAATCTCAAATTGAAACAGAAGGTTCCAACAGCATTGACTAAATGGAAGCAG
AGTAACTCCCATCCTTTGATTTTGCGTCCGTTAGTGGGTAATATGAGGCATGAGTTAA
ATTTGCTAAATATGAAGAGTGTTTTAGATCGATTAATGCACGCTCATGAGAGTGAAC
TTTCTTATTCCAAACTAGATGTGGAGAAGTTTATTAACTTAGCCACAAGAAGCAAAA
AGCAAAACCCATTCCAAAAGTCAATTGAAAAGCCAATTTCAAAGTTCCATTTAGTTTT
ATGCAACAAAACCTCTAATATGTTGGACGTCAACATACAATTGACAACTAATGAGCT
GTTTGTCAATCTAATCATCAATATGACAATTATTAGATTTGAAACAGAAGACGATTTT
AAGAACAATGTCAATGGTATTAACGTTCTACAGCTTGGGTTCAGTGATTTCAATGAA
ATCGAAGAATGCTTGGATTGGTCGATCCAAAATTTTGTATAGGACACAACATTTTCTG
ATTTTAAAGAAGTAGAGGACTTCCTACATTTTATTGTCGCTGAGTACATCCAGCAAAA
GAAGGTGTAA

Human GENBANK Accession Number: AB015617.1
Human nucleic acid sequence: SEQ ID NO: 146
ATGTATGGAAGTGCCCGCTCTGTTGGGAAGGTGGAGCCGAGCAGCCAGAGCCCTGG
GCGTTCACCCAGGCTTCCACGTTCCCCTCGCTTGGGTCACCGTCGAACCAACAGTACG
GGAGGGAGTTCGGGAAGCAGTGTTGGAGGTGGCAGTGGGAAAACCCTTTCAATGGA
AAATATACAATCTTTAAATGCTGCCTATGCCACCTCTGGCCCTATGTATCTAAGTGAC

FIGURE 80 (CONT'D)

CATGAAAATGTGGGTTCAGAAACACCTAAAAGCACCATGACACTTGGCCGTTCTGGG
GGACGTCTGCCTTACGGTGTTCGGATGACTGCTATGGGTAGTAGCCCCAATATAGCT
AGCAGTGGGGTTGCTAGTGACACCATAGCATTTGGAGAGCATCACCTCCCTCCTGTG
AGTATGGCATCCACTGTACCTCACTCCCTTCGTCAGGCGAGAGATAACACAATCATG
GATCTGCAGACACAGCTGAAGGAAGTATTAAGAGAAAATGATCTCTTGCGGAAGGAT
GTGGAAGTAAAGGAGAGCAAATTGAGTTCTTCAATGAATAGCATCAAGACCTTCTGG
AGCCCAGAGCTGAAGAAGGAACGAGCCCTGAGAAAAGATGAAGCTTCCAAAATCAC
CATTTGGAAGGAACAGTACAGAGTTGTACAGGAGGAAAACCAGCACATGCAGATGA
CAATCCAGGCTCTCCAGGATGAATTGCGGATCCAGAGGGACCTGAATCAGCTGTTTC
AGCAGGATAGTAGCAGCAGGACTGGCGAACCTTGTGTAGCAGAGCTGACAGAGGAG
AACTTTCAGAGGCTTCATGCTGAGCATGAGCGGCAGGCCAAAGAGCTGTTTCTTCTT
CGAAAGACATTGGAGGAAATGGAGCTGCGTATTGAGACTCAAAAGCAGACCCTAAAT
GCTCGGGATGAATCCATTAAGAAGCTTCTGGAAATGTTGCAGAGCAAAGGACTTTCT
GCCAAGGCTACCGAGGAAGACCATGAGAGAACAAGACGACTGGCAGAGGCAGAGAT
GCACGTTCATCACCTAGAAAGCCTTTTGGAGCAGAAGGAAAAAGAGAACAGTATGTTG
AGAGAGGAGATGCATCGAAGGTTTGAGAATGCTCCTGATTCTGCCAAAACAAAAGCT
CTGCAAACTGTTATTGAGATGAAGGATTCAAAAATTTCCTCTATGGAGCGTGGGCTT
CGAGACCTGGAAGAGGAAATTCAGATGCTGAAATCGAATGGTGCTTTGAGTACTGAG
GAAAGGGAAGAAGAAATGAAGCAAATGGAAGTGTATCGGAGCCATTCTAAATTTAT
GAAAAATAAGATTGGCCAGGTGAAACAGGAGCTGTCCAGAAAGGACACAGAACTAC
TCGCCCTGCAGACAAAGCTAGAAACACTCACAAACCAGTTCTCAGATAGTAAACAGC
ACATTGAAGTGTTGAAGGAGTCCTTGACTGCTAAGGAGCAGAGGGCTGCCATCCTGC
AGACTGAGGTGGATGCTCTCCGATTGCGTTTGGAAGAGAAGGAAACCATGTTGAATA
AAAAGACAAAACAAATTCAGGATATGGCTGAAGAGAAGGGGACACAAGCTGGAGAG
ATACATGACCTCAAGGACATGTTGGATGTGAAGGAGCGGAAGGTTAATGTTCTTCAG
AAGAAGATTGAAAATCTTCAAGAGCAGCTTAGAGACAAGGAAAAGCAGATGAGCAG
CTTGAAAGAACGGGTCAAATCCTTGCAGGCTGACACCACCAACACTGACACTGCCTT
GACAACTTTGGAGGAGGCCCTTGCAGAGAAAGAGCGGACAATTGAACGCTTAAAGG
AGCAGAGGGACAGAGATGAGCGAGAGAAGCAAGAGGAAATTGATAACTACAAAAAA
GATCTTAAAGACTTGAAGGAAAAAGTCAGCCTGTTGCAAGGCGACCTTTCAGAGAAA
GAGGCTTCACTTTTGGATCTGAAAGAGCATGCTTCTTCTCTGGCATCCTCAGGACTGA
AAAAGGACTCACGGCTTAAGACACTAGAGATTGCTTTGGAGCAGAAGAAGGAGGAG
TGTCTGAAAATGGAATCACAATTGAAAAAGGCACATGAGGCAGCATTGGAAGCCAGA
GCCAGTCCAGAGATGAGTGACCGAATACAGCACTTGGAGAGAGAGATCACCAGGTA
CAAAGATGAATCTAGCAAGGCCCAGGCAGAAGTTGATCGACTCTTAGAAATCTTGAA
GGAGGTGGAAAATGAGAAGAATGACAAAGATAAGAAGATAGCTGAGTTGGAAAGTC
TCACCTCAAGGCAAGTGAAAGACCAGAATAAGAAGGTAGCAAATCTGAAGCACAAG
GAACAGGTGGAAAAAAAGAAGAGTGCACAAATGTTAGAGGAGGCGCGACGACGGGA
GGACAATCTCAACGACAGCTCTCAGCAGCTACAGGTGGAGGAGTTACTGATGGCCAT
GGAGAAGGTAAAGCAGGAACTAGAATCCATGAAAGCAAAGCTGTCCTCCACCCAGC
AGTCTCTGGCAGAAAAGGAAACTCACTTGACTAATCTTCGGGCAGAGAGAAGGAAAC
ACTTAGAGGAAGTTCTGGAGATGAAGCAAGAAGCTCTTCTGGCTGCCATTAGTGAAA

FIGURE 80 (CONT'D)

AAGACGCCAATATAGCTCTCTTGGAGCTTTCGTCCTCTAAGAAGAAGACCCAAGAGG
AAGTGGCTGCCCTGAAGCGGGAGAAGGATCGTCTGGTACAGCAGCTTAAGCAGCAG
ACGCAAAATCGAATGAAGCTAATGGCCGACAACTACGAG

Saccharomyces cerevisiae orf name: YER127W
Saccharomyces cerevisiae gene name: LCP5
GENBANK Accession Number: AAC03225.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 125
ATGTCTGAACTTAATGCATTATTAAAAGATATCAACGGCTCGCTCACTGCGACATCAGAA
TCCTTGGAGAGGTTGTCTGGGATTTATAGTAATTCTGCGACCGATGAGATTCCTGAAAGT
AACCAACTACATGAGCATCTATTTTACGACGCTAAGAAGCCTGCTGAGAAAGTATCG
CTGCTATCCTTAAAAAATGGGAGCATGCTAGGGTACATAAATTCTCTATTGATGCTTA
TAGGCAATAGGCTAGACGACGAGTGCAAAGATCCTTCTGCTATGGATGCACGTGAAC
GCTCTATTCAACACCGTGTGGTATTAGAGCGTGGTGTTAAACCACTAGAAAAAAAGT
TGGCTTACCAATTGGACAAGCTGACTAGAGCATATGTGAAAATGGAAAAGGAATATA
AAGACGCTGAGAAGCGTGCACTGGAAAAATCTACCTTAGTGAATCATAGCGGCAACG
ACGATAGCGAAGATGATGAGTCTAGTGAGGATGAAATAGCATACAGGCCAAATACCT
CTGGAATTATCAACACAAATAAAAAATCATCAGCATACAGGGTGGAGGAAACGGCTA
AGCAAGAAAACGGGGAAGAAAACGATGACAATGAGACTGGCGTGTATAAACCACCA
AAGATTACGGCTGTTCTACCACCGCAACAAACGCATTTTGAAGATAGATTCGATGCC
AGAGAACACAAAGATCGTAGTAACAAATCGCGTATGCAAGCCATGGAAGAATATATT
AGAGAGTCATCGGACCAACCGGACTGGAGTGCATCTATTGGTGCTGACATTGTGAAC
CATGGAAGAGGCGGTATCAAATCTTTGAGAGACACAGAGAAGGAACGTAGAGTCAC
TTCATTCGAAGAAGATAATTTTACCAGATTGAATATTACAAATAAAGCTGAAAAAAG
GAAGCAAAAGCAACGAGAAAGAAATGCAAGGATGAACGTTATCGGTGGTGAAGATT
TTGGTATATTCAGCTCAAAGAGGAAGCTGGAAGATAGCACTTCGAGA

Candida albicans nucleic acid: SEQ ID NO: 126
ATGTCAAAGGTAGACACTGTATTAAAGGAAATCATCTCGTCTACCAAGTCAACTGAA
GCTTCAGTGAAAGAGTTGATAGCTTTTGTCAAGGACTCGTCTTCCCAACATCCAGAAT
TGGTGCGGAACTTGTTAGCAAAATCAAACCTGCTGTTAGAAGGGGTATCGTTGTTGG
GGTTGAAAAACGAATCGTTGGTGTCCTATATCAACAATATAGTGCTTGTTGTTTTGTC
TCATCTAGAGCGTCTAGAAAGCGATCTGGAGACGGGATCCAGCGCTGTCGAACGATC
GATAATTCAAAGGGTGACATTGGAAAAGGGCGTTAAACCTCTAGAAAAGAAACTCAG
TTATCAGTTGGATAAAATGATCAGGGCATATGGACGGATGGAACAAGACGAAATCAA
AGCTGAACAGAAGTTAAACGATAGAGGAAGTGGGGAGAACGATGAGAACGATGAGA
ACGATTCTGAGGAAGATTCTGAAGAAGATTCTGAAGACGACTCTGAGGACGACGAAT
TGGCTTATAGACCAGATGCATCATCGTTTGCTAAATTGACATCGGCCAAAACCAAAC
TGAAACCAACATCATCAGCAGTCTCTACATCGAATGAAAAGTATAGACCACCAAAGA
TATCAGCAATGGCACCTCCAACTGCAGTAAAGAGCCACGACCTTGATGCCAACACCA

FIGURE 80 (CONT'D)

CGTCGTCAAAGAACCGTAAATTACAGAGCATGGAAGAGTACTTGCAAGAGCAAAGTG
ATATGCCAATGGTGGAGGCATCGGTGGGGTCTACAATTGTGGAGCATGGAAGAGGTGG
TGTTAAAACACAGCACGATCGTAAGAAAGAACGAGAGATACAAACGTATGAAGAGG
ATAATTTTGTCAGACTACCAACCAGTCAAACAAAGAAAAGTTTCAAGGAAAAACAAC
GTGATATCCGTAATCAATTTGCTGGTGAAGACTGGTCGATGTTTAATAATAACAAGG
ATGTGACCCGTCAAGGCACATCGCGAAAGAGAAAGGCAACCACCGTTTGGGACAAA
GTCAAGAAAAAGAAGAATACTTAGATGGTAAGTAGACGCTGACATTTTGCTGCAGTA
TAG

Human GENBANK Accession Number: AL050003
Human nucleic acid sequence: SEQ ID NO: 127
GGGGGCTTTGCGAAGATGGCGGCGCTGGGGGTGCTGGAGTCCGACCTGCCAAGTGC
CGTGACACTTCTGAAAAATCTCCAGGAGCAAGTGATGGCTGTAACTGCACAAGTGAA
ATCACTGACACAAAAAGTTCAAGCTGGTGCCTATCCTACAGAAAAGGGTCTCAGCTT
CTTGGAAGTGAAAGACCAGCTGCTGCTCATGTACCTTATGGATTTGACCCACCTCATT
CTGGACAAAGCCTCAGGAGGATCTCTTCAGGGACATGATGCAGTTTTGAGACTGGTG
GAGATTCGCACGGTTTTGGAAAAGCTTCGTCCCTTGGACCAAAAGCTGAAGTATCAA
ATTGACAAGCTGATCAAGACTGCAGTGACAGGCAGCCTTAGTGAGAATGACCCACTT
CGTTTTAAGCCTCATCCCAGCAATATGATGAGCAAGTTGAGCTCTGAGGATGAGGAG
GAAGATGAAGCAGAAGATGACCAGTCTGAGGCTTCAGGGAAGAAATCTGTGAAGGG
AGTGTCTAAGAAATATGTTCCTCCACGCTTGGTTCCAGTACATTATGATGAAACAGA
AGCTGAGCGGGAGAAGAAGCGTCTAGAACGAGCCAAGAGACGGGCATTGAGCAGCT
CTGTCATTCGTGAACTTAAGGAGCAGTACTCAGATGCTCCAGAGGAAATCCGTGATG
CTCGGCATCCCCATGTTACCCGCCAGAGTCAGGAGGACCAACACAGGATTAACTATG
AGGAGAGCATGATGGTGCGTTTGAGCGTCAGTAAGCGAGAGAAAGGACGGCGAAAA
CGAGCAAATGTCATGAGCTCACAACTTCATTCCCTTACACACTTCAGTGACATCAGTG
CTTTGACAGGGGGAACTGTTCATCTTGATGAGGATCAGAATCCTATTAAGAAGCGGA
AGAAGATACCTCAGAAAGGTCGGAAGAAAAAAGGCCAGTGAACTGCTGGGACTTAG
GTGATCAGGTGCAAGGTGGGGAGTACAAATTGAGTCTCTTTGGATTTGCCATTCTGG
GTCTCACCAAGCCCTGTAGTATCTCTTCCATACTGGGCAATAATCTCCTTAGGTGGGC
GTGGGGCCAAGAAGACTCGTTCTGCCTGGGATAGAGCTCAAAGGAGACTGTAG

Saccharomyces cerevisiae orf name: YFR027W
Saccharomyces cerevisiae gene name: ECO1
GENBANK Accession Number: BAA09266.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 130
ATGAAAGCTAGGAAATCGCAGAGAAAAGCGGGCAGTAAACCAAATCTTATCCAGTCT
AAATTGCAAGTTAATAATGGTTCGAAATCGAATAAAATAGTCAAGTGTGATAAATGT
GAGATGTCATATTCCTCGACATCAATAGAAGATCGCGCCATCCACGAGAAATACCAC
ACTTTACAGCTGCATGGACGTAAATGGTCGCCGAATTGGGGTTCTATAGTATACACA

FIGURE 80 (CONT'D)

GAGCGAAACCATTCAAGGACGGTGCATCTATCAAGATCGACAGGGACAATAACGCCA
TTGAACTCCTCACCTTTGAAAAAAAGTAGTCCGTCTATTACCCATCAGGAGGAGAAG
ATTGTATATGTGAGACCAGATAAGTCGAATGGTGAAGTCCGAGCCATGACGGAGATA
ATGACACTAGTGAATAACGAGCTGAATGCGCCACACGATGAGAATGTCATTTGGAAC
AGTACCACAGAAGAAAAAGGCAAAGCGTTTGTATACATAAGAAATGACAGGGCGGT
CGGAATAATAATTATAGAGAACCTTTATGGGGGCAATGGTAAAACATCTAGTCGTGG
ACGTTGGATGGTTTATGATTCTAGAAGATTGGTACAGAATGTGTACCCCGATTTTAA
GATTGGCATATCGAGAATTTGGGTGTGCAGGACAGCAAGGAAGTTGGGTATCGCAAC
CAAATTGATTGACGTTGCAAGAGAAAATATTGTTTACGGTGAAGTTATTCCTAGGTA
CCAGGTAGCATGGTCGCAACCCACAGACAGCGGTGGAAAACTGGCTAGCAAATACA
ACGGCATTATGCATAAATCAGGCAAGTTACTATTGCCGGTATAC

Candida albicans nucleic acid: SEQ ID NO: 131
ATGGGCTCCATTAATTCTCAAAAACCTCAAAAAATCCAATCAATTCTTGCATTACCAT
CTAATTTCAAAAAAATTACTTGTTCAACATGTGATATGACATATAATCCCCATATATC
TCAAGATAAATTACTACATAACAAATACCACACAAATTTCATCAATGGAATACCCTG
GAATTATAAAACTGATAATGATGTTTTAATAATTGAGAATTTTACATTAGTTGAAACC
CCGAAATTGAATTCCACGGGGAAATCATTAAAGCTGACAAAAACGCGTCAGACATTT
AAAGGTTCTATAATTTGTATAAATAAATCCAACAAACGACATATACAAAAAGTGGAA
CTACTATTAAACATGGTGAATCAAGAGTTGAATGCTAGTCAAGATTCAGGACAATGG
AAGAAACCTGAATTTGATAGAAGTAAAGCATTTGTGATAATAATAGACAGTAAGGCC
ATTGGATTATGCACAACAGATACAATTCAACCTGATCAAGGAAGGTGGATGATACAT
AAAACACAATCTATAGTACCTAATCAGATTAATAAAAATGTTGTCATTGGAATTTCAA
GAATATGGATAAGTCGGAAATGGAGACAATATGGATTAGGTAAAAAACTTTTAAATG
TTGTTTTGAAAAATTCTATTTACAGTGTGCAATTATTGAAGAATCAAGTTGCCTTTAG
TCAACCAAGTTTTAGTGGTGGAATGTTGGCAAAATCATTCAATGGGGTGAAACATAA
AAGTGGTGAAATGTTGTTACCCGTATATATTGAATGATCCTTTCAGGTTTTCGGAGGC
GGCGGTGATTATGGGTGTACATATTTGTATATTTTTTGT

Saccharomyces cerevisiae orf name: YGL122C
Saccharomyces cerevisiae gene name: NAB2
GENBANK Accession Number: CAA96830.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 82
ATGTCTCAAGAACAGTACACAGAAAACTTGAAGGTTATCGTTGCCGAAAAACTGGCT
GGTATACCAAACTTTAACGAAGATATCAAGTATGTTGCGGAGTATATTGTCTTATTGA
TCGTTAACGGTGGTACTGTTGAATCTGTCGTAGACGAGCTGGCTAGTTTGTTTGATAG
TGTTTCGAGAGATACGCTTGCAAATGTTGTTCAAACAGCCTTTTTCGCATTAGAAGCT
CTGCAACAGGGAGAAAGTGCTGAAAATATTGTTTCCAAAATTAGAATGATGAATGCG
CAAAGCTTGGGACAATCGGATATCGCACAACAGCAACAACAGCAACAACAACAACA
GCAACCAGACATCGCGCAACAGCAACCTCAACAGCAACCTCAACAGCAACCTCAACA

FIGURE 80 (CONT'D)

GCAACCTCAACAGCAACCTCAACAGCAACCTCAACAGCAACCTCAACAGCAACCTCA
ACAGCAACCTCAACTTCAACCACTTCAGCCACAACTAGGGACCCAGAATGCAATGCA
GACAGATGCTCCTGCAACTCCATCCCCCATATCAGCCTTTTCCGGCGTTGTTAACGCT
GCAGCTCCCCCTCAGTTTGCGCCTGTAGATAACAGCCAAAGGTTCACTCAACGTGGC
GGAGGCGCCGTTGGAAAGAATCGTAGAGGTGGTCGCGGTGGGAACCGTGGAGGACG
CAACAATAATTCCACACGTTTTAATCCGTTAGCAAAAGCACTTGGAATGGCGGGTGA
GAGTAATATGAACTTCACTCCAACCAAGAAAGAGGGGCGTTGCAGATTGTTTCCTCA
CTGTCCTCTTGGTAGATCATGCCCACATGCACACCCAACTAAGGTATGTAATGAATAT
CCAAATTGTCCAAAGCCTCCCGGAACTTGTGAGTTTTTACATCCAAATGAAGATGAA
GAGTTGATGAAGGAAATGGAAAGAACTCGTGAAGAATTTCAAAAAAGAAAAGCTGA
TTTATTGGCGGCAAAAAGGAAACCGGTACAAACTGGTATCGTTCTGTGTAAATTTGG
GGCTCTGTGTTCCAATCCATCATGCCCATTTGGTCATCCAACACCAGCAAATGAAGAT
GCGAAAGTCATTGATCTAATGTGGTGTGACAAGAATTTGACATGTGATAATCCTGAG
TGTAGAAAGGCCCACTCTTCATTGTCGAAGATCAAGGAAGTAAAACCAATAAGCCAG
AAGAAAGCAGCTCCACCTCCGGTTGAAAAGTCCTTAGAACAATGTAAGTTCGGTACG
CACTGCACCAATAAACGTTGCAAATATAGACATGCTCGTTCTCATATTATGTGCCGTG
AAGGAGCAAACTGTACTAGAATTGATTGTTTATTTGGCCATCCAATTAATGAAGATT
GTAGATTTGGTGTCAATTGTAAGAATATTTACTGTCTATTCAGACATCCTCCAGGCAG
AGTACTTCCGGAAAAGAAAGGCGCTGCACCCAATTCAAACGTTCCTACCAATGAAAG
GCCATTTGCATTGCCAGAAAACGCAATAATTGAAAATGCTCCTCCGCAAACCAGTTTT
ACGCACCAAGAACAA

Candida albicans nucleic acid: SEQ ID NO: 83
ATGCAATTTGCTCCAGATAACCAAATAGGCAAAGAGTTACAGCAAAACTTGATTCAA
GAAATACAAAGGCGTTTCAATAAACCGGCTGATGATGCCGTAGATATTGCTGACTAT
ATCATCTACTTGATTGTGGCAAAAAAGAGCGAACAAGAAATAGTCGCAGAAGTCAAA
GATATTGCTGACATATCTATTGATGTTGGGTTTATTGGGGATGTTTATCTGGAAATCA
GAAAGTTGGAAGTAAAATATAATCAACCTCCTGCTGCAGTGGAGGAAGCTTCTCAAC
CTCAACAAGAACAGCAACAGCAATCTCAAGCTTCTGTAGTGGCTCCACAAATTCCTA
TTGGTCCTAAGAAACAATTAACTGAGGAAGAGAAGATTGCCCTTCGAAGTCAAAGAT
TTGGAACTACTACTAGATTGAGTGGGCGAGGTGGACGTGGTGGTATAACTAAAACTA
GAACCGATTTCAGAAATGGGCACAATAATAAGAACTTCCTAGACCCTAAAAAATTAG
ACCAAATAATTTCTGGTGCCAATAATGGGGCTATTAAGTTTGTACCACTCCCACCAAA
AGGTAGATGTCCAGATTTCCCATATTGTAAGAATCAGAATTGTGAAAAAGCTCATCC
AACAAAAAACTGTTTCAACTACCCGGATTGCCCTAACCCACCGGGAACATGTAATTTT
TTGCATCCGGATCAAGACCAAGAGTTGATTGCTAAATTAGAAACATCTAAAAAAGAA
TTTGAAGAAAAGAAAAAGAATCAACTTATGGTCAAACAAGGCTCATGTAAATATGGT
TTGAAATGTGCTAAAGAAAATTGTCCATTTGCTCACCCAACACCAGCTAATCCTGAAT
CTGGTAAGATTGAAACTTTGGAATGGTGTCCACAAGGTAAGAATTGTCAAGATAGAA
ATTGTACTAAATCACATCCACCTCCACCTACGGCAAACTCAGAAAAATTATTATCAGC
TGCTGACTTGGCATTGGAACAATGTAAATTTGGTTCACAATGTACTAATCTCAAATGT

FIGURE 80 (CONT'D)

CCAAGAAGACATGCAACTTCGGCTGTGCCATGTCGTGCTGGTGCTGAATGTAGAAGA
GTCGATTGTACATTTTCCCATCCATTGAAAGAACCATGCCGTTTTGGAACAAAATGTA
CAAATAAAGTGTGTATGTACCAACATCCTGAAGGAAGAACTATTGCCTCTCACACTT
GGACCAAGGATGGTAGTGGCAATAATAACAGTACCTCAAATCGATCATTTGCTGTTT
CTGAAGATCAGATTATGGAACAAGTTGCTCAATAG

Human GENBANK Accession Number: AF155107.1
Human nucleic acid sequence: SEQ ID NO: 84
ACCCACAGCAGTTGCACTTGCTGAGCAGGCAGCTTGAGGACCCAAATGGTAGCTTTT
CTAACGCTGAGATGAGTGAACTGAGTGTGGCACAGAAACCAGAAAAACTTTTGGAGC
GCTGCAAGTACTGGCCTGCTTGTAAAAATGGGGATGAGTGTGCCTACCATCACCCCA
TCTCACCCTGCAAAGCCTTCCCCAATTGTAAATTTGCTGAAAAATGTTTGTTTGTTCA
CCCAAATTGTAGATACGGAAATGAACTGAAATATGATGCAAAGTGTACTAAACCAGA
TTGTCCCTTCACTCATGTGAGTAGAAGAATTCCAGTACTGTCTCCAAAACCAGTTGCA
CCACCAGCACCACCTTCCAGTAGTCAGCTCTGCCGTTACTTCCCTGCTTGTAAGAAGA
TGGAATGTCCCTTCTATCATCCAAAACATTGTAGGTTTAACACTCAATGTACAAGACC
GGACTGCACATTCTACCATCCCACCATTAATGTCCCACCACGACATGCCTTGAAATGG
ATTCGACCTCAAACCAGCGAATAGCACCCAGTCCTGCCTGGCAGAAGATCATGCAGT
TTGGAAGTTTTCATGTCTGATGAAAGATCTCTACAGAACTTGTCAAATCTTTGAAACT
TGGAATATATTGCTTTCATAATATGAAGGTTTATTGGCTATCTAAAA

Saccharomyces cerevisiae orf name: YGR195W
Saccharomyces cerevisiae gene name: SKI6
GENBANK Accession Number: CAA97221.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 119
ATGTCAAGACTAGAAATATACTCGCCAGAAGGGCTACGTCTCGATGGACGTCGATGG
AATGAACTCCGCCGTTTTGAAAGTTCCATCAACACACATCCGCACGCTGCAGACGGT
TCATCCTACATGGAACAAGGTAACAACAAAATTATCACTCTTGTTAAAGGTCCAAAA
GAGCCAAGATTGAAATCTCAAATGGATACCTCAAAGGCTTTATTGAACGTATCGGTA
AACATTACAAAATTCTCCAAATTCGAAAGAAGTAAATCAAGCCACAAGAATGAAAGG
CGTGTTCTTGAGATACAAACCTCCCTGGTGAGGATGTTTGAGAAGAATGTCATGCTG
AATATCTACCCCAGAACAGTTATCGATATCGAGATCCATGTCCTTGAGCAAGATGGC
GGTATTATGGGATCTTTAATCAACGGTATTACCCTCGCTTTAATAGATGCCGGTATAT
CAATGTTCGATTACATAAGTGGTATATCCGTCGGGCTGTACGATACTACCCCATTATT
AGATACCAATTCATTAGAAGAAAATGCTATGAGTACAGTGACACTAGGTGTGGTAGG
GAAGTCAGAAAAACTTTCTCTTTTATTGGTGGAAGACAAAATTCCGTTAGATAGGTT
AGAGAACGTTCTTGCCATCGGCATCGCAGGTGCTCATAGGGTAAGAGATTTGATGGA
TGAAGAACTGAGGAAACATGCTCAGAAAAGAGTC

FIGURE 80 (CONT'D)

Candida albicans nucleic acid: SEQ ID NO: 120
ATGGAATTATATTCACCTGAGGGACTTAGAATAGACGGAAGAAGATGGAACGAATTG
CGTAGATTTGAATGCCGTATCAACACTCATCCAAACTCATCGGATGGCTCCTCATATG
TCGAACAAGGTAATACCAAAGTGATGTGCACAGTACAAGGACCAA
TAGAACCAGCATTAAGATCTCAACAACATTCAGAACGAGCAAATATAGAAGTGAATT
TGAATATTGCTAGTTTTTCAACTTTTGAAAGGAAAAAACGAAGTAGAAATGAAAGAA
GATTAGTTGAACTTAAAACTACTTTAGAAAAAACATTTGAAGAAAGTGTTATGATAA
ATTTATATCCAAGAACAAATATTGTTATAAATGTTCAAGTATTATGCCAGGATGGTGG
GATGTTAGCTGCAGTTATCAACTCTATTACATTAGCACTCATTGACGCTGGTATATCA
ATGTATGATTATGTGAGTGGTGTATCTTGTGGATTATATGATCAAACACCATTATTAG
ATGTAAATAACTTAGAAGAACACGATATGAGTTGTTTAACAGTTGGTGTTATTGGTA
AAAGTGAGAAATTGGCATTAATGTTGTTAGAAGATAAAATGCCATTGGATAGATTGG
AATCAGTATTGTCAATTGGTATTGCTGGAAGTCATAAAATAAGAGAATTAATGGATC
AAGAAGTGAGGAAGCATGGAATTATTAGGGCTTCTAAAATGCAATAA

Human GENBANK Accession Number: AK000598.1
Human nucleic acid sequence: SEQ ID NO: 121
AGAGAGCGGACCTGGCGGCCGGGCAGCATGGCGGGGCTGGAGCTCTTGTCGGACCA
GGGCTACCGGGTGGACGGGCGGCGCGCCGGGGAGCTGCGCAAGATCCAGGCGCGGA
TGGGCGTGTTCGCGCAGGCTGACGGCTCGGCCTACATTGAGCAGGGCAACACCAAGG
CACTGGCTGTGGTCTACGGCCCGCACGAGATCCGGGGCTCCCGGGCTCGAGCCCTGC
CGGACAGGGCCCTAGTGAACTGTCAATATAGTTCAGCGACCTTCAGCACAGGTGAGC
GCAAGCGACGGCCACATGGGGACCGTAAGTCCTGTGAGATGGGCCTGCAGCTCCGCC
AGACTTTCGAAGCAGCCATCCTCACACAGCTGCACCCACGCTCCCAGATTGATATCTA
TGTGCAGGTGCTACAGGCAGATGGTGGGACCTATGCAGCTTGTGTGAATGCAGCCAC
GCTGGCAGTGCTGGATGCCGGGATACCCATGAGAGACTTTGTGTGTGCGTGCTCAGC
TGGCTTCGTGGACGGCACAGCCCTGGCGGACCTCAGCCATGTGGAGGAAGCAGCTGG
TGGCCCCCAGCTGGCCCTGGCCCTGCTGCCAGCCTCAGGACAGATTGCGCTGCTTGA
GATGGATGCCCGGCTGCACGAGGACCACCTGGAGCGGGTGTTGGAGGCTGCTGCCCA
GGCTGCCCGAGATGTGCACACCCTCTTAGATCGAGTGGTCCGGCAGCATGTGCGTGA
GGCCTCTATCTTGCTGGGGGACTGACCACCCAGCCACCCATGTCCAGAATAAAACCC
TCCTCTGCCCACACAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Saccharomyces cerevisiae orf name: YHR005C-A
Saccharomyces cerevisiae gene name: TIM10
GENBANK Accession Number:AAB68435.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 141
ATGTCTTTCTTAGGTTTCGGTGGTGGTCAGCCTCAATTATCATCTCAACAAAAGATTCAA
GCTGCGGAAGCTGAACTAGATTTGGTCACAGACATGTTCAATAAATTGGTTAATAACTGT
TATAAAAAATGTATCAATACTTCTTATTCCGAGGGTGAGCTGAATAAGAATGAATCTTCG

FIGURE 80 (CONT'D)

TGCCTAGACAGATGTGTGGCCAAATATTTGAGACCAATGTTCAAGTCGGTGAAAAC
ATGCAGAAAATGGGCCAATCATTTAACGCAGCCGGTAAGTTTTAG

Candida albicans nucleic acid: SEQ ID NO: 142
ATGTTTGGCTTAGGTGGTACTACTCCTCAAATTTCATCTCAACAAAAACTTCAAGCTG
CTGAAGCTGAATTAGATATGGTTACTGGCATGTTCAATGCTTTAGTTTCCCAATGTCA
CACCAAATGTATCAACAAATCATATAATGAAGCTGATATTTCAAAGCAAGAATCTTT
ATGTCTTGATAGATGTGTTGCCAAATATTTTGAAACCAATGTTCAAGTTGGTGAAAAT
ATGCAAAAAATTAGGTCAATCTGGTCAATTTATGGGTAGAAGATAAAT

Human GENBANK Accession Number: NM_012456.1
Human nucleic acid sequence: SEQ ID NO: 143
GGAGCCTCACGRGAGCGKGGTAACGTTATAGTATTTGTCAGAAGTTGGGGTCTCCGT
GGGCATTGTGATCCGTCCCAGGCAGTGGATTAGGAGGCCAGAAGGAGATCCCTTCCA
CGGTGCTAGGCTGAGATGGATCCTCTCAGGGCCCAACAGCTGGCTGCGGAGCTGGAG
GTGGAGATGATGGCCGATATGTACAACAGAATGACCAGTGCCTGCCACCGGAAGTGT
GTGCCTCCTCACTACAAGGAAGCAGAGCTCTCCAAGGGCGAGTCTGTGTGCCTGGAC
CGATGTGTCTCTAAGTACCTGGACATCCATGAGCGGATGGGCAAAAAGTTGACAGAG
TTGTCTATGCAGGATGAAGAGCTGATGAAGAGGGTGCAGCAGAGCTCTGGGCCTGCA
TGAGGTCCCTGTCAGTATACACCCTGGGGTGTACCCCACCCCTTCCCACTTTAATAAA
CGTGCTCCCTGTTGGGTGTCATCTGTGAAGACTGCCAGGCCTAGGCTCTCTGTAGAG
AGTCTTCAAGATCCCGGAGTGGTAGCGCTGTCTCCTGGTGAAGGAGTATTTGTCACA
CTGGAATGTGACTGTGTGTGTATGTATGTGTATATATATATATATATATATATATAAA
CAAGTTTGTTGACACCTACAAAAAAAAAA

Saccharomyces cerevisiae orf name: YKL186C
Saccharomyces cerevisiae gene name: MTR2
GENBANK Accession Number: CAA82029.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 88
ATGAACACCAATAGTAATACTATGGTAATGAATGACGCAAATCAAGCACAAATAACG
GCCACATTTACGAAGAAGATATTAGCGCATTTGGATGATCCGGACTCCAACAAATTG
GCCCAATTCGTACAGCTTTTTAATCCAAACAACTGCAGAATAATATTTAATGCTACCC
CCTTCGCGCAAGCAACAGTTTTTCTGCAAATGTGGCAAAACCAGGTCGTACAAACAC
AACATGCCCTAACAGGAGTAGACTATCACGCTATTCCGGGATCCGGCACGTTGATAT
GCAACGTCAATTGCAAAGTCAGATTCGACGAAAGCGGCAGAGACAAGATGGGGCAA
GACGCGACTGTTCCCATTCAACCAAATAACACTGGGAACAGAAATCGACCCAACGAT
ATGAACAAGCCAAGACCTCTATGGGGTCCATATTTTGGCATTTCCCTGCAGCTGATCA
TCGACGACCGCATATTTAGAAATGATTTTAATGGTGTAATATCGGGGTTTAACTATAA
CATGGTTTACAAACCCGAGGATTCTCTGCTAAAAATTTAG

FIGURE 80 (CONT'D)

Candida albicans nucleic acid: SEQ ID NO: 89
CATCCTATAGCACAACAACTAGAGCCGTTTCTCAAACGATTTCTTGCATCGTTAGATT
TACTGTACACACAGCCAACATCACAACCATTCCCCAACGTTGAATCGTATGCCACTCA
GTTAGGATCAAACTTAAAGCGGTCAAGTGCAATTATAGTGAACGGCCAGCCTATTAT
ACCGAGCCCACAAGAAGACTGTAAATTACAATTCCAAAAGAAATGGTTACAAACTCC
GTTATCGTCACACCAATTGACAAGTTACGATGGGCATTTAATTCCAGGCACGGGGAC
CTTTGTCGTTCATTTTTCAGCAAAAGTAAGATTTGATCAAAGTGGAAGGAACCGGTT
AGGTGAATCTGCCGACTTGTTTCAGGAAAATAATTCAATTGTTTCCAAAACCAATCAA
AGACCTATTTGGGGTTCGTGGTTTGGAGTCGACGTCAATTTGGTTGTTGACGAAAAC
GTTATGCAAGATGGAGAGATTATAAATAGTATGGATTATAGATTTACCTATGTACCT
AACGATAGCATTATAAAAGTATAA

Saccharomyces cerevisiae orf name: YKR062W
Saccharomyces cerevisiae gene name:TFA2
GENBANK Accession Number: CAA82141.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 79
ATGAGTAAAAACAGGGACCCTCTACTGGCTAATTTGAACGCTTTCAAAAGCAAAGTG
AAGTCTGCCCCGGTGATCGCACCCGCTAAAGTTGGACAGAAGAAGACCAATGACACA
GTGATTACTATAGATGGAAACACTAGGAAGAGGACGGCCTCCGAACGTGCGCAAGA
AAACACTTTGAACTCTGCGAAAAATCCTGTGTTAGTGGATATCAAGAAAGAAGCTGG
GAGCAATAGCTCTAATGCTATTTCATTAGATGACGACGATGACGACGAAGATTTTGG
TAGCTCTCCTTCAAAAAAAGTAAGGCCTGGCTCTATTGCTGCAGCCGCTTTACAAGCA
AATCAAACAGATATTTCCAAGAGTCACGATTCTTCAAAGTTGCTTTGGGCGACTGAA
TACATTCAAAAGAAAGGTAAGCCCGTTTTGGTGAATGAGTTATTGGACTACTTGTCA
ATGAAAAAAGATGACAAGGTTATTGAGCTTTTAAAAAAATTAGATAGAATAGAGTTT
GACCCCAAGAAGGGGACTTTCAAATACCTTTCCACCTACGATGTCCATTCCCCTTCGG
AACTGCTGAAGTTGTTACGTTCACAAGTAACATTCAAAGGTATTTCCTGCAAAGACTT
GAAAGACGGTTGGCCACAATGCGATGAAACGATTAACCAACTGGAGGAAGACAGCA
AAATTTTGGTGTTAAGAACTAAAAAGGATAAAACTCCAAGATACGTTTGGTATAACA
GCGGTGGTAACTTGAAATGTATTGACGAGGAGTTTGTTAAAATGTGGGAAAATGTGC
AATTACCGCAATTTGCAGAATTGCCAAGAAAGCTGCAAGATTTAGGTCTAAAGCCTG
CTAGTGTCGATCCTGCTACTATCAAAAGACAAACAAAGAGAGTTGAAGTTAAAAAGA
AGAGACAAAGAAAGGGTAAGATTACTAACACTCATATGACCGGTATC

Candida albicans nucleic acid: SEQ ID NO: 80
ATGTCCGACTTATCAGCTCAACTTTCAGCTTTTAAGAATAAGATCAAAAGTGGACCAT
CGGTGATTGTTCCTAGAAAGGCAACTTTTACTCAATCTCCATCATCACCATTATCATC
ATCAACCACAACAACAACACTGAAGAATGACGCCAATGTGAAGAAGAGATCAACGA
CGGATTCAGTAACCCGAGTATTGAAGAAACAAAAGGCAAATATGGGAGAAATGACG
GGATCACATTTATCGACACAATTACACCTTGCTGTTGAATATATCAAGGAACATGACC

FIGURE 80 (CONT'D)

AACCAATATCGGTGGAGAAGTTGCAGAATTATTTATCATTTGATATATCACATACTTT
ATTGCCATTATTGAATGAAATTGATCGAGTGAAATACGACGAATCTAAGGGTACAT
TGGAATATGTTTCATTGCATAATATTCGTAGTAGTGATGATTTATTGGAATTTTTGAG
ACGTCAAACCACATTCAAGGGCACTTCCGTAAAAGAATTAAAAGATGGTTGGGCTGG
TTGTGTTGCCGCTATAGACGAATTAGAATCACAAGGCAAAATTTTGGTGTTGCGTAA
CAAGAAGGAAAATGCTCCAAGATTAGTATGGGCTAATAATGGTGGTGAGTTGGGTTA
TATTGACACAGAATTCAAGGATATGTGGGATCAAGTGAAATTGCCGGAACCAGATGT
ATTGTATCAGAAATTATTGGATCAAGGATTGAAACCTACGGGAGCTGATCCTAATTT
GATCAAAAAGCAACCACAACAAAAGGAAAAGAAACAAAAGAAAGCAAGAAGAGGAAA
GATTACAAATACACATATGAAAGGTATTTTGAAGGATTATTCTCAATTAGTTTGA

Human GENBANK Accession Number: NM_002095.1
Human nucleic acid sequence: SEQ ID NO: 81
CTTAAATTACCCACTACGTTGTCCAGTCGCCGCCTCAGCTACCGCCGCTGCCGCCGCCGC
CGCCGCCACCGCCAGTGGTGAGACCCCGACCTGGCGGGTCAGCGCTGGGCGTGCGTG
CGGGCAGGCGGGGGCGCTGACGAGAAGCAGGAAGAGGGTGCAGTGCCGGCGTGGGC
GGCCGGCCGAGGCGGAGGCGCAGGAAGGGGGCGGCGAGTCGTGCGAGGCTGCCCTT
CTCACTCAGCATTATGGATCCAAGCCTGTTGAGAGAAAGGGAGCTGTTCAAAAAACG
AGCTCTTTCTACTCCTGTAGTAGAAAAACGTTCAGCATCTTCTGAGTCATCATCATCA
TCGTCAAAGAAGAAGAAAACAAAGGTAGAACATGGAGGATCGTCAGGCTCTAAACA
AAATTCTGATCATAGCAATGGATCATTTAACTTGAAAGCTTTGTCAGGAAGCTCTGG
ATATAAGTTTGGTGTTCTTGCTAAGATTGTGAATTACATGAAGACACGGCATCAGCG
AGGAGATACGCATCCTCTAACCTTAGATGAAATTTTGGATGAAACACAACATTTAGA
TATTGGACTCAAGCAGAAACAATGGCTAATGACTGAGGCTTTAGTCAACAATCCCAA
AATTGAAGTAATAGATGGGAAGTATGCTTTCAAGCCCAAGTACAACGTGAGAGATAA
GAAGGCCCTACTTAGGCTCTTAGATCAGCATGACCAGCGAGGATTAGGAGGAATTCT
TTTAGAAGACATAGAAGAAGCACTGCCCAATTCCCAGAAAGCTGTCAAGGCTTTGGG
GGACCAGATACTATTTGTAAATCGTCCCGATAAGAAGAAAATACTTTTCTTCAATGAT
AAGAGCTGTCAGTTTTCTGTGGATGAAGAATTTCAGAAACTGTGGAGGAGTGTCACT
GTAGATTCCATGGACGAGGAGAAAATTGAAGAATATCTGAAGCGACAGGGTATTTCT
TCCATGCAGGAATCTGGACCAAAGAAAGTGGCCCCTATTCAGAGAAGGAAAAAGCCT
GCTTCACAGAAAAAGCGACGCTTTAAGACTCATAACGAACACTTGGCTGGAGTGCTG
AAGGATTACTCTGACATTACTTCCAGCAAATAGGGAACAGTTTTGCCCTGGAACAGA
GTTACAGATACACAATCAAGAGTGTTCTTGCTGATGCTCGGGGTCTGAAGACTGTCTT
CCTATCTGCTTCTTGCGGCTGAGGAGAGGAGCAGTTCAGTTTACAAAACAAGTGCAA
ATTACCAAACTCAAAGCTTATTTGAGTAGAATGGGCTCATGGGCAATGTGATGTTCC
CTGTTAACCTTCTGTTACTCCCTGGGAGAAAGGCGCTGAGCGTGGCATGCAGGTGTC
TTTGCTGTGTTTTTCTCCACTTCTAAATGGTTCCTGGTTCCTTTCTTCCTCGTTTGTTA
CTTTAGAGCAAGTTTGCCCATAGTCTTGAATGCAATATTTGTTTATTCCAAAAGAACA
TATTTATAATAA

FIGURE 80 (CONT'D)

Saccharomyces cerevisiae orf name: YLR078C
Saccharomyces cerevisiae gene name: BOS1
GENBANK Accession Number: CAA97636.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 90
ATGAACGCTCTTTACAACCATGCTGTGAAGCAAAAAAATCAACTACAACAAGAGTTG
GCCAGGTTTGAAAAGAATTCTGTGACCGCCCCTATTTCTTTACAAGGGTCCATCTCTG
CAACTCTGGTCTCACTGGAGAAAACAGTTAAGCAATATGCAGAACATTTAAACAGAT
ATAAAGAAGATACTAATGCAGAGGAAATTGATCCTAAGTTCGCTAATCGACTAGCAA
CTTTAACACAGGATCTGCACGACTTTACTGCCAAGTTTAAGGATTTAAAACAATCCTA
CAACGAAAATAATTCCAGAACTCAGTTGTTTGGCTCAGGAGCATCGCATGTTATGGA
CTCCGATAACCCCTTTAGTACATCAGAGACCATCATGAATAAAAGGAACGTTGGTGG
TGCGAGTGCAAATGGTAAAGAGGGCTCTAGCAACGGTGGGGGACTACCGTTGTACCA
AGGGCTACAAAAGGAACAGTCTGTTTTCGAAAGGGGTAACGCTCAATTAGATTACAT
TCTAGAAATGGGCCAACAATCATTCGAAAATATAGTGGAACAAAACAAAATTTTATC
CAAGGTACAAGATAGAATGTCAAATGGCCTAAGAACATTGGGTGTTTCGGAACAAAC
TATCACCTCTATCAATAAACGGGTGTTCAAAGATAAACTAGTCTTTTGGATCGCGTTA
ATTCTCTTGATCATAGGTATTTATTATGTGTTG

Candida albicans nucleic acid: SEQ ID NO: 91
ATGAATTCAATATATAATCATGGTTTAAAACAAACCCAAACTATAACTAAAGATTTAA
CTCAATTCGAGAAAAACTTATCCACATCACCATTATCATTACAAGTGCAATCACAACA
TCATTAACTGCATTCAGGAAAACTATCGAAGAATATGATGATTTATTGGAAGTAAAT
GTCTATGATACATCTGATACCATAGATGAGGGTAGATTAGATATATTCAATCCAGATT
TAAATGAATACACTCTGAAATATGATACTTTAAATAAGCTACGTGAGTTTCTTCTCCA
TCAAGCTAATAAACAAGAATTATTAGGAGAAGGACACTTATCACCAACAGCAACAGC
AGCATTGGATCGACATCATCAGATAATCCGTATGAATCTAGCTCAAATCCATCTCAAC
AACAACAACAGCAATTACAAGATGAACAAAACACCATGTCTTATAGAGAAGGATTAT
ATCATGAAAAGAATTCTCTAGA

Human GENBANK Accession Number: NM_003569.1
Human nucleic acid sequence: SEQ ID NO: 92
GAGGGAGCCGTGGAGGTCCAGGTGACTGCTTAGAAAACTGCACAGCATCTGATGAA
ATTAGCGAATAAGAACATCAACCATGTCTTACACTCCAGGAGTTGGTGGTGACCCCA
CCCAGTTGGCCCAGAGGATCTCTTCTAACATCCAGAAGATCACACAGTGTTCTGTGG
AAATACAAAGAACTCTGAATCAACTTGGAACACCTCAAGATTCACCTGAATTGAGGC
AACAGTTGCAACAGAAGCAGCAGTATACTAACCAGCTTGCCAAAGAAACAGATAAGT
ACATTAAAGAGTTTGGATCTCTGCCCACCACCCCCAGTGAACAGCGTCAAAGGAAAA
TACAGAAGGATCGCTTAGTGGCAGAGTTCACAACATCACTGACAAACTTCCAGAAGG
TCCAGAGGCAGGCTGCTGAGCGAGAGAAAGAGTTTGTTGCTCGAGTAAGAGCCAGTT
CCAGAGTGTCTGGCAGTTTTCCTGAGGACAGCTCAAAAGAAAGGAATCTTGTATCCT

FIGURE 80 (CONT'D)

GGGAAAGCCAAACTCAACCTCAAGTGCAGGTGCAGGATGAAGAAATTACAGAGGAT
GACCTCCGTCTTATTCATGAGAGAGAATCTTCTATCAGGCAACTTGAAGCTGATATTA
TGGATATTAATGAAATATTTAAAGATTTGGGAATGATGATTCATGAACAAGGAGATG
TAATAGATAGCATAGAAGCCAATGTGGAAAATGCAGAGGTGCACGTTCAGCAAGCA
AATCAGCAGCTGTCAAGGGCAGCAGATTATCAGCGCAAATCCAGAAAAACCCTGTGC
ATCATCATTCTTATCCTTGTCATTGGAGTTGCGATTATCAGTCTCATCATATGGGGAT
TGAACCACTGAAGTTATAAAGGAGCACACTGTCGCACTACATTGTCTAAATTATGTA
GGAAGATTCCTGTAATCATGTTTTTTAATTATTATTTTAAAGCTATTGTATAAAGGA
TGGTTCCCATACTTTGTTATTTTTATTGGGGGGGTTGGGCGGGTTCCTTTGGATTAAA
TCTGATATTTTCTAATACTGAAAGATTTTCTAAATGTCACTGCTGACATAACTCCCTT
GGTCTTCAATTTAATAGTTGTTAAGTTTTGGGCCACATTGCATATGCCTTTCATTTAT
AATTTATTTACCCTGCTTGACTTAGTTTGGGGAATTCGGAAATTTAAGGTGTGTGTAT
TCTGTTGGGATCTCCCTGCCACGTGAACACACCAAGATGTGTGTTACTTCAAGTTAAAA
CTCCCCAAAATTTAATTTTTGATTTGCTTCCACCAGGGGAAAATATTCTCCAATAATGTA
AAATAATTAAGGTCCAATACATGGGTTGTATTTTTCTGGTTCACAACAGCACAAAGTGTC
TTTCATTTTTTTGTTGGATTTCCTTTAAGATCTTTTTTACCCTGAAGTCGGTGAACACTT
TTCTAGTTAATTTGATACTCTTTCTGTGTATATAATAAGCTTTTGCTGTAGATTGCCTAG
TAAAATTACTAAGGATAGGTTGTTTTTACATATGGTCTATTTAAGTCTGATGTTTACGGG

Saccharomyces cerevisiae orf name: YLR291C
Saccharomyces cerevisiae gene name: GCD7
GENBANK Accession Number: AAB67337.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 116
ATGTCCTCTCAAGCATTCACTTCAGTACATCCGAATGCGGCAACATCTGATGTGAATGTT
ACCATTGACACTTTCGTTGCTAAGTTAAAAAGAAGACAAGTGCAAGGTTCATACGCCATC
GCCTTGGAAACTTTACAACTGTTAATGCGATTTATCTCTGCAGCTCGTTGGAACCATGTT
AATGACCTTATTGAACAAATCAGAGATTTAGGTAATAGTCTAGAAAAAGCTCATCCTACT
GCTTTCAGTTGCGGTAACGTAATTAGAAGAATACTGGCTGTTTTGAGGGATGAAGTA
GAAGAAGACACTATGAGCACAACTGTCACATCCACATCCGTTGCTGAACCTTTGATTT
CCTCTATGTTTAATTTATTACAGAAACCGGAGCAACCTCATCAGAATAGAAAAAAATA
GTTCAGGGAGCTCTAGTATGAAAACCAAGACTGATTACCGTCAAGTAGCCATTCAGG
GTATCAAGGATCTTATAGATGAGATAAAAAACATTGATGAAGGTATTCAGCAAATTG
CTATTGATTTGATTCACGATCATGAGATTTTATTAACTCCCACACCTGATTCAAAAAC
CGTATTAAAATTTCTGATTACTGCTCGCGAACGTAGTAATAGAACATTTACGGTTTTA
GTTACAGAGGGGTTCCCTAATAACACCAAGAATGCACATGAGTTTGCCAAAAAATTA
GCACAGCACAACATAGAAACCCTAGTAGTCCCAGACTCAGCTGTTTTTGCTTTAATGT
CCCGTGTGGGTAAGGTTATTATCGGCACTAAAGCCGTTTTTGTCAATGGGGGGACTA
TCTCGTCAAATTCAGGTGTATCATCCGTTTGTGAATGCGCCCGAGAATTTAGAACCCC
TGTATTTGCTGTTGCAGGTTTGTATAAGCTTTCTCCTCTATATCCGTTCGACGTAGAG
AAGTTTGTCGAATTTGGTGGGTCCCAACGTATATTACCTAGAATGGATCCAAGAAAA
AGATTAGATACAGTTAATCAAATTACCGATTATGTTCCGCCTGAAAATATTGATATCT

FIGURE 80 (CONT'D)

ACATTACAAACGTCGGTGGGTTCAATCCAAGTTTTATATATCGTATTGCGTGGGATAA
TTACAAGCAAATTGATGTGCATTTGGATAAAAATAAG

Candida albicans nucleic acid: SEQ ID NO: 117
ATGTCGAAATTGCTTACTCCTGAAATTCTAGCGCTCATAGACCCAGTGGTGTCTAGTT
TGAAACGTCATCAGCTTGTGGATGATAAGGAGATAGCATTAACAATTGCCCAGTTGT
TGATGAAAGTCATATCAGCAGCAAGATGGTCTAATACATATGATTTAATTGAATTGA
TAAGACAAGTTGGTGTTATATTTACCGAAGCATATCCTAGAAAAGTCATTCCAGGAA
ATATTGTGAGAAGAGTGTTAGCTTTAATACGTGATGAAACCGAAACTGAAACTGAGA
CAGAGACTGAACAAACAGATAACATCCCAATGATGAGCTCTATGTTTAGTTTATTGG
CAACACATAACAAAAATGAAACTATAAAGGAACAAACACAATTACAACTGAAGAAAC
AAACAAGCGATATGAGAGCCATAATTATACAAGGGATTAGAGATTTAGTTGATGAAA
TTTCCAATGTTAATGATGGGATTGAAACTATGGCGGTTGATTTGATTCATGACGATGA
AATATTATTAACTCCAACCCCTAATTCGGAAACAGTGCAACATTTTTTAATCAAAGCA
AGATTGAAAAGAAAATTCACAGTAGTTGTTACTGAAAACTATCCAAACGACATCAAG
GCAGCCCACAAGTTTGTAAAGACACTAGCTGAACACAACATCGAAACAATTTTAATT
CCAGACACAACAATTTATGCAGTGATGTCAAGAGTTGGGAAAGTTATAATAGGTACT
AATGCTGTATTTGCCAATGGTGGCTGTTTGTCAGATTCAGGTGTTGCCAATGTAGTTG
AATGTGCCAAAGAACACAGAACACCTGTGTTTGCTGTGGCAGGGTTATTCAAATTAT
CTCCATTGTATCCATTTACAAGAAACGATTTGATTGAAGTAGGAAACTCCGGGAAGG
TTTTGAACTACGACGATTTTGAATTGGTACAAAATGTTGATGTTGTGACTAATCCTTT
GGAAGATTATATACCTCCTCAACATATCGACATTTTTATGACCAATATTGGAGGGTTT
TCTCCTTCATTTATTTATAGAATTGTTTTGGATAATTATAAAGCTGAAGACAACAAAC
TTGAATAA

Human GENBANK Accession Number: L40395.1
Human nucleic acid sequence: SEQ ID NO: 118
AAAAAGGGTTCGGAGTTGTCAGAGAGGATCGAGAGCTTCGTGGAGACCCTGACGCG
GGGTGGTGGGCCGCGCAGGTCCGAGGAAATGGTCGGGAGACCCTAGGGTTGCTGCG
CCAGATCATCACGGACCACCGATGGAGAAACGCGGGGGAGCTGATGGAGCTGATCC
GCAGAGAGGGCAGGAGGATGACGGCCGCTCAGCCCTCCGAGACCACCGTGGGCAAC
ATGGTGCGGAGAGTGCTCAAGATTATCCGGGAGGAGTATGGAGACTCCATGGACGC
AGCGACGGAGAGTGATCAGCAGGAGTCCCTGGACAAACTGTTGACAYCCGGAGGCC
TAAACGAGGATTTCAGCTTCCATTATGSCCAACTCCAGTCCAACATCATTGAGGCGAT
TAATGAGCTGCTAGTGGAGCTGGAAGGGACAATGGAGAACATTGCAGCCCAGGCTCT
GGAGCACATTCACTCCAATGAGGTGATCATGACCATTGGCTTCTCCCGAACAGTAGA
GGCCTTCCTCAAAGAGGCTGCCCGAAAGAGGAAATTCCATGTCATTGTAGCAGAGTG
TGCTCCTTTCTGCCAGGGTCATGAAATGGCTGTGAATTTGTCCAAAGCAGGTATTGA
GACAACTGTCATGACTGATGCTGCCATTTTTGCCGTTATGTCAAGAGTCAACAAGGT
GATCATTGGCACCGAAGACCATCCTGGCCAATGGGGCCCTGAGAGCTGTGACAGGAA

FIGURE 80 (CONT'D)

CTCACACTCTGGCACTGGCAGCAAAACACCATTCCACCCCACTCATCGTCTTGTGCAC
CTATGTTCAAACTTTCTCCACAGTTCCCCAATGAAGRRGMCYCATWWMATAAGTTTG
GTGGCTCCTGAAGAAGTCCTGCCATTCACAGAAGGGGAMATYCTGGAGAAGGTCAG
CGTGCATTGYCCTGTGTTTGACTACGYTCCCCCAGAGCTCAWTACCCTCTTTAGCGTGA
TCTCCAACATTGGTGGGAATGCACCTTCTTACATCTACCGCCTGATGAGTGAACTCTACC
ATCCTGATGAWCATGTTTTATGACCGACCACACGTGTCCTAAGCAGATTGCTTAGGC
AGATACAGAWTGAAGAGGAGACTTGAGTGTTGCTGCTGAAGCACATCCTTGCAATGT
GGGAGTGCACAGGAGTCCACCWAAAAAAAAAATCCTTGATACTGTTGCCTGCCTTTT
TAGTCACCCCGTAACAAGGGCACACATMCAGCAYTGTGTCTTGCCTTTCAGATCTTA
ACAGAGCAGCAGGGCTTAACTTGTTGATTTKGGAGSCTCTTAGTGACCTGGTTGCGTC
TGTGTCAGGAACTTAAACTTTCTGGTTCAGTAGTGTGKTAAACATAACRCTGWANAC
CTTACTGGGATACAGATTTTTGCTCAGAAATGGCTATGACACTTTTTCTAGGCTCTAC
CAATAAAARCCACTTGAAGGTTC

Saccharomyces cerevisiae orf name: YMR005W
Saccharomyces cerevisiae gene name: MPT1
GENBANK Accession Number:CAA88520.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 85
ATGGCAAATTCGCCGAAAAAGCCATCTGATGGCACTGGAGTATCAGCGTCAGACACG
CCTAAATATCAACATACCGTCCCAGAAACGAAACCAGCATTTAATTTGTCACCAGGT
AAAGCTAGTGAGCTATCACATAGCCTTCCGTCGCCTAGCCAGATAAAATCAACCGCA
CATGTATCTTCAACTCACAATGATGCGGCAGGTAATACGGATGATTCTGTTCTTCCTA
AAAATGTATCACCCACAACTAATTTGAGAGTTGAAAGTAATGGAGATACAAACAATA
TGTTCTCTAGCCCTGCTGGACTAGCTCTACCAAAAAAGGATGATAAAAAAAAAAACA
AGGGTACGAGTAAAGCAGATTCTAAAGATGGCAAAGCATCCAACTCCTCAGGACAGA
ATGCACAACAACAATCAGACCCAAATAAAATGCAAGATGTCCTTTTTTCCGCAGGTA
TCGATGTTAGGGAGGAGGAGGCTCTTCTAAATTCATCTATTAATGCCTCAAAATCCCA
AGTTCAAACAAATAACGTTAAGATCCCCAACCATTTACCATTCCTTCACCCGGAACAA
GTTTCCAATTATATGAGGAAAGTCGGAAAAGAGCAAAACTTCAACCTGACCCCTACA
AAGAATCCTGAAATTTTGGACATGATGTCAAGTGCCTGCGAAAACTATATGAGAGAT
ATCCTAACAAATGCCATTGTCATCTCCCGACATAGAAGAAAAGCAGTCAAGATAAAT
TCTGGTAGAAGAAGTGAAGTTTCTGCGGCTTTAAGAGCCATTGCACTAATTCAAAAA
AAAGAAGAAGAAAGGCGTGTGAAAAAAAGAATTGCGTTGGGACTCGAGAAGGAAGA
TTATGAAAATAAGATTGATTCCGAAGAGACGTTACACAGAGCATCGAACGTTACGGC
TGGCCTTAGAGCAGGTAGTAAAAAACAGTATGGTTGGCTAACTTCATCAGTAAATAA
GCCGACGTCCTTGGGAGCAAAATCTTCAGGCAAAGTCGCCTCCGACATCACGGCTAG
AGGAGAAAGTGGGCTAAAGTTTAGAGAAGCTAGAGAGGAGCCTGGTATAGTAATGA
GGGATTTACTCTTTGCTCTCGAAAATAGGCGCAACAGCGTTCAGACTATTATTTCA

FIGURE 80 (CONT'D)

Candida albicans nucleic acid: SEQ ID NO: 86
AATCACCGAATTATATCACATAAATCCATGACAAGTACACCTCAAGAATCCTCTAATT
TAAAGAGACAATTAGAAAACAGTGAGGACTCCAGCTCACCAAATAAGGAATCTAAAA
CAGAGACTACCACGGAAAACCAGAGCTCATGGGAGTCTGACTTTAATAGTTTACCAG
TGGAATTACTACAAACTGAAACAAATGGTACATCACCAGCACCAGCACCAGCAACAC
CGATCGATACCACCAATGCATCAAGCACAAAGGAACGTGATCAGGATACTTCTAAAT
TAAATGACGCGATTGCTGCTGCAGGAGTTGATATTCAACAAGAAGAAGAGATATTAT
TACAACAACAATTAAATAGAAAATCTGCAGAGGGTATGGCAAGCAATCTAAAAAGTG
TGATCAGGTCCAGCAAACTGCCTCCATTTCTACACAATTACCATTTAGCTGCCTTTAT
TGATAAAGTGGCTAAACAAAATGGAATTCAACAGAATTTCTTAATGGATGGTGAGAT
GTTGGAATTAATTTCAGCTGCTTGTGAGACTTGGTTAAGTAATCTAGCAACAAAAAC
GATAATCTTGTCACGCCACAGGAGAAGGGGAATACCTGTTATTAATAAGAAGTCAGG
AAGTAGTTCAGTTCCAAGATCAGAAATTTCAAAAGAATTGAGAAGCTTGGCCTTAAA
ACAAAAGGAAATGGAAGAGAAACGAGTGAATAAAAGAGTGATGTTGGGGTTGGAAA
AAAGCACCAAAGACGCATCCAAAAATGACGAAAATGGTGAATCAAAAGCTGGTGCTGA
AGAAACATTACATCGTGCAGCAAATGCTACAGCTGCAATGATGACTATGAATCCCGG
GAGAAAGAAATATAGTTGGATGACTTCAAGTGCTACAGCAGGCGGTGGGTCAGACTT
TGGTAAATCAAGTGGTGGCTCATCAAAGGACTCGGGAAAACACCAAAGTCCTATTAT
TTCAGTACGTGGTGATAATGGCCTTAGGTTTAGAGAAATAAGGTCAGGTAATTCCAT
TATTATGAAAGATTTGTTAGGCGCAATTGAAGATGAAAAAATGGGTACGAGAAATGC
TGTAATAAAAGGATATGCAAAATTGAAAGATTAA

Human GENBANK Accession Number: Y11354.1
Human nucleic acid sequence: SEQ ID NO: 87
ATGGCGGCGGGCTCGGATCTGCTGGACGAGGTCTTCTTCAACAGCGAGGTGGACGAG
AAAGTGGTGAGCGACCTGGTGGGCTCGCTGGAGTCGCAGCTGGCGGCCAGCGCGGC
CCACCACCACCACCTCGCGCCGCGCACGCCCGAGGTGCGGGCCGCGGCCGCCGGCGC
GCTCGGGAACCATGTTGTGAGCGGCAGCCCGGCCGGAGCCGCGGGCGCAGGGCCGG
CCGCCCCCGCCGAGGGCGCGCCCGGAGCGGCGCCGGAGCCGCCCCCGCAGGTAGA
GCGCGGCCGGGGGGCGGGGGGCCGCAGCGCCCGGGCCCCCCCTCACCGCGCCGCCC
CCTTGTCCCCGCAGGGCCCGCGCCGCCCGCCGCGAAGCTGAGGCCGCCGCCCGAGGG
CAGCGCGGGGGCCTGCGCCCCGGTGCCCGCCGCCGCCGCCGTCGCCGCGGGGCCCG
AGCCCGCCCCCGCCGGCCCCGCCAAGCCCGCCGGCCCCGCCGCGCTGGCCGCCCGCG
CCGGCCCCGGCCCCGGGCCCGGCCCCGGCCCCGGCCCCGGCCCTGGCAAGCCCGCCG
GCCCCGGCGCCGCGCAAACTTTGAATGGGAGCGCCGCGCTGCTGAACTCGCACCACG
CCGCCGCACCTGCTGTCAGCCTGGTCAACAACGGGCCCGCCGCGCTGCTGCCGCTGC
CCAAGCCCGCCGCCCCCGGCACTGTCATCCAGACGCCCCCCTTCGTGGGCGCCGCCG
CGCCCCCCGCGCCCGCCGCGCCCTCGCCCCCGCCGCCCCCGCGCCCGCCGCCCCCG
CCGCCGCCCCGCCCCCGCCACCCCCGCGCCCGCCACCCTGGCCCGGCCGCCCGGCC
ACCCCGCCGGACCCCCGACCGCCGCGCCCGCCGTGCCGCCCCCGCCGCCAAGGGTT
ATGCCAAGATCAGAGATTAAGCCCAGAACGGGGCAGCGCCGGGGCAGCCCCCGCC

FIGURE 80 (CONT'D)

CCCGCCCCGGCCGCCGGGGGCCCCGCTGGGGTCAGCGGCCAGCCCGGGCCCGGCGC
GGCGGCTGCGGCGCCGGCGCCGGGGGTCAAGGCCGAGTCGCCCAAGAGGGTGGTGC
AGGCGGCGCCCCCGGCGGCGCAGACCCTGGCGGCCAGCGGCCCGGCCAGCACGGCG
GCCAGCATGGTCATCGGGCCAACTATGCAAGGGGCGCTGCCCAGCCCGGCCGCCGTC
CCGCCGCCCGCCCCCGGGACCCCCACCGGGCTGCCCAAAGGCGCGGCCGGCGCAGTG
ACCCAGAGCCTGTCCCGGACGCCCACGGCCACCACCAGCGGGATTCGGGCCACCCTG
ACGCCCACCGTGCTGGCCCCCCGCTTGCCGCAGCCGCCTCAGAACCCGACCAACATC
CAGAACTTCCAGCTGCCCCCAGGAATGGTCCTCGTCCGAAGTGAGAATGGGCAGTTG
TTAATGATTCCTCAGCAGGCCTTGGCCCAGATGCAGGCGCAGGCCCATGCCCAGCCT
CAGACCACCATGGCGCCTCGCCCTGCCACCCCCACAAGTGCCCCTCCCGTCCAGATCT
CCACCGTACAGGCACCTGGAACACCTATCATTGCACGGCAGGTGACCCCAACTACCA
TAATTAAGCAAGTGTCTCAGGCCCAGACAACGGTGCAGCCCAGTGCAACCCTGCAGCGC
TCGCCCGGCGTCCAGCCTCAGCTCGTTCTGGGTGGCGCTGCCCAGACGGCTTCACTTGGG
ACGGCGACGGCTGTTCAGACGGGGACTCCTCAGCGCACGGTACCAGGGGCGACCAC
CACTTCCTCAGCTGCCACGGAAACTATGGAAAACGTGAAGAAATGTAAAAATTTCCT
ATCTACGTTAATAAAACTGGCTTCATCTGGCAAGCAGTCTACAGAGACAGCAGCTAA
TGTGAAAGAGCTCGTGCAGAATTTACTGGATGGAAAAATAGAAGCAGAAGATTTCAC
AAGCAGGTTATACCGAGAACTTAATTCTTCACCTCAACCTTACCTTGTGCCTTTCCTG
AAGAGGAGCTTACCCGCCTTGAGACAGCTGACCCCCGACTCCGCGGCCTTCATCCAG
CAGAGCCAGCAGCAGCCGCCACCGCCCACCTCGCAGGCCACCACTGCGCTCACGGCC
GTGGTGCTGAGTAGCTCGGTCCAGCGCACGGCCGGGAAGACGGCGGCCACCGTGAC
CAGTGCCCTCCAGCCCCCTGTGCTCAGCCTCACGCAGCCCACGCAGGTCGGCGTCGG
CAAGCAGGGGCAACCCACACCGCTGGTCATCCAGCAGCCTCCGAAGCCAGGAGCCCT
GATCCGGCCCCCGCAGGTGACGTTGACGCAG

Saccharomyces cerevisiae orf name: YMR131C
Saccharomyces cerevisiae gene name:RSA2
GENBANK Accession Number: CAA88556.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 96
ATGTCGAAAAGGTCTATCGAGGTCAACGAGGAACAAGATAGAGTGGTCTCTGCTAAA
ACAGAATCTCACTCTGTTCCTGCTATTCCCGCCTCTGAAGAGCAAGATGCTCCCAAGA
ATGACCTAGAAGAACAATTGAGTGATGAATTTGATAGTGATGGTGAAATTATTGAAA
TTGATGGCGATGATGAGATTAATGACGAAGATGACCTTAGGAAAAAGCAAGAAGAA
GCTGAAACTTTAGTACAAAAGGACCAATCCGAAGGCAACAAAGAAAAGATCCAGGA
GCTTTACTTACCCCATATGTCTCGTCCATTAGGGCCAGATGAAGTCCTTGAGGCTGAT
CCCACTGTTTATGAAATGCTACATAATGTCAATATGCCATGGCCATGCTTGACATTAG
ATGTCATTCCAGATACACTAGGTTCTGAACGTAGAAACTATCCACAGTCTATTTTGTT
GACCACGGCTACTCAATCTTCCAGGAAAAAGGAGAATGAACTAATGGTTCTAGCACT
TTCTAATTTAGCGAAAACACTTTTGAAAGACGATAATGAAGGTGAAGATGATGAAGA
GGATGATGAAGATGATGTGGATCCAGTCATTGAGAATGAAAATATACCATTGAGAGA
TACAACCAATAGATTAAAGGTTTCTCCTTTTGCCATTTCTAATCAAGAGGTGTTAACC

FIGURE 80 (CONT'D)

GCTACAATGAGCGAAAATGGTGATGTTTATATATACAATCTAGCTCCACAAAGCAAA
GCTTTTTCCACACCAGGTTATCAGATTCCGAAGTCTGCTAAGCGTCCTATTCACACTG
TAAAAAATCATGGGAATGTTGAAGGCTACGGGTTGGATTGGTCACCATTGATCAAGA
CTGGTGCGTTACTATCAGGTGATTGCTCAGGACAAATATATTTTACCCAAAGGCACA
CATCGAGATGGGTGACTGATAAACAACCATTTACTGTTTCAAACAATAAATCCATAG
AAGATATCCAGTGGTCTCGCACTGAATCCACCGTTTTTGCAACCGCAGGATGTGATG
GATATATAAGGATTTGGGACACAAGATCAAAAAAACATAAACCTGCTATCTCTGTTA
AAGCTTCTAATACTGACGTAAATGTCATAAGTTGGAGTGATAAAATTGGTTACTTGCT
AGCAAGCGGTGACGATAACGGTACATGGGGAGTATGGGATTTAAGACAGTTTACGCC
AAGTAATGCTGACGCCGTCCAACCGGTTGCTCAATATGACTTCCATAAGGGAGCCATT
ACTTCCATTGCATTCAACCCATTAGATGAGTCTATCGTTGCGGTAGGCTCAGAAGATAAT
ACTGTGACTTTGTGGGATTTGTCTGTAGAAGCTGACGATGAGGAAATTAAACAACAG
GCCGCCGAAACAAAAGAGCTACAAGAAATTCCACCACAATTATTGTTTGTTCACTGG
CAAAAGGAAGTTAAAGATGTCAAATGGCATAAGCAAATCCCAGGTTGTTTAGTAAGT
ACCGGTACT

Candida albicans nucleic acid: SEQ ID NO: 97
ATGTCAAAAAGATCAGCTGAAGATGATTTAAGTGGCAATAGATCCACCAGTCATACT
GCCATTAAAACTAATAAAGATTCTCTTCCAACTACTACAAATGGAAAGGAAGAAGAA
CCAGACAATATGGATATTGGGGAATTTGAAGATCCATACGGTGATGAATTTGAAAGT
GATGAAGAAATTATAGAATTAGACGATAACAATGATGAAGAAGATGATGAAATGATT
GATGAAAATTCAACACAAGCCAAAATTGAAGAATTAGAAGCCAAAGAACAAGAACA
AGAACAACAATCATCAATATATTTACCTCATAAATCAAAACCATTAGGACCAGATGA
AGTCTTAGAAGCCGATCCAACAGTCTATGAAATGTTGCATAATATCAATTTACCATGGC
CATGTTTGACTGTTGATATTTTACCAGATTCTTTAGGTAATGAAAGAAGATCATATCC
AGCAACAGTTTATTTAGCTACTGCGACTCAAGCTGCTAAAGCCAAAGATAATGAATT
GTTAGCTATGAAAGCATCTTCATTGGCCAAAACATTAGTTAAAGATGAAAATGAAGA
AGATGAGGAAGATGAAGACGATGACGATGATGTTGATAGTGATCCAATATTAGATTC
AGAATCTATTCCATTAAGACATACTACAAATAGAATAAGAGTAAGTCCTCATGCTCA
ACAAACTGGGGAATACTTAACTGCTTCAATGTCAGAAAATGGTGAAGTTTATATATT
TGATTTACTGGCACAATATAAGGCATTTGACACACCAGGTTATATGATTCCTAAATCA
TCGAAAAGACCAATTCATACTATTCGTGCCCATGGGAATGTTGAAGGTTATGGATTA
GATTGGTCTCCATTAGTAAATACAGGGGCTTTATTATCTGGAGATATGTCAGGGAGA
ATTTATTTAACTAATAGAACGACATCAAGTTGGACCACTGATAAAACTCCATTTTTTG
CATCACAATCTTCAATTGAAGATATTCAATGGTCAACTGGTGAAACTACAGTGTTTGC
CACGGGTGGATGTGATGGATATATTTGTATTTGGGATACAAGATCGAAAAAACATAA
ACCTGCATTATCAGTAATTGCTTCTAAATCTGATGTTAATGTGATATCTTGGAGTTCT
AAAATCAATCATTTATTGGCATCAGGACATGACGATGGTAGTTGGGGTGTATGGGAT
TTAAGAAATTTCACAAACAATACCACCAGTAATCCTTCACCTGTGGCTAATTATGATT
TCCATAAATCGCCAATCACATCAATTTCATTCAATCCATTAGATGAATCAATCATTGC
TGTTTCATCAGAAGATAATACTGTTACATTATGGGATCTTGCTGTTGAAGCTGATGAT

FIGURE 80 (CONT'D)

GAAGAAATTTCTCAACAAAGAAAAGAAGCTCAAGAATTACATGATATTCCACCACAA
TTATTATTTGTCCATTGGCAAAGAGATGTTAAAGATGTTAGATGGCATCCACAAATTC
CTGGTTGTTTGGTATCTACTGGTGGTGATGGATTAAACATTTGGAAAACTATATCTGT
GTAA

Human GENBANK Accession Number: NM_005610.1
Human nucleic acid sequence: SEQ ID NO: 98
CGCGCGCACAGAGCGAGCTCTTGCAGCCTCCCCGCCCCTCCCGCAACGCTCGACCCC
AGGATTCCCCCGGCTCGCCTGCCCGCCATGGCCGACAAGGAAGCAGCCTTCGACGAC
GCAGTGGAAGAACGAGTGATCAACGAGGAATACAAAATATGGAAAAAGAACACCCC
TTTTCTTTATGATTTGGTGATGACCCATGCTCTGGAGTGGCCCAGCCTAACTGCCCAG
TGGCTTCCAGATGTAACCAGACCAGAAGGGAAAGATTTCAGCATTCATCGACTTGTC
CTGGGGACACACACATCGGATGAACAAAACCATCTTGTTATAGCCAGTGTGCAGCTC
CCTAATGATGATGCTCAGTTTGATGCGTCACACTACGACAGTGAGAAAGGAGAATTT
GGAGGTTTTGGTTCAGTTAGTGGAAAAATTGAAATAGAAATCAAGATCAACCATGAA
GGAGAAGTAAACAGGGCCCGTTATATGCCCCAGAACCCTTGTATCATCGCAACAAAG
ACTCCTTCCAGTGATGTTCTTGTCTTTGACTATACAAAACATCCTTCTAAACCAGATC
CTTCTGGAGAGTGCAACCCAGACTTGCGTCTCCGTGGACATCAGAAGGAAGGCTATG
GGCTTTCTTGGAACCCAAATCTCAGTGGGCACTTACTTAGTGCTTCAGATGACCATAC
CATCTGCCTGTGGGACATCAGTGCCGTTCCAAAGGAGGGAAAAGTGGTAGATGCGAA
GACCATCTTTACAGGGCATACGGCAGTAGTAGAAGATGTTTCCTGGCATCTACTCCA
TGAGTCTCTGTTTGGGTCAGTTGCTGATGATCAGAAACTTATGATTTGGGATACTCGT
TCAAACAATACTTCCAAACCAAGCCACTCAGTTGATGCTCACACTGCTGAAGTGAAC
TGCCTTTCTTTCAATCCTTATAGTGAGTTCATTCTTGCCACAGGATCAGCTGACAAGA
CTGTTGCCTTGTGGGATCTGAGAAATCTGAAACTTAAGTTGCATTCCTTTGAGTCACA
TAAGGATGAAATATTCCAGGTTCAGTGGTCACCTCACAATGAGACTATTTTAGCTTCC
AGTGGTACTGATCGCAGACTGAATGTCTGGGATTTAAGTAAAATTGGAGAGGAACAA
TCCCCAGAAGATGCAGAAGACGGGCCACCAGAGTTGTTGTTTATTCATGGTGGTCAT
ACTGCCAAGATATCTGATTTCTCCTGGAATCCCAATGAACCTTGGGTGATTTGTTCTG
TATCAGAAGACAATATCATGCAAGTGTGGCAAATGGCAGAGAACATTTATAATGATGAA
GACCCTGAAGGAAGCGTGGATCCAGAAGGACAAGGGTCCTAGATATGTCTTTACTTG
TTGTGATTTTAGACTCCCCTTTTTTCTTCTCAACCCTGAGAGTGATTTAACACTGGTTT
TGAGACAGACTTTATTCAGCTATCCCTCTATATAATAGGTACCACCGATAATGCTATT
AGCCCAAACCGTGGGTTTTTCTAAATATTAATAGGGGGGCTTGATTCAACAAAGCCA
CAGACTTAACGTTGAAATTTTCTTCAGGAATTTTCTAGTAACCCAGGTCTAAAGTAGC
TACAGAAAGGGGAATATTATGTGTGATTATTTTTCTTCTTATGCTATATCCCCAAGTT
TTTCAGACTCATTTAAGTAAAGGCTAGAGTGAGTAAGGAATAGAGCCAAATGAGGTA
GGTGTCTGAGCCATGAAGTATAAATACTGAAAGATGTCACTTTTATTCAGGAAATAG
GGGGAGTTCAAGTCGTATAGATTCCTACTCGAAAATCTTGACACCTGACTTTCCAGG
ATGCACATTTTCATACGTAGACCAGTTTCCTCTTGGTTTCTTCAGTTAAGTCAAAACA
ACACGTTCCTCTTTCCCCATATATTCATATATTTTTGCTCGTTAGTGTATTTCTTGAGC

FIGURE 80 (CONT'D)

TGTTTTCATGTTGTTTATTTCCTGTCTGTGAAATGGTGTTTTTTTTTTTGTTGTTGGTT
TTTTTTTTTTTTTTTTAACTTGGGACCACCAAGTTGTAAAGATGTATGTTTTTACCTGA
CAGTTATACCACAGGTAGACTGTCAAGTTGAGAAGAGTGAATCAATAACTTGTATTT
GTTTTAAAAATTAAATTAATCCTTGATAAGAGTTGCTTTTTTTTTTTAGGAGTTAGTC
CTTGACCACTAGTTTGATGCCATCTCCATTTTGGGTGACCTGTTTCACCAGCAGGCCT
GTTACTCTCCATGACTAACTGTGTAAGTGCTTAA

Saccharomyces cerevisiae orf name: YMR235C
Saccharomyces cerevisiae gene name: RNA1
GENBANK Accession Number: CAA90206.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 113
ATGGCTACCTTGCACTTCGTTCCTCAGCACGAGGAAGAACAAGTTTACTCCATCTCTGGG
AAGGCACTCAAGTTAACAACCAGTGACGATATCAAACCATACCTGGAAGAATTGGCA
GCTTTGAAAACCTGTACCAAATTAGACCTTTCAGGGAATACAATCGGTACTGAAGCT
TCGGAAGCATTAGCTAAATGCATCGCTGAAAATACACAGGTCAGGGAATCTTTGGTT
GAAGTAAATTTTGCTGACTTATACACTTCGAGGTTGGTTGACGAAGTCGTTGATTCGT
TGAAGTTTTTATTGCCTGTTCTGTTGAAATGTCCTCACTTGGAGATTGTGAACCTTTC
TGATAATGCGTTTGGGCTAAGAACAATCGAGTTACTAGAAGATTACATTGCACATGC
CGTGAATATCAAACATTTGATCTTAAGTAACAATGGTATGGGCCCTTTTGCTGGTGAA
AGGATTGGTAAGGCCCTATTTCATCTCGCTCAAAATAAGAAAGCTGCTTCCAAACCA
TTTTTGGAAACTTTTATCTGTGGTAGAAATAGATTAGAGAATGGATCCGCAGTCTACT
TAGCTCTGGGTTTGAAAAGCCACTCCGAAGGTTTGAAAGTCGTAAAGCTGTACCAAA
ATGGTATTAGGCCTAAAGGTGTCGCCACGCTAATTCATTACGGTTTACAGTACTTGAA
AAACTTGGAAATCTTGGATCTTCAAGACAATACTTTCACGAAACATGCTTCTTTGATC
CTTGCTAAGGCCTTGCCTACATGGAAGGATAGTTTATTTGAATTGAATTTGAACGACT
GTCTTTTGAAAACTGCTGGTTCAGATGAAGTCTTTAAAGTATTCACCGAAGTTAAATT
CCCCAATTTGCATGTCTTGAAATTCGAATATAATGAAATGGCTCAAGAAACCATTGA
AGTATCCTTCTTACCGGCTATGGAAAAGGGAAATTTACCTGAATTGGAAAAGCTAGA
AATAAATGGTAACAGATTAGATGAAGATTCTGATGCTTTAGATTTGCTCCAAAGCAA
ATTTGATGATTTAGAGGTTGACGATTTTGAAGAGGTCGATAGTGAAGATGAGGAAGG
CGAGGACGAGGAAGACGAGGACGAGGATGAAAAACTCGAAGAAATTGAAACGGAAA
GGCTTGAAAAGGAACTGCTAGAAGTACAAGTAGATGATCTTGCTGAACGT

Candida albicans nucleic acid: SEQ ID NO: 114
ATGGCATCAGTAGAAGTTGAATTAGGAGTTACTCCAGAAACCACTTATTCAATTTCA
GGAAAACAACTAAAATTTGATTCTGAATCGGATATTGCTCCATATATCAAGGAATTG
ACGGAAAAAGAAAATGTCAAAAAAGTTGATTTTTCAGGAAATACTATTGGTATTGAAG
CATCAAAAGCATTAAGTGAAGCATTATTAAAACATAAAGACACTATCGTTGAAATCA
ACTTTTCTGATTTATACACTGGTAGATTGAATACTGAAATTCCTCAATCTTTAGAGTA
TTTGTTACCAGCATTGTCGAAATTGCCAAATTTGAAATTGATCAACTTGAGTGACAA

FIGURE 80 (CONT'D)

TGCTTTTGGATTGCAAACTATTGATCCAATTGAAGCTTACTTGGCCAAAGCTGTTTCC
ATCGAGCATTTGATTTTGTCAAACAATGGTATGGGTCCATTTGCTGGGTCAAGAATTG
GAGGATCTTTGTTTAAGTTAGCTAAGGCTAAGAAAGCAGAAGGAAAGGAGTCTTTGA
AAACATTTATTTGTGGTAGAAACAGATTGGAAAATGGTTCTGTTAACTATTTATCTGT
TGGGTTAAGAAATCACAAGGATTTGGAAGTGGTTAGATTGTATCAAAATGGTATTAG
ACCTGCTGGTATTTCTAAATTGGTTGAGCAAGGTTTATCTAACAACAAAAAAATTAAA
AGTGCTTGATTTGCAAGACAATACCATCACTACCAGAGGAGCTATTCACATTGCAGA
ATCATTATCTAACTGGCCACTTTTGGTTGAGTTGAATCTTAACGATTCCTTATTGAAG
AACAAAGGTTCTTTGAAATTAGTCGAAGCCTTCCATGCTGGAGATGAAAAACCGCAA
TTAATTACCTTGAAATTACAATATAATGAGTTAGAAACAGATAGTTTAAGAGTTTTGG
CTGATGCAATTGCCAGTAAATTACCACAATTGAAGTTCTTGGAATTGAACGGTAATA
GATTTGAAGAGGATTCCGAACATATCGATAAAATCAATGGAATCTTCGAAGAAAGAG
GCTATGGCGAAATAGATGAATTGGATGAATTAGAAGAGCTTGATAGTGAAGAAGAA
GAAGATGACGAGGATGACGAAGGAGAAGACGACACATTAGAGGAAGACCTTGATTT
GACACAATTAGAAGAAGAATTGGCTGGAGTTTCTTTGGAAGACAAAGATGGTAACGTGG
ATGAAATTGCCGAAGAATTATCCAAAACTCATATTAAATAG

Human GENBANK Accession Number: X82260.1
Human nucleic acid sequence: SEQ ID NO: 115
ATGGCCTCGGAAGACATTGCCAAGCTGGCAGAGACACTTGCCAAGACTCAGGTGGCC
GGGGGACAGCTGAGTTTCAAAGGCAAGAGCCTCAAACTCAACACTGCAGAAGATGCT
AAAGATGTGATTAAAGAGATTGAAGACTTTGACAGCTTGGAGGCTCTGCGTCTGGAA
GGCAACACAGTGGGCGTGGAAGCAGCCAGGGTCATCGCCAAGGCCTTAGAGAAGAA
GTCGGAGTTGAAGCGCTGCCACTGGAGTGACATGTTCACGGGAAGGCTGCGGACCG
AGATCCCACCAGCCCTGATCTCACTAGGGGAAGGACTCATCACAGCTGGGGCTCAGC
TGGTGGAGCTGGACTTAAGCGACAACGCATTCGGGCCCGACGGTGTGCAAGGCTTCG
AGGCCCTGCTCAAGAGCTCAGCCTGCTTCACCCTGCAGGAACTCAAGCTCAACAACT
GTGGCATGGGCATTGGCGGCGGCAAGATCCTGGCTGCAGCTCTGACCGAATGTCACC
GGAAATCCAGTGCCCAAGGCAAGCCTCTGGCCCTGAAGGTCTTTGTGGCTGGCAGAA
ACCGTCTGGAGAATGATGGCGCCACTGCCTTGGCAGAAGCTTTTAGGGTCATCGGGA
CCCTGGAGGAGGTCCACATGCCACAGAATGGGATCAACCACCCTGGCATCACTGCCC
TGGCCCAGGCTTTCGCTGTCAACCCCCTGCTGCGGGTCATCAACCTGAATGACAACA
CCTTCACTGAGAAGGGCGCCGTGGCCATGGCCGAGACCTTGAAGACCTTGCGGCAGG
TGGAGGTGATTAATTTTGGGGACTGCCTGGTGCGCTCCAAGGGTGCAGTTGCCATTG
CAGATGCCATCCGCGGCGGCCTGCCCAAGCTAAAGGAGCTGAACTTGTCATTCTGTG
AAATCAAGAGGGATGCTGCCCTGGCTGTTGCTGAGGCCATGGCAGACAAAGCTGAGC
TGGAGAAGCTGGACCTGAATGGCAACACCCTGGGAGAAGAAGGCTGTGAACAGCTT
CAGGAGGTGCTGGAGGGCTTCAACATGGCCAAGGTGCTGGCGTCCCTCAGTGATGAC
GAGGACGAGGAGGAGGAGGAGGAAGGAGAAGAGGAAGAAGAGGAAGCAGAAGAAG
AGGAGGAGGAAGATGAGGAAGAGGAGGAAGAAGAGGAGGAGGAGGAGGAAGAAGA
GCCTCAGCAGCGAGGGCAGGGAGAGAAGTCAGCCACGCCCTCACGGAAGATTCTGG

FIGURE 80 (CONT'D)

ACCCTAACACTGGGGAGCCAGCTCCCGTGCTGTCCTCCCCACCTCCTGCAGACGTCTC
CACCTTCCTGGCTTTTCCCTCTCCAGAGAAGCTCCTGCGCCTAGGGCCCAAGAGCTCC
GTGCTGATAGCCCAGCAGACTGACACGTCTGACCCCGAGAAGGTGGTCTCTGCCTTC
CTAAAGGTGTCATCTGTGTTCTTAGCTGAAACTGAAATCAAATAGAAGGACGAAGCT
ACTGTGAGGATGGCAGTGCAGGATGCAGTAGATGCCCTGATGCAGAAGGCTTTCAAC
TCCTCGTCCTTCAACTCCAACACCTTCCTCACCAGGCTCCTCGTGCACATGGGTCTGC
TCAAGAGTGAAGACAAGGTCAAGGCCATTGCCAACCTGTACGGCCCCCTGATGGCGC
TGAACCACATGGTGCAGCAGGACTATTTCCCCAAGGCCCTTGCACCCCTGCTGCTGG
CGTTCGTGACCAAGCCCAACAGCGCCCTGGAATCCTGCTCCTTCGCCCGCCACAGTCTG
CTGCAGACGCTGTACAAGGTCTAG

Saccharomyces cerevisiae orf name: YMR309C
Saccharomyces cerevisiae gene name: NIP1
GENBANK Accession Number: A46417
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 122
ATGTCCCGTTTCTTTTCGTCTAATTACGAATACGATGTAGCCAGTTCTTCATCCGAAGAA
GATCTTTTATCTTCGTCTGAAGAAGATTTGTTAAGCTCTTCCTCCTCTGAGTCTGAATTG
GACCAAGAATCTGACGACTCCTTTTTCAATGAAAGTGAAAGTGAAAGTGAAGCTGAT
GTAGACTCTGATGATTCTGATGCAAAGCCTTATGGTCCTGACTGGTTCAAGAAATCTG
AGTTCAGAAAACAAGGTGGAGGTTCAAATAAATTTTTGAAAAGCTCTAACTATGATT
CCAGTGATGAAGAATCCGATGAAGAAGATGGCAAGAAGGTAGTCAAGTCTGCCAAA
GAAAAACTATTGGATGAAATGCAAGACGTTTATAATAAGATCTCTCAAGCTGAGAAC
TCTGATGACTGGTTGACTATTTCTAATGAGTTTGATTTGATCTCGCGTCTCTTAGTTA
GGGCTCAACAACAAAACTGGGGGACTCCAAATATTTTCATCAAGGTTGTTGCCCAAG
TGGAGGACGCTGTGAATAATACACAACAAGCTGATTTGAAGAATAAAGCTGTTGCAA
GAGCTTATAACACTACAAAGCAAAGAGTCAAGAAAGTTTCTAGAGAAAATGAAGACT
CAATGGCTAAATTCAGAAATGATCCTGAATCATTTGATAAGGAACCAACCGCAGATT
TGGATATTTCTGCTAATGGATTCACAATTTCTTCGTCTCAAGGCAATGACCAAGCGGT
ACAAGAAGATTTCTTCACTAGATTACAAACAATAATTGACTCAAGAGGTAAGAAGAC
TGTCAATCAACAATCCTTGATTTCTACTTTGGAGGAGTTATTAACTGTAGCTGAAAAA
CCATATGAATTCATAATGGCTTATTTGACTTTGATTCCATCAAGATTCGATGCCTCAG
CTAACCTATCTTACCAACCAATTGATCAATGGAAATCTTCATTCAACGATATTAGTAA
ATTATTGTCTATTTTAGACCAGACAATTGACACCTACCAAGTTAATGAATTTGCTGAT
CCAATCGATTTCATTGAAGATGAACCTAAAGAAGATTCTGATGGTGTCAAGAGGATT
CTGGGTTCCATTTTCTCATTTGTTGAAAGATTAGATGACGAATTCATGAAATCCCTGT
TAAACATCGATCCTCATTCCAGTGATTATTTGATCCGTTTAAGGGATGAACAATCAAT
CTATAATTTGATCCTAAGAACTCAATTGTACTTTGAAGCGACTTTGAAAGATGAACAC
GACCTAGAAAGAGCATTGACACGTCCATTCGTCAAGAGATTGGATCATATCTACTAT
AAATCCGAAAATTTGATAAAAATTATGGAAACTGCTGCTTGGAATATCATACCTGCT
CAATTCAAATCTAAATTTACTTCAAAAGACCAGCTCGATTCTGCTGATTATGTCGACA
ATTTAATAGACGGATTATCGACAATCTTATCCAAGCAAAACAACATTGCTGTTCAAAAA

FIGURE 80 (CONT'D)

CGTGCTATTTTATACAACATTTACTACACTGCATTAAACAAAGATTTCCAAACTGCTAAA
GATATGTTACTAACTTCCCAAGTTCAAACAAATATCAACCAATTCGATTCATCCCTACAA
ATTTTATTCAACAGGGTTGTTGTTCAATTGGGTCTATCCGCCTTTAAATTATGTTTGATT
GAAGAATGTCATCAAATTTTGAATGATCTTCTGTCAAGTTCTCACTTAAGAGAAATTTTG
GGCCAACAATCCCTACACAGAATATCTCTCAATTCTAGTAACAATGCTTCAGCTGATGAG
CGTGCTAGACAATGTTTGCCATATCACCAACACATCAATCTCGATTTAATCGATGTCGTC
TTCTTAACATGTTCCTTATTGATCGAAATTCCAAGAATGACTGCCTTCTATTCCGGTATT
AAGGTCAAGAGAATTCCTTACTCTCCAAAATCCATTCGTCGTTCCTTAGAACATTACGAC
AAGTTAAGTTTCCAAGGTCCACCAGAAACTTTAAGAGATTATGTCTTGTTTGCTGCCAAA
TCAATGCAAAAAGGTAACTGGAGAGACTCTGTTAAATACTTAAGAGAAATAAAATCT
TGGGCTTTATTACCAAACATGGAAACGGTGTTGAATAGTTTAACGGAAAGAGTACAA
GTTGAATCTTTGAAGACTTATTTCTTTTCTTTCAAGAGGTTCTATTCAAGTTTTTCTGT
TGCTAAACTAGCCGAATTATTTGATCTTCCAGAAAATAAGGTGGTTGAAGTTTTGCAA
TCTGTTATCGCAGAATTGGAAATCCCAGCCAAATTAAACGACGAGAAGACCATCTTT
GTTGTCGAAAAG

Candida albicans nucleic acid: SEQ ID NO: 123
ATGTCTCGTTTTTTTGTTTCAGGATACACTTCTGACTCTTCTTCTGAAGAGGAGGATT
TATTGAGTACTTCTGAAGAAGAGTTATTATCTTCTTCTGATGAAGGAGAAGACAACG
AATCAGATAGTTCATTTTTTGGTGAAGATGATGATGAATCAGAAGAATCTAGTTCTG
ATGATGAAGATGGTCGACCATCTGGTCCAGCATATTTTTTAAAGAAATCATTTTTAAA
AGGAGCTGGAGGAGATGATTCTGACAGTGATAGTGATGATGAAGGTCGTAAAGTTGT
TAAATCAGCTAAAGATAAATTATTAGATGATATGAAATCTTCAATTGAAATTATAAAT
TCCAACAAATATAATAACAATTGGAGTATAGTTTTAGGTGAATTTGATAAGTTTGGTA
GATTTTTGATTAGATGTAATCAAACCAATTTGGGTACACCAAAATTTTATATTAAATT
GTTGACTAGTTTAGATAACTCCATAACTGAAACTAGTAATAATGAAAGAGATGATAA
AACATTAAAAGCTGATGAAGCCAGAGCTTTCAATACTTTGAGACAAAGAATTAAAAA
ACAAATAAGAGAATTCCAAGTTTATTATGATTTGTATAAGGAAAATCCAGAAGAATT
TGATGAAAATGAAGATGAACCATTAGAATCTGTTCAAGCTGGTCTTAACGATAATGT
TAAAAATGAAGCTGATAATTCTAATGTTGGTGCTCTTGCGTCAAACAGAGTATTGAG
TCCTATTTTCCATACTTTGAAAACTATTTCCGAAAGTCGTGGTAAAAAGAATATTGAT
AAATTGGAACAAATTGCTACTTTGGAAAAATTATTAGAAGCAAATGTTTCTAAAAGT
TCACCATTTGAATTGATTTCTATTTATCAGATGTTATTATCAGTTAGATTTGATGCTTC
ATCTAATCAAGCTTTTATGCCTTTGGAACAATGGCAAAAGAATGAACACGATTTAGG
TAAATTATTGGATTTGTTGGAAGCTAATGTTGATACTTATCAAGTTTCTGAATTGGGT
TCAACTACTGATGATATTGATATTGAACCAGTTGCTAATGCCCAAGGTGTTAAAGTTA
TTTTCGGATCAATCACTTCTTCTATTGATAGATTGGACGATGAATTGACCAAATCTTT
ACAACATACTGACCCACATTCTATTGAATATGTTGAAAGATTGAAGGATGAAAGTAC
TATTTACAATTTGATTGTTAGAGGTCAAGCATATGTTGAATCCATAACTCCAGAAGAT
GTCAAGTATAATTCTGAACAATTGGCAAGAATTGTTTTGAGAAGATTGGAACACATT

FIGURE 80 (CONT'D)

TATTATAAACCAAAACAATTGATTAAAGCTAATGAAGAAGAAGCTTGGCGTAATATT
GAATACAATTCATCTATTGTCAGTAAAGGTTCTTCAGTTGATGAAGTTATTGATCAATTG
ACGGAATTTTTACAAAAGCAACAAAAAAACAAAACTTATGGGAAACATGCTATACTA
TTCTCCATTTATTATTATGCTGTCAATAGTCAATATGAAAAGGCTAAAGAATTATTTT
TGAGATCTCAATTTTATAGTAACATCAATTCTGCTGAATCTTCTTTACAAGTTCAATA
TAATCGTGCTTTAGTTCAATTAGGTTTAAGTGCTTTTAGAGCAGGTAGTATTGAAGAA
TCTCATAAAATTTTGAATGAAATTGTCAATTCTCAAAGATCTAAAGAATTATTGGGTC
AAGGTTTCAATTCTAAATTCCCCAATCAAGCTACTGTTTTGGAAAGACAAAAATTATT
ACCATTCCATCAACATATTAATTTGGAATTATTGGAATGTGTATTTATGACTTGTTCT
TTATTAATTGAAATTCCAACTTTGGCTGCTATTGCTAATAATCATAAGGATTCAAAAC
GTAAAAATGCTTCATTGAAATCTTTCAAAAGTAAATTGGATTTCCATGATAGACAATT
TTTCACTGGTCCACCAGAAAGTATTAAAGATCATATTGTGGTGATGAAATTACTAAAT
TGGAAGAAGCAATGGTAAAATTGAACAAAGAATATAAAATCGCTAAAGAACGTCTTA
ACCCACCATCAAATCGTCGTTGA

Human GENBANK Accession Number: U46025.1
Human nucleic acid sequence: SEQ ID NO: 124
TGACTCGCGGGCTCAGCTGGTCCGGCCGTAGCACCTCCGCGCCGTCGCCATGTCGCGGTT
TTTCACCACCGGTTCGGACAGCGAGTCCGAGTCGTCCTTGTCCGGGGAGGAGCTCGT
CACCAAACCTGTCGGAGGCAACTATGGCAAACAGCCATTGTTGCTGAGCGAGGATGA
AGAAGATACCAAGAGAGTTGTCCGCAGTGCCAAGGACAAGAGGTTTGAGGAGCTGA
CCAACCTTATCCGGACCATCCGTAATGCCATGAAGATTCGTGATGTCACCAAGTGCCT
GGAAGAGTTTGAGCTCCTGGGAAAAGCATATGGGAAGGCCAAAAGCATTGTGGACA
AAGAAGGTGTCCCCCGGTTCTATATCCGCATCCTGGCTGACCTAGAGGACTATCTTA
ATGAGCTTTGGGAAGATAAGGAAGGGAAGAAGAAGATGAACAAGAACAATGCCAAG
GCTCTGAGCACCTTGCGTCAGAAGATCCGAAAATACAACCGTGATTTCGAGTCCCAT
ATCACAAGCTACAAGCAGAACCCCGAGCAGTCTGCGGATGAAGATGCTGAGAAAAA
TGAGGAGGATTCAGAAGGCTCTTCAGATGAGGATGAGGATGAGGACGGAGTCAGTG
CTGCAACTTTCTTGAAGAAGAAATCAGAAGCTCCTTCTGGGGAGAGTCGCAAGTTCC
TCAAAAAGATGGATGATGAAGATGAGGACTCAGAAGATTCCGAAGATGATGAAGAC
TGGGACACAGGTTCCACATCTTCCGATTCCGACTCAGAGGAGGAAGAAGGGAAACAA
ACCGCGCTGGCCTCAAGATTTCTTAAAAAGGCACCCACCACAGATGAGGACAAGAAG
GCAGCCGAGAAGAAACGGGAGGACAAAGCTAAGAAGAAGCACGACAGGAAATCCAA
GCGCCTGGATGAGGAGGAGGAGGACAATGAAGGCGGGGAGTGGGAAAGGGTCCGG
GGCGGAGTGCCGTTGGTTAAGGAGAAGCCAAAAATGTTTGCCAAGGGAACTGAGAT
CACCCATGCTGTTGTTATCAAGAAACTGAATGAGATCCTACAGGCACGAGGCAAGAA
GGGAACTGATCGTGCTGCCCAGATTGAGCTGCTGCAACTGCTGGTTCAGATTGCAGC
GGAAAACAACCTGGGAGAGGGCGTCATTGTCAAGATCAAGTTCAATATCATCGCCTC
TCTCTATGACTACAACCCCAACCTGGCAACCTACATGAAGCCAGAGATGTGGGGGAA
GTGCCTGGACTGCATCAATGAGCTGATGGATATCCTGTTTGCAAATCCCAACATTTTT
GTTGGAGAGAATATTCTGGAAGAGAGTGAGAACCTGCACAACGCTGACCAGCCACTG

FIGURE 80 (CONT'D)

CGTGTCCGTGGCTGCATCCTAACTCTGGTGGAACGAATGGATGAAGAATTTACCAAA
ATAATGCAAAATACTGACCCTCACTCCCAAGAGTACGTGGAGCACTTGAAGGATGAG
GCCCAGGTGTGTGCCATCATCGAGCGTGTGCAGCGCTACCTGGAGGAGAAGGGCACT
ACCGAGGAGGTCTGCCGCATCTACCTGCTGCGCATCCTGCACACCTACTACAAGTTT
GATTACAAGGCCCATCAGCGACAGCTGACCCCGCCTGAGGGCTCCTCAAAGTCTGAG
CAAGACCAGGCAGAAAATGAGGGCGAGGACTCGGCTGTGTTGATGGAGAGACTGTG
CAAGTACATCTACGCCAAGGACCGCACAGACCGGATCCGCACATGTGCCATCCTCTG
CCACATCTACCACCATGCTCTGCACTCGCGCTGGTACCAGGCCCGCGACCTCATGCTC
ATGAGCCACTTGCAGGACAACATTCAGCATGCAGACCCGCCAGTGCAGATCCTTTAC
AACCGCACCATGGTGCAGCTGGGCATCTGTGCCTTCCGCCAAGGCCTGACCAAGGAC
GCACACAACGCCCTGCTGGACATCCAGTCGAGTGGCCGAGCCAAGGAGCTTCTGGGC
CAGGGCCTGCTGCTGCGCAGCCTGCAGGAGCGCAACCAGGAGCAGGAGAAGGTGGA
GCGGCGCCGTCAGGTCCCCTTCCACCTGCACATCAACCTGGAGCTGCTGGAGTGTGT
CTACCTGGTGTCTGCCATGCTCCTGGAGATCCCCTACATGGCCGCCCATGAGAGCGA
TGCCCGCCGACGCATGATCAGCAAGCAGTTCCACCACCAGCTGCGCGTGGGCGAGCG
ACAGCCCCTGCTGGGTCCCCCTGAGTCCATGCGGGAACATGTGGTCGCTGCCTCCAA
GGCCATGAAGATGGGTGACTGGAAGACCTGTCACAGTTTTATCATCAATGAGAAGAT
GAATGGGAAAGTGTGGGACCTTTTCCCCGAGGCTGACAAAGTCCGCACCATGCTGGT
TAGGAAGATCCAGGAAGAGTCACTGAGGACCTACCTCTTCACCTACAGCAGTGTCTA
TGACTCCATCAGCATGGAGACGCTGTCAGACATGTTTGAGCTGGATCTGCCCACTGT
GCACTCCATCATCAGCAAAATGATCATTAATGAGGAGCTGATGGCCTCCCTGGACCA
GCCAACACAGACAGTGGTGATGCACCGCACTGAGCCCACTGCCCAGCAGAACCTGGC
TCTGCAGCTGGCCGAGAAGCTGGGCAGCCTGGTGGAGAACAACGAACGGGTGTTTG
ACCACAAGCAGGGCACCTACGGGGGCTACTTCCGAGACCAGAAGGACGGCTACCGC
AAAAACGAGGGCTACATGCGCCGCGGTGGCTACCGCCAGCAGCAGTCTCAGACGGC
CTACTGAGCTCTCCACTCTGTTTCCCGCCTGGGCCATCCAACCTTGAAGTCCTAAACC
ACACCTCAGTCACTAAAGGTCTGTTTAAAGTTGTTCTGGTTGATTGCTTGTTGCCA

Saccharomyces cerevisiae orf name: YNL036W
Saccharomyces cerevisiae gene name: NCE103
GENBANK Accession Number: CAA95901.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 128
ATGAGCGCTACCGAATCTTCATCTATATTCACATTGAGTCACAACTCAAACCTACAAGAT
ATCTTGGCCGCCAATGCCAAATGGGCCTCCCAGATGAACAACATACAGCCAACTTTGTTC
CCAGATCACAATGCGAAGGGCCAGTCCCCTCACACTCTTTTCATCGGCTGCTCCGATTCG
CGTTACAACGAAAACTGTTTAGGTGTCTTGCCCGGCGAAGTGTTCACTTGGAAAAATGTT
GCTAACATATGTCACTCAGAGGATTTAACTTTGAAGGCCACTTTAGAGTTTGCCATTATT
TGTCTAAAAGTTAACAAAGTTATTATTTGTGGCCACACTGATTGTGGTGGTATAAAGACA
TGTTTAACTAACCAAAGGGAAGCCTTACCAAAAGTTAACTGTTCTCATCTGTACAAGTAC
TTAGACGATATTGACACCATGTACCATGAAGAGTCACAAAATTTGATCCATTTGAAAACG
CAACGTGAAAAATCTCATTACCTGTCGCACTGTAACGTCAAAAGGCAGTTTAATAGGATT

FIGURE 80 (CONT'D)

ATTGAAAACCCTACTGTGCAAACTGCTGTACAAAATGGAGAATTACAGGTATACGGT
CTGCTTTACAACGTAGAGGACGGTCTACTGCAAACAGTTAGCACTTACACAAAAGTT
ACCCCAAAATAG

Candida albicans nucleic acid: SEQ ID NO: 129
ATGGGTAGAGAAAATATTTTGAAATATCAATTGGAACATGATCATGAATCTGATCTT
GTTACTGAAAAAGATCAATCATTATTACTTGATAATAATAACAACCTAAACGGGATG
AATAATACCATTAAAACTCATCCGGTACGTGTTAGTTCAGGAAATCATAATAATTTTC
CTTTCACTTTATCTTCAGAATCTACATTACAAGATTTTTTAAATAATAATAAATTTTTT
GTTGATTCCATAAAACATAATCATGGTAATCAAATATTTGATTTGAATGGTCAAGGTC
AATCTCCTCATACATTATGGATAGGGTGTAGTGATTCAAGAGCAGGTGATCAATGTT
TAGCTACATTACCAGGAGAAATATTTGTTCATAGAAACATTGCTAATATAGTCAATGC
CAATGATATAAGTAGTCAAGGGGTTATACAATTTGCTATTGATGTATTAAAAGTGAA
AAAAATCATTGTTTGTGGTCATACTGATTGTGGTGGTATTTGGGCATCATTATCAAAG
AAAAAAATTGGTGGTGTTTTAGATTTATGGTTAAATCCAGTTAGACATATTCGTGCTG
CTAATTTAAAATTATTAGAAGAATATAATCAAGATCCTAAATTAAAGGCCAAAAAAT
TGGCTGAATTAAATGTCATTTCTTCTGTAACAGCATTGAAAAGACATCCTAGTGCTAG
TGTTGCATTAAAGAAGAATGAAATTGAAGTTTGGGGGATGTTATATGATGTGGCAAC
TGGTTATTTATCTCAAGTAGAGATTCCTCAAGATGAATTTGAGGATTTATTCCATGTT
CATGATGAACATGATGAAGAAGAATATAACCCTCATTGA

Saccharomyces cerevisiae orf name: YNL126W
Saccharomyces cerevisiae gene name: SPC98
GENBANK Accession Number:CAA96007.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 107
ATGGAACTAGAGCCCACTCTTTTTGGTATAATAGAGGCATTGGCTCCTCAATTATTGTCG
CAGAGTCATTTGCAGACATTTGTATCTGATGTAGTCAATTTACTGCGATCATCCACCAAA
TCGGCAACTCAATTAGGCCCTTTAATTGATTTTTACAAATTACAATCACTAGATTCGCCT
GAAACAACAATTATGTGGCATAAAATTGAGAAATTTCTCGATGCTTTATTTGGAATCCAG
AACACCGATGATATGGTAAAGTACCTCTCTGTCTTTCAATCTTTGCTTCCATCAAATTAC
AGAGCAAAAATTGTCCAAAAATCATCTGGGCTCAATATGGAGAACCTTGCTAACCAT
GAACATTTACTTAGCCCAGTGCGGGCTCCAAGTATATATACAGAAGCTTCATTTGAA
AACATGGACCGATTTTCTGAAAGAAGGTCCATGGTATCTTCGCCTAATCGTTACGTTC
CCTCTTCAACCTACAGTTCTGTTACTTTGAGACAGTTGTCAAATCCTTATTATGTGAA
CACTATACCCGAGGAAGATATCCTAAAATACGTATCATATACATTATTAGCTACGAC
ATCGGCACTATTTCCGTTTGATCATGAGCAAATACAAATTCCGTCTAAGATACCCAAT
TTTGAGAGTGGACTTTTACATTTAATATTTGAAGCGGGTTTATTATATCAAAGTTTGG
GTTATAAAGTGGAGAAGTTTAGGATGTTGAATATATCTCCAATGAAAAAAGCATTGA
TTATAGAAATTTCAGAAGAATTACAAAACTACACAGCATTTGTGAACAATCTGGTCTC
TTCAGGGACAGTAGTGTCATTGAAATCGTTATATCGTGAAATATATGAAAATATAAT

FIGURE 80 (CONT'D)

AAGGCTTCGAATATACTGTAGGTTTACAGAACACCTTGAAGAATTGAGCGGAGATAC
ATTCTTGATTGAATTAAATATTTTCAAATCCCACGGAGATCTTACTATAAGAAAAATA
GCAACGAATTTGTTTAATTCAATGATTTCTCTTTATTATGAGTATTTAATGAATTGGT
TGACTAAAGGTCTACTCCGAGCTACTTATGGAGAATTCTTCATTGCTGAAAACACTGA
TACAAATGGTACAGACGATGATTTTATTTACCACATTCCTATAGAGTTCAACCAAGAA
AGAGTTCCGGCCTTCATACCGAAAGAGTTGGCATATAAAATATTCATGATCGGCAAA
TCGTATATCTTCCTAGAAAAGTACTGTAAAGAGGTTCAATGGACAAACGAATTTTCTA
AAAAGTATCATGTCCTGTACCAGAGCAATTCTTATCGGGGAATATCAACGAACTTTTT
TGAAATTATAAATGATCAATATTCTGAAATTGTTAATCATACTAATCAAATTCTAAAT
CAGAAGTTTCATTACAGAGACGTGGTATTTGCGTTAAAGAATATTCTTCTCATGGGTA
AATCTGATTTTATGGATGCTCTTATAGAAAAGGCCAATGATATTCTCGCGACACCATC
GGATTCATTGCCAAATTATAAGTTAACAAGGGTTTTACAGGAAGCCGTGCAGCTTTC
TTCCTTAAGACATTTAATGAATAGTCCCCGTAATAGTTCTGTCATTAATGGATTGGAT
GCGAGGGTACTCGATCTTGGACATGGATCCGTGGGTTGGGATGTTTTTACTTTAGATT
ACATCCTCTACCCCCCTTTGAGTTTAGTATTAAACGTAAATCGTCCTTTTGGCAGGAA
AGAGTATCTACGAATTTTCAATTTTTTATGGAGATTTAAAAAGAACAATTATTTCTAT
CAAAAGGAAATGTTGAAGAGTAATGATATAATCAGATCATTCAAGAAAATCAGAGGT
TACAACCCGCTCATCCGTGATATTATCAATAAACTTTCTAGAATCAGTATACTTAGAA
CTCAATTCCAGCAATTCAACTCGAAGATGGAATCTTATTATTTGAACTGCATTATAGA
GGAAAATTTTAAAGAAATGACCCGGAAACTGCAACGCACAGAGAATAAAAGCCAAA
ACCAATTCGACTTAATTAGATTAAATAATGGCACCATAGAATTAAATGGGATTTTAAC
CCCAAAAGCTGAAGTACTAACAAAGTCTTCAAGCAGTAAACCCCAAAAACACGCAAT
CGAAAAGACGCTGAATATTGATGAATTAGAAAGTGTACATAACACGTTCTTGACGAA
TATTCTTTCTCATAAGCTTTTTGCAACTAACACAAGTGAAATAAGCGTTGGTGATTAT
TCTGGGCAACCATACCCAACTTCATTGGTTTTACTTTTAAATTCGGTTTACGAGTTCG
TCAAAGTTTATTGTAATTTGAACGACATTGGATACGAAATCTTCATTAAAATGAATCT
CAATGATCACGAAGCATCTAACGGATTATTGGGAAAATTTAATACGAATTTAAAGGA
AATTGTTAGCCAGTATAAAAATTTTAAA

Candida albicans nucleic acid: SEQ ID NO: 108
ATGGCGTTAAACAAGGTACAACTAATAAAATTATATTCCAATCGATTAGTGAAATCA
TTGGTTCCTGTGGAATTCGGTGAGGCATTCATCCAAAGTATAATCAATGACTTGCAA
ACCACTTTACTAAATACTTCTTCTGAAGAACAAAATTTGTCAATAATTATAAACAAGC
TTAAAATGCAATTTTTAAGTAACAATTTAAAAAATGAATGGGTCGAATTTCAAAACA
TTGTTAATTCATTAAGCAAATTCAAGTCGTTGGATCAGATTTGTAATTATCTCGCATT
TCTTGATGCTTTAAGAGATGAGAAACCAGAAGATATATTATCAACATCAACAGCGAG
CTTGTCTCCCGGTAAGCAAAATGTAATGATCAATACGGTAAACACAGCATTGACGTT
ATCACAGTTAATCGAGCCTTACTATGATACTTTATCGGAACAAACCATTTTAACCTAC
TTACCCTACACGATGTTAGGTCTGGATTCCAAAATATTCACCTTCAGCAATAATTATA
CACGATTGGAGATACCGAAAGATATAAACAACAGTTTCAGCTCATTGCTACGCGAAG
TTTTTGAGTTTGCAATACTATATAAACAATTGGCAATTGTTGTTGATAGGTATAAAGG

FIGURE 80 (CONT'D)

AACTTTAGTACTGGCCATAAAGACAGCTTACATAGCAATACTAGAGGCTCAATTGAA
CAAATATGTGAATGATATTAACAATATCTTCAATAATAAACCGAATTCCATATTAGTT
GTTTACAATTCCATTTTCCCCTGGATATCTATACTACGATTTTTATATCGAGTCTCAAA
CAGACTAAACAGATTAGATGGTTATGAATTTCTCACATTTATTTATAGTTTCACCAAC
CATGGAGATCCCAAAATACGGGGCATTGCTGTGACTGCATTCACCGAGGTTGTCAAA
CCGTATTATAATATTGTGGAACATTGGATAGTGAAAGGGGAGTTGATTGATAATAAT
AACGAGTTTTTCATTATCTTTGATCAAGAGCAGAATGAATTCAATAGTATAATTAAAT
TATTGCCCAAAAAAATACCAGCCTTTATTAAATCGAGTGATAAAATATTTCAGATTGG
GAAAACATTAATTTTTCTAAATAAATATTGTCGTGAACTAAAATGGGTAAATCAGTAT
AACGTGAAATATTCTGCTATATTGTTCAATAACCATCAAGGCTTGGCATCCATGACAA
CAAATGAAATGATCAAATTGATTGATCTGCAATATAATGAGATATTAACGTTTCTCAC
CCAAATAATCCAAGGAAACAATAAATTGTTTACTCATGTTTATAATTTCAAGAGGTTT
TATTTTATGGAGACCAATGATTTTATTGATGCGATTATGGTGAAAGGGAAGGACGTT
TTTAATGAGTCTTCTGTTAATATTTCATCAACCTATCTTAGGAAAGTCTTACAAGACG
CTATACAAATTTCGTCGGTGAAAAATTTTGAGTATGTTGACAGACTCGATTCGAGAG
TGTTGAATCCCCAACACGGGAATTTGGGCTGGGAATCGTTCACCATTGAATACAAAA
TTGATGATCTTCCCATGAGTTATTTATTTGAAGGTCACCAACATTTACAATATTTAAA
AATGTTTCATTTTCTATGGAAATTAAGACAATTGAATAATTTATTAAATTGGCATTTT
GAGATGTTTAATGAGTTGAATCATAATGTGGTGACGAAGTTGTCAAGCAGAAATAGA
AGACCTTTGGCGAAATCATTGAGCATAATCACCAGTATAAGATTCCATTTTACCCAGT
TTCTTAACGAACTAATAGCTTATTTGTCTTATGATGTTATTGAAGAAAATTTTCGACA
GACTGTATATTTTTAGGGCAGATTTAAAGAACGATGGCGATGAAGAGCTTTTCTTATT
GAGCAAATCGCTCCGTTAA

Human GENBANK Accession Number: AF042378.1
Human nucleic acid sequence: SEQ ID NO: 109
CAGGAAGGGCGCGGGCCGCGGTCCCTGCGCGTGCGGCGGCAGTGGCGGCTCTGCCC
GGACCACCGTGCACGGCTCCGGGCGAGGATGGCGACCCCGGACCAGAAGTCGCCGA
ACGTTCTGCTGCAGAACCTGTGCTGCAGGATCCTGGGCAGGAGCGAAGCTGATGTAG
CCCAGCAGTTCCAGTATGCTGTGCGGGTGATTGGCAGCAACTTCGCCCCAACTGTTG
AAAGAGATGAATTTTTAGTAGCTGAAAAAATCAAGAAAGAGCTTATTCGACAACGAA
GAGAAGCAGATGCTGCATTATTTTCAGAACTCCACAGAAAACTTCATTCACAGGGAG
TTTTGAAAAATAAATGGTCAATACTCTACCTCTTGCTGAGCCTCAGTGAGGACCCACG
CAGGCAGCCAAGCAAGGTTTCTAGCTATGCTACGTTATTTGCTCAGGCCTTACCAAG
AGATGCCCACTCAACCCCTTACTACTATGCCAGGCCTCAGACCCTTCCCCTGAGCTAC
CAAGATCGGAGTGCCCAGTCAGCCCAGAGCTCCGGCAGCGTGGGCAGCAGTGGCAT
CAGCAGCATTGGCCTGTGTGCCCTCAGTGGCCCCGCGCCTGCGCCACAATCTCTCCTC
CCAGGACAGTCTAATCAAGCTCCAGGAGTAGGAGATTGCCTTCGACAGCAGTTGGGG
TCACGACTCGCATGGACTTTAACTGCAAATCAGCCTTCTTCACAAGCCACTACCTCAA
AAGGTGTCCCCAGTGCTGTGTCTCGCAACATGACAAGGTCCAGGAGAGAAGGGGATA
CGGGTGGTACTATGGAAATTACAGAAGCAGCTCTGGTAAGGGACATTTTGTACGTCT

FIGURE 80 (CONT'D)

TTCAGGGCATAGATGGCAAAAACATCAAAATGAACAACACTGAAAATTGTTACAAAG
TAGAAGGAAAGGCAAATCTAAGTAGGTCTTTGAGAGACACAGCAGTCAGGCTTTCTG
AGTTGGGATGGTTGCATAATAAAATCAGAAGATACACGGACCAGAGGAGCCTGGAC
CGCTCATTCGGACTCGTCGGGCAGAGCTTTTGTGCTGCCTTGCACCAGGAACTCAGA
GAATACTATCGATTGCTCTCTGTTTTACATTCTCAGCTACAACTAGAGGATGACCAGG
GTGTGAATTTGGGACTTGAGAGTAGTTTAACACTTCGGCGCCTCCTGGTTTGGACCTAT
GATCCCAAAATACGACTGAAGACCCTTGCGGCCCTAGTGGACCACTGCCAAGGAAGG
AAAGGAGGTGAGCTGGCCTCAGCTGTCCACGCCTACACAAAAACAGGAGACCCGTAC
ATGCGGTCTCTGGTGCAGCACATCCTCAGCCTCGTGTCTCATCCTGTTTTGAGCTTCC
TGTACCGCTGGATATATGATGGGGAGCTTGAGGACACTTACCACGAATTTTTTGTAG
CATCAGATCCAACAGTTAAAACAGATCGACTGTGGCACGACAAGTATACTTTGAGGA
AATCGATGATTCCTTCGTTTATGACGATGGATCAGTCTAGGAAGGTCCTTTTGATAGG
AAAATCAATAAATTTCTTGCACCAAGTTTGTCATGATCAGACTCCCACTACAAAGATG
ATAGCTGTGACCAAGTCTGCAGAGTCACCCCAGGACGCTGCAGACCTATTCACAGAC
TTGGAAAATGCATTTCAGGGGAAGATTGATGCTGCTTATTTTGAGACCAGCAAATAC
CTGTTGGATGTTCTCAATAAAAAGTACAGCTTGCTGGACCACATGCAGGCAATGAGG
CGGTACCTGCTTCTTGGTCAAGGAGACTTTATAAGGCACTTAATGGACTTGCTAAAA
CCAGAACTTGTCCGTCCAGCTACGACTTTGTATCAGCATAACTTGACTGGAATTCTAG
AAACCGCTGTCAGAGCCACCAACGCACAGTTTGACAGTCCTGAGATCCTGCGAAGGC
TGGACGTGCGGCTGCTGGAGGTCTCTCCAGGTGACACTGGATGGGATGTCTTCAGCC
TCGATTATCATGTTGACGGACCAATTGCAACTGTGTTTACTCGAGAATGTATGAGCCA
CTACCTAAGAGTATTTAACTTCCTCTGGAGGGCGAAGCGGATGGAATACATCCTCAC
TGACATACGGAAGGGACACATGTGCAATGCAAAGCTCCTGAGAAACATGCCAGAGTT
CTCCGGGGTGCTGCACCAGTGTCACATTTTGGCCTCTGAGATGGTCCATTTCATTCAT
CAGATGCAGTATTACATCACATTTGAGGTGCTTGAATGTTCTTGGGATGAGCTTTGGA
ACAAAGTCCAGCAGGCCCAGGATTTGGATCACATCATTGCTGCACACGAGGTGTTCT
TAGACACCATCATCTCCCGCTGCCTGCTGGACAGTGACTCCAGGGCACTTTTAAATCA
ACTTAGAGCTGTGTTTGATCAAATTATTGAACTTCAGAATGCTCAAGATGCAATATAC
AGAGCTGCTCTGGAAGAATTGCAGAGACGATTACAGTTTGAAGAGAAAAAGAAACAG
CGTGAAATTGAGGGCCAGTGGGGAGTGACGGCAGCAGAGGAAGAGGAGGAAAATAA
GAGGATTGGAGAATTTAAAGAATCTATACCAAAAATGTGCTCACAGTTGCGAATATT
GACCCATTTCTACCAGGGTATCGTGCAGCAGTTTTTGGTGTTACTGACGACCAGCTCT
GACGAGAGTCTTCGGTTTCTTAGCTTCAGGCTGGACTTCAACGAGCATTACAAAGCC
AGGGAGCCCAGGCTCCGTGTGTCTCTGGGTACCAGGGGGCGGCGCAGCTCCCACACG
TGAAGCTCGCGGTCCTCCCAGGGAGCTGCGGGTGATGTTCGTTGCACTGCTAGACAC
GAAATTCCCATTGACGTCCTGCAGGAACTGCATGCTGCAGGTGTCCTGCCCTTCCGCC
CACGAGTGCGCCATGTTTCAGCGGAGCGGCGTGTGGGAGAAGCCACGTCGTGTTTCA
CATGTCGGAGTCGAATGCATTTGTAAATCCCTAAGTCAAGTAGGCTGGCTGCACTGT
TCACATTTGTCTCTAAAAGTCTTCATCGCTAAAAGATACCATAATTTGCTGAGGCTTC
TTAAGCTTTCTATGTTATAATTTATATTTGTCACTTTAAAAAATCCATTTCTTTTAGAA
AAAATTAGGGTGATAGGATATTCATTAGTTAAGATGGTAACGTCATTGCTATTTTTTT
AACATCCTCTTTAGAGGTAATTTTTGTTAACATAACCAAAAATTAAATTGAAACAAAA

FIGURE 80 (CONT'D)

TGTCCCAACTAAGAAAATATATAGAGCATTTTATTTTTTTTTAGTGTTGTAAAATATT
AACCTCTGTGAGATCCTTTGTATCTTAATGCATTACCTTTACACATATTTATTCTTATT
TTCTCTCCTTTCAGAGTTTACATTTTTATATTTAATTTACTATTTCAGATTTTTAAAAT
AGTATAGAAAAAAGTAGGAGTGATAGAGAACAAAAATACTCTTATACAGTGCAACCC
AAATACCGCGAATGCATCAGCTAAAGCAGCGTGTAAATAGGAGTGATGAGAAAGTTA
ATGGAGTATTTTATTTTCAAAGTTCCTGATAAGCATTGGAAAGAAATCGACATGGAT
AATGAAGATTTCCTTTTTCCTTGCCTATTTTTTCATTGTAAATATTTATATACTACTGA
CCAAGATGTTGGGGTGGGGGGATTGTTTTTGTAAAAATGTCATTATCAGGTCACA
TAAATCTGCCTTTATGTTGCATAAGTGAAAATTTAGAAAATTAAAAGCAATTATCTTT
CAAAAAAAATGGAATAAATTGCTTTTCTACATAAAAAAAAA

Saccharomyces cerevisiae orf name: YNL282W
Saccharomyces cerevisiae gene name: POP3
GENBANK Accession Number: CAA96194.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 77
ATGTCCGGGTCGTTAAAATCTCTAGACAAGAAAATAGCTAAAAGAAGGCAGGTGTAT
AAGCCCGTGCTAGACAATCCGTTCACAAACGAAGCACATATGTGGCCGCGCGTGCAT
GATCAGCCATTGATTTGGCAGCTGCTGCAATCCTCTATCATAAATAAGTTGATTCACA
TTCAATCGAAGGAGAACTACCCTTGGGAGCTGTATACAGATTTCAATGAAATTGTGC
AGTATTTGAGCGGCGCTCACGGAAACAGCGACCCAGTATGTCTATTTGTGTGCAATA
AGGACCCTGATGTACCGCTTGTGCTCTTGCAGCAAATCCCGCTATTATGCTATATGGC
GCCCATGACGGTTAAACTGGTGCAGTTGCCCAAGAGTGCCATGGATACCTTCAAGTC
GGTTTCTAAATATGGAATGCTGCTGCTGCGGTGCGACGATAGGGTCGACAAGAAATT
CGTATCGCAGATCCAGAAGAACGTTGATCTGCTTCAGTTTCCCTGGTTAAATGCTATC
AAGTATCGGCCCACATCTGTCAAGCTGTTGAAAACTACAGTGCCAATTGTCTCGAAG
AAGAGGCAAAAGTAG

Candida albicans nucleic acid: SEQ ID NO: 78
ATGAATAAATCAAATAAAGTCAAGAAACCTTCGGTGGCCAAAGTCTCAACTAAAGCT
GCTTCATCATCACTCAAGTCTCAGGAAGCAAAGAGAAAACAAGTTTTCCGTCCAATT
CTCGATAACTCATTTACACAATCAAACCAATGGCCATTTATAGAACCAACTATTGCAA
ACGATATTGTTGATCTACTAGAAGTATTGCTAAAAATGCAAGACTCTACATTTAAATA
CCGTGGGTTTAATCCAACTGTGTCTGCTCTTGAAAAACAAGCAGCTGCTAATCGTGGT
ATACATAAAAATGCTTGTGTACAAATAAAGTATGTATTTGTGTGCAAGTACGATATAT
CCCCAGCAACGCTCACAAATGTGTTTCCTACGTTGTGTTTCACGGCGTCAAAAAGTGC
TGAAGATCGGGTTAAGCTAATCCAGTTACCAAGAGGAAGTCTAGAACGGTTATCGAA
AGCACTTGGGGTAGATAGAGTTGGTATATTTGGTCTAACTAAAGATACTGAAGGGGC
ACAACCGTTATTTGATCTTATAAATGAAAATGTCAAAGATATTGAAGCTCCTTGGCTA
GACTGTATTTTCCGTGAGGAGATGGTATTTAATCAACCTAACACAAAGCATGTGGCAAGT
ACTGTAGGTAGAAAGAAAAACAAGTAG

FIGURE 80 (CONT'D)

Saccharomyces cerevisiae orf name: YNR003C
Saccharomyces cerevisiae gene name:RPC34
GENBANK Accession Number:CAA96279.1
Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 74
ATGAGTGGAATGATAGAAAATGGGTTACAGCTATCGGACAATGCTAAAACCTTACAT
AGCCAGATGATGTCGAAAGGAATAGGCGCATTATTTACACAGCAAGAACTCCAAAAA
CAAATGGGAATCGGGTCGTTAACAGACTTGATGTCCATTGTACAGGAATTGCTAGAC
AAGAACTTGATCAAATTAGTAAAACAAAACGACGAATTAAAATTTCAAGGTGTCTTA
GAATCTGAGGCGCAAAAGAAAGCCACCATGTCGGCTGAAGAGGCACTGGTATATTCT
TATATCGAGGCTAGCGGTAGAGAAGGGATATGGTCCAAGACTATCAAGGCAAGAAC
CAATCTCCATCAGCATGTAGTTCTTAAATGCTTGAAGAGTTTAGAATCCCAAAGATAC
GTGAAGAGTGTTAAGAGTGTAAAGTTTCCCACAAGGAAAATCTACATGTTGTACAGC
TTACAACCCTCTGTGGACATCACAGGAGGTCCATGGTTCACAGATGGAGAGCTGGAT
ATAGAATTTATCAATAGTTTATTGACTATTGTTTGGAGGTTCATATCAGAGAACACCT
TCCCTAATGGCTTCAAGAATTTCGAAAATGGACCCAAAAAAAACGTCTTTTATGCTCC
AAACGTAAAAAATTACTCTACCACACAAGAAATTTTGGAATTTATTACAGCGGCACA
AGTGGCCAATGTCGAGTTAACCCCTTCAAATATCAGATCTTTGTGTGAAGTCTTAGTG
TACGACGACAAGCTGGAAAAAGTCACGCATGACTGCTATAGAGTGACCTTAGAGAGC
ATTCTACAAATGAACCAAGGTGAGGGCGAGCCGGAGGCAGGTAATAAGGCTTTGGA
GGATGAAGAAGAATTTTCCATCTTTAACTACTTCAAGATGTTT

Candida albicans nucleic acid: SEQ ID NO: 75
ATGAGTGAGATGTTAGTATCAGATAAAGCACGTCATCTTTATACAAAGATGAGGGAG
TATCCAACTTCCAAACTTTTTGATCAAGATGAATTACAAACACTATTTGATATTAAAA
AGGGATCAGAATTAATGGAATATTTACAAGAATTAGTCAATGGTAAATATGTTAAAA
TTAGTAAAATGGGAGATCAATTAAAATTTCAAACTGTTGCTGAAGAAGAAGCCAAAA
AAGTATCGTCAATGTCTGATGATGAAGCAATGATTTATTCTTATATTGAAGCTTCAGG
TCGTGAAGGGATTTGGACTAAAACCATTAAAGCTAAAACTAATTTACATCAACATAT
TGTTCAAAAAATGTTTAAAAAATTTAGAAAATAATCGATACATTAAAAGTATTAAATC
AGTGAAACATCCAACAAGAAAAATTTATATGTTGTATAATTTACAACCTAGTATTGAT
GTTACTGGTGGTCCTTGGTTTACTGATTCAGAATTAGATACTGAATTTATAGAAACTT
TATTGGAAGTGTGTTGGAGATTTATTGTTGGGAAAACCATGTATATAAAGGATGAAG
AAGCTGATAATGAAGATATAAATCCACTTCAAACAACATATCACAATCATCATCCAG
GGGTGAATTTGGATCAACTTGTTGAATTTATAAACAATAGTAATATCACCAGTGTTGA
GTTGGGTATTAATGATATTAGATCATTATGTGATGTGCTAATCTATGACGATAGAATA
GAAGAAGTTGGTGGGAATCAAGAAAATAGTGGGATTTTTAAAGCTACTTGGCAAAGT
ATAATAGATAAAGGTAACACTATTTTGCAAAATAATTATCAGGATTTGAAAAAATGTT
GTTTCTGAAGATTGTTTTAATTATTTACAACAAAATCAATCAGATTTTAGTGTTTTTC
AATATAAATCTACTATTCAAGATCTTCAAGATGAATCGGATCTAGTGTATTTAGATAG
CTGGATAAATGAATAA

FIGURE 80 (CONT'D)

Human GENBANK Accession Number: U93869
Human nucleic acid sequence: SEQ ID NO: 76
CGACCCGGGTTCCGCCGCTTGCTACCGGGCTGCTCCGTGCATCTTTCCCCCCAGGCGTCA
GGAACTGCGCCTCATGGGCGAGGTGAAGGTGAAGGTGCAGCCGCCTGACGCCGATC
CGGTCGAAATAGAAAACAGGATTATAGAATTATGTCACCAGTTCCCTCATGGAATCA
CAGACCAAGTAATTCAGAATGAAATGCCTCAATATAGAAGCCCAGCAGCGGGCAGTA
GCATCAATAGGTTGTTGTCTATGGGTCAGTTGGATCTCTTAAGGAGCAATACGGGCC
TTTTATATAGAATAAAGGACTCTCAGAATGCTGGTAAAATGAAGGGATCCGATAACC
AAGAAAAACTAGTATATCAAATCATAGAGGATGCAGGAAATAAAGGAATATGGAGC
AGAGATATCCGCTATAAAAGTAATTTGCCATTAACAGAAATCAACAAAATTCTGAAG
AATCTGGAAAGTAAAAAGCTTATCAAAGCTGTTAAGTCTGTAGCAGCCTCAAAAAAG
AAGGTGTATATGCTCTATAACCTGCAGCCAGACCGGTCTGTGACTGGTGGAGCCTGG
TACAGTGACCAGGATTTTGAATCTGAATTTGTAGAGGTGCTTAACCAACAGTGTTTTA
AATTCCTACAGTCCAAGGCAGAAACAGCACGAGAAAGCAAACAGAACCCAATGATA
CAAAGAAATAGTTCATTTGCCTCATCACATGAAGTGTGGAAATATATCTGCGAATTG
GGAATCAGTAAGGTAGAGTTATCCATGGAAGACATTGAAACCATCCTGAATACACTC
ATTTATGATGGAAAAGTGGAGATGACGATTATTGCCTGCAAAAGAAGGCACAGTTGG
CAGTGTAGATGGACACATGAAACTGTACAGGGCAGTCAATCCAATCATCCCTCCCAC
AGGTTTGGTCCGGGCCACCCTGTGGACTCTGCCCCGGTTTTTGATGACTGCCACGAA
GGTGGTGAGATTTCACCATCTAACTGTATTTACATGACAGAGTGGCTCGAATTTTAAT
AGAGAGCTATGAACTTTATTGACATTTTGCAAATGAAGTTACTTAGGGAGCAGATAA
TTTAATTCATGATGGAACACGAAATCTCCTTGAAAGCAAACTTCACAATAATGGACG
TAGACTTGCTGCTATGAAAACATATTTTTTTTATTTATGAAGACTAAATTTATATTGG
TAAAATAGCCAGTAGAATATGAAAGAAATAAGGTTAGTAGTGAAATTCATTCTTCAA
TAAATAAAACACTTTGAAACTCCGGAGGACCACATCTTTCAAGACTTCTGATGGGCG
AAGCCCCCGGCTTCAAAACACGACAAGGAAGTGGTCTATTTCGATGAATGGACAATT
TGAAAAGATGCCAACATACCCGTATTTACCAAGTACTATGATAATGGCTAGAGTATA
AAAATGTTCTTTTTAAAGTTATTTATTAAGTTCTTCATTGGACGCTTTTTTTTATATCT
GGTTCACTACCACCATTTTCTGTTTCCTACTTTCTCAGTGGTTTCATTGAAAAGAAAT
TAGAAGGGGTTAAAGGCAGGAATAGCAAAGAGTGCAAACTTGGGGTATGACTGGGG
GAGAGTGGAACATGCCTTTTCCGCACAATATTAATTCCTTTTTGTATCAGAAAGGNNC
TNTTAGGAGTTATGCTACCATACTTACTTCAAACCCAATGACTACTGTCAAGGTCATA
TTTTCAGTACATAAATACTATCATTTTCATTCTAAAGAATATTTTCACTGTTCCTTCTT
TCTTAAAGTCTTATGTTTCACTCTTTAACTCAAATGTATTCTTTGTTAGAATTTACCCT
AGATTCTTATTTAATGTCTGCAGTAGACTGAATGTTTGTGTGCCCCCAGAATTCTAAT
GTTGAAATCTCATTTCCAATGTGATGGTATTTGGAGGTGGGGCTTTTGGTAAGTGATA
GGTCAGGAGAGTAACAGCGCTCATGAATGGGATTAGTGCCCTTATATAAAGAGACCC
AGAGAGCTCCATCACCCCTTCTGCCATGTGAAAGGGAGAAGACAAACATCCACGAAC
CAGGAAGTGGGTCCTCACCAGAAAACAAATCTGTAAGCACCTTGATCTTGGACTTCC
CAGCCTCCAGAATTGTGAGAAATAAATTTCTGTTGTTGATTTTTTTTTTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTT

FIGURE 80 (CONT'D)

::ODMA\WORLDOX\M:\0342\0G548\LWJ4450.WPD

SEQUENCE LISTING

<110> ANADYS PHARMACEUTICALS, INC.
THOMPSON, Craig
MOORE, Jeffrey
BUURMAN, Ed T.
BRADLEY, John
DESILVA, Thamara
HARRIS, Sandra
KOMARNITSKY, Svetlana
MENDILLO, Marc
MOORE, Daniel
MCCOY, Melissa
SANDERSON, Karen
HAQ, Tariq
ZHU, Shuhao
LONG, Fan
DAVIDOV, Eugene

<120> ANTIFUNGAL COMPOUNDS AND METHODS OF USE

<130> 0342/1G548-US1

<150> US 60/215,164
<151> 2000-06-29

<150> US 60/224,457
<151> 2000-08-10

<160> 146

<170> PatentIn version 3.1

<210> 1
<211> 316
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 74

<400> 1

Met Gly Glu Val Lys Val Lys Val Gln Pro Pro Asp Ala Asp Pro Val
1 5 10 15

Glu Ile Glu Asn Arg Ile Ile Glu Leu Cys His Gln Phe Pro His Gly
20 25 30

Ile Thr Asp Gln Val Ile Gln Asn Glu Met Pro His Ile Glu Ala Gln
35 40 45

Gln Arg Ala Val Ala Ile Asn Arg Leu Leu Ser Met Gly Gln Leu Asp
50 55 60

Leu Leu Arg Ser Asn Thr Gly Leu Leu Tyr Arg Ile Lys Asp Ser Gln
65 70 75 80

Asn Ala Gly Lys Met Lys Gly Ser Asp Asn Gln Glu Lys Leu Val Tyr
85 90 95

Gln Ile Ile Glu Asp Ala Gly Asn Lys Gly Ile Trp Ser Arg Asp Ile
100 105 110

Arg Tyr Lys Ser Asn Leu Pro Leu Thr Glu Ile Asn Lys Ile Leu Lys
115 120 125

Asn Leu Glu Ser Lys Lys Leu Ile Lys Ala Val Lys Ser Val Ala Ala
130 135 140

Ser Lys Lys Lys Val Tyr Met Leu Tyr Asn Leu Gln Pro Asp Arg Ser
145 150 155 160

Val Thr Gly Gly Ala Trp Tyr Ser Asp Gln Asp Phe Glu Ser Glu Phe
165 170 175

Val Glu Val Leu Asn Gln Gln Cys Phe Lys Phe Leu Gln Ser Lys Ala
180 185 190

Glu Thr Ala Arg Glu Ser Lys Gln Asn Pro Met Ile Gln Arg Asn Ser
195 200 205

Ser Phe Ala Ser Ser His Glu Val Trp Lys Tyr Ile Cys Glu Leu Gly

210 215 220

Ile Ser Lys Val Glu Leu Ser Met Glu Asp Ile Glu Thr Ile Leu Asn
225 230 235 240

Thr Leu Ile Tyr Asp Gly Lys Val Glu Met Thr Ile Ile Ala Ala Lys
245 250 255

Glu Gly Thr Val Gly Ser Val Asp Gly His Met Lys Leu Tyr Arg Ala
260 265 270

Val Asn Pro Ile Ile Pro Pro Thr Gly Leu Val Arg Ala Pro Cys Gly
275 280 285

Leu Cys Pro Val Phe Asp Asp Cys His Glu Gly Gly Glu Ile Ser Pro
290 295 300

Ser Asn Cys Ile Tyr Met Thr Glu Trp Leu Glu Phe
305 310 315

<210> 2
<211> 330
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 75

<400> 2

Met Ser Glu Met Leu Val Ser Asp Lys Ala Arg His Leu Tyr Thr Lys
1 5 10 15

Met Arg Glu Tyr Pro Thr Ser Lys Leu Phe Asp Gln Asp Glu Leu Gln
20 25 30

Thr Leu Phe Asp Ile Lys Lys Gly Ser Glu Leu Met Glu Tyr Leu Gln
35 40 45

Glu Leu Val Asn Gly Lys Tyr Val Lys Ile Ser Lys Met Gly Asp Gln
50 55 60

Leu Lys Phe Gln Thr Val Ala Glu Glu Glu Ala Lys Lys Val Ser Ser
65 70 75 80

Met Ser Asp Asp Glu Ala Met Ile Tyr Ser Tyr Ile Glu Ala Ser Gly
85 90 95

Arg Glu Gly Ile Trp Thr Lys Thr Ile Lys Ala Lys Thr Asn Leu His
100 105 110

Gln His Ile Val Gln Lys Cys Leu Lys Asn Leu Glu Asn Asn Arg Tyr
115 120 125

Ile Lys Ser Ile Lys Ser Val Lys His Pro Thr Arg Lys Ile Tyr Met
130 135 140

Leu Tyr Asn Leu Gln Pro Ser Ile Asp Val Thr Gly Gly Pro Trp Phe
145 150 155 160

Thr Asp Ser Glu Leu Asp Thr Glu Phe Ile Glu Thr Leu Leu Glu Val
165 170 175

Cys Trp Arg Phe Ile Val Gly Lys Thr Met Tyr Ile Lys Asp Glu Glu
180 185 190

Ala Asp Asn Glu Asp Ile Asn Pro Leu Gln Thr Thr Tyr His Asn His
195 200 205

His Pro Gly Val Asn Leu Asp Gln Leu Val Glu Phe Ile Asn Asn Ser
210 215 220

Asn Ile Thr Ser Val Glu Leu Gly Ile Asn Asp Ile Arg Ser Leu Cys
225 230 235 240

Asp Val Leu Ile Tyr Asp Asp Arg Ile Glu Glu Val Gly Gly Asn Gln
245 250 255

Glu Asn Ser Gly Ile Phe Lys Ala Thr Trp Gln Ser Ile Ile Asp Lys
260 265 270

Gly Asn Thr Ile Leu Gln Asn Asn Tyr Gln Asp Leu Lys Asn Val Val
275 280 285

Ser Glu Asp Cys Phe Asn Tyr Leu Gln Gln Asn Gln Ser Asp Phe Ser
290 295 300

Val Phe Gln Tyr Lys Ser Thr Ile Gln Asp Leu Gln Asp Glu Ser Asp
305 310 315 320

Leu Val Tyr Leu Asp Ser Trp Met Asn Glu
325 330

<210> 3
<211> 317
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human Genbank Accession No: U93869

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 76

<400> 3

Met Ser Gly Met Ile Glu Asn Gly Leu Gln Leu Ser Asp Asn Ala Lys
1 5 10 15

Thr Leu His Ser Gln Met Met Ser Lys Gly Ile Gly Ala Leu Phe Thr
20 25 30

Gln Gln Glu Leu Gln Lys Gln Met Gly Ile Gly Ser Leu Thr Asp Leu
35 40 45

Met Ser Ile Val Gln Glu Leu Leu Asp Lys Asn Leu Ile Lys Leu Val
50 55 60

Lys Gln Asn Asp Glu Leu Lys Phe Gln Gly Val Leu Glu Ser Glu Ala
65 70 75 80

Gln Lys Lys Ala Thr Met Ser Ala Glu Glu Ala Leu Val Tyr Ser Tyr
85 90 95

Ile Glu Ala Ser Gly Arg Glu Gly Ile Trp Ser Lys Thr Ile Lys Ala
100 105 110

Arg Thr Asn Leu His Gln His Val Val Leu Lys Cys Leu Lys Ser Leu
115 120 125

Glu Ser Gln Arg Tyr Val Lys Ser Val Lys Ser Val Lys Phe Pro Thr
130 135 140

Arg Lys Ile Tyr Met Leu Tyr Ser Leu Gln Pro Ser Val Asp Ile Thr
145 150 155 160

Gly Gly Pro Trp Phe Thr Asp Gly Glu Leu Asp Ile Glu Phe Ile Asn
165 170 175

Leu Leu Thr Ile Val Trp Arg Phe Ile Ser Glu Asn Thr Phe Pro
180 185 190

Asn Gly Phe Lys Asn Phe Glu Asn Gly Pro Lys Lys Asn Val Phe Tyr
195 200 205

Ala Pro Asn Val Lys Asn Tyr Ser Thr Thr Gln Glu Ile Leu Glu Phe
210 215 220

Ile Thr Ala Ala Gln Val Ala Asn Val Glu Leu Thr Pro Ser Asn Ile
225 230 235 240

Arg Ser Leu Cys Glu Val Leu Val Tyr Asp Asp Lys Leu Glu Lys Val
245 250 255

Thr His Asp Cys Tyr Arg Val Thr Leu Glu Ser Ile Leu Gln Met Asn
260 265 270

Gln Gly Glu Gly Glu Pro Glu Ala Gly Asn Lys Ala Leu Glu Asp Glu
275 280 285

Glu Glu Phe Ser Ile Phe Asn Tyr Phe Lys Met Phe Pro Ala Ser Lys
290 295 300

His Asp Lys Glu Val Val Tyr Phe Asp Glu Trp Thr Ile
305 310 315

<210> 4
<211> 195
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 77

<400> 4

Met Ser Gly Ser Leu Lys Ser Leu Asp Lys Lys Ile Ala Lys Arg Arg
1 5 10 15

Gln Val Tyr Lys Pro Val Leu Asp Asn Pro Phe Thr Asn Glu Ala His
20 25 30

Met Trp Pro Arg Val His Asp Gln Pro Leu Ile Trp Gln Leu Leu Gln
35 40 45

Ser Ser Ile Ile Asn Lys Leu Ile His Ile Gln Ser Lys Glu Asn Tyr
50 55 60

Pro Trp Glu Leu Tyr Thr Asp Phe Asn Glu Ile Val Gln Tyr Leu Ser
65 70 75 80

Gly Ala His Gly Asn Ser Asp Pro Val Cys Leu Phe Val Cys Asn Lys
85 90 95

Asp Pro Asp Val Pro Leu Val Leu Leu Gln Gln Ile Pro Leu Leu Cys
100 105 110

Tyr Met Ala Pro Met Thr Val Lys Leu Val Gln Leu Pro Lys Ser Ala
115 120 125

Met Asp Thr Phe Lys Ser Val Ser Lys Tyr Gly Met Leu Leu Leu Arg
130 135 140

Cys Asp Asp Arg Val Asp Lys Lys Phe Val Ser Gln Ile Gln Lys Asn
145 150 155 160

Val Asp Leu Leu Gln Phe Pro Trp Leu Asn Ala Ile Lys Tyr Arg Pro
165 170 175

Thr Ser Val Lys Leu Leu Lys Thr Thr Val Pro Ile Val Ser Lys Lys
180 185 190

Arg Gln Lys
195

<210> 5
<211> 220
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 78

<400> 5

Met Asn Lys Ser Asn Lys Val Lys Lys Pro Ser Val Ala Lys Val Ser

1 5 10 15

Thr Lys Ala Ala Ser Ser Ser Leu Lys Ser Gln Glu Ala Lys Arg Gln
20 25 30

Val Phe Arg Pro Ile Leu Asp Asn Ser Phe Thr Gln Ser Asn Gln Trp
35 40 45

Pro Phe Ile Glu Pro Thr Ile Ala Asn Asp Ile Val Asp Leu Leu Glu
50 55 60

Val Leu Leu Lys Met Gln Asp Ser Thr Phe Lys Tyr Arg Gly Phe Asn
65 70 75 80

Pro Thr Val Ser Ala Leu Glu Lys Gln Ala Ala Ala Asn Arg Gly Ile
85 90 95

His Lys Asn Ala Cys Val Gln Ile Lys Tyr Val Phe Val Cys Lys Tyr
100 105 110

Asp Ile Ser Pro Ala Thr Leu Thr Asn Val Phe Pro Thr Leu Cys Phe
115 120 125

Thr Ala Ser Lys Ser Ala Glu Asp Arg Val Lys Leu Ile Gln Leu Pro
130 135 140

Arg Gly Ser Leu Glu Arg Leu Ser Lys Ala Leu Gly Val Asp Arg Val
145 150 155 160

Gly Ile Phe Gly Leu Thr Lys Asp Thr Glu Gly Ala Gln Pro Leu Phe
165 170 175

Asp Leu Ile Asn Glu Asn Val Lys Asp Ile Glu Ala Pro Trp Leu Asp
180 185 190

Cys Ile Phe Arg Glu Glu Met Val Phe Asn Gln Pro Asn Thr Lys His
195 200 205

Val Ala Ser Thr Val Gly Arg Lys Lys Asn Lys Lys
210 215 220

<210> 6
<211> 328
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 79

<400> 6

Met Ser Lys Asn Arg Asp Pro Leu Leu Ala Asn Leu Asn Ala Phe Lys
1 5 10 15

Ser Lys Val Lys Ser Ala Pro Val Ile Ala Pro Ala Lys Val Gly Gln
20 25 30

Lys Lys Thr Asn Asp Thr Val Ile Thr Ile Asp Gly Asn Thr Arg Lys
35 40 45

Arg Thr Ala Ser Glu Arg Ala Gln Glu Asn Thr Leu Asn Ser Ala Lys
50 55 60

Asn Pro Val Leu Val Asp Ile Lys Lys Glu Ala Gly Ser Asn Ser Ser
65 70 75 80

Asn Ala Ile Ser Leu Asp Asp Asp Asp Asp Asp Glu Asp Phe Gly Ser
85 90 95

Ser Pro Ser Lys Lys Val Arg Pro Gly Ser Ile Ala Ala Ala Ala Leu
100 105 110

Gln Ala Asn Gln Thr Asp Ile Ser Lys Ser His Asp Ser Ser Lys Leu
115 120 125

Leu Trp Ala Thr Glu Tyr Ile Gln Lys Lys Gly Lys Pro Val Leu Val
130 135 140

Asn Glu Leu Leu Asp Tyr Leu Ser Met Lys Lys Asp Asp Lys Val Ile
145 150 155 160

Glu Leu Leu Lys Lys Leu Asp Arg Ile Glu Phe Asp Pro Lys Lys Gly
165 170 175

Thr Phe Lys Tyr Leu Ser Thr Tyr Asp Val His Ser Pro Ser Glu Leu
180 185 190

Leu Lys Leu Leu Arg Ser Gln Val Thr Phe Lys Gly Ile Ser Cys Lys
195 200 205

Asp Leu Lys Asp Gly Trp Pro Gln Cys Asp Glu Thr Ile Asn Gln Leu
210 215 220

Glu Glu Asp Ser Lys Ile Leu Val Leu Arg Thr Lys Lys Asp Lys Thr
225 230 235 240

Pro Arg Tyr Val Trp Tyr Asn Ser Gly Gly Asn Leu Lys Cys Ile Asp
245 250 255

Glu Glu Phe Val Lys Met Trp Glu Asn Val Gln Leu Pro Gln Phe Ala
260 265 270

Glu Leu Pro Arg Lys Leu Gln Asp Leu Gly Leu Lys Pro Ala Ser Val
275 280 285

Asp Pro Ala Thr Ile Lys Arg Gln Thr Lys Arg Val Glu Val Lys Lys
290 295 300

Lys Arg Gln Arg Lys Gly Lys Ile Thr Asn Thr His Met Thr Gly Ile
305 310 315 320

Leu Lys Asp Tyr Ser His Arg Val

325

<210> 7
<211> 284
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 80

<400> 7

Met Ser Asp Leu Ser Ala Gln Leu Ser Ala Phe Lys Asn Lys Ile Lys
1 5 10 15

Ser Gly Pro Ser Val Ile Val Pro Arg Lys Ala Thr Phe Thr Gln Ser
20 25 30

Pro Ser Ser Pro Leu Ser Ser Ser Thr Thr Thr Thr Thr Ser Lys Asn
35 40 45

Asp Ala Asn Val Lys Lys Arg Ser Thr Thr Asp Ser Val Thr Arg Val
50 55 60

Leu Lys Lys Gln Lys Ala Asn Met Gly Glu Met Thr Gly Ser His Leu
65 70 75 80

Ser Thr Gln Leu His Leu Ala Val Glu Tyr Ile Lys Glu His Asp Gln
85 90 95

Pro Ile Ser Val Glu Lys Leu Gln Asn Tyr Leu Ser Phe Asp Ile Ser
100 105 110

His Thr Leu Leu Pro Leu Leu Asn Glu Ile Asp Arg Val Lys Tyr Asp
115 120 125

Glu Ser Lys Gly Thr Leu Glu Tyr Val Ser Leu His Asn Ile Arg Ser
130 135 140

Ser Asp Asp Val Leu Glu Phe Leu Arg Arg Gln Thr Thr Phe Lys Gly
145 150 155 160

Thr Ser Val Lys Glu Leu Lys Asp Gly Trp Ala Gly Cys Val Ala Ala
165 170 175

Ile Asp Glu Leu Glu Ser Gln Gly Lys Ile Leu Val Leu Arg Asn Lys
180 185 190

Lys Glu Asn Ala Pro Arg Leu Val Trp Ala Asn Asn Gly Gly Glu Leu
195 200 205

Gly Tyr Ile Asp Thr Glu Phe Lys Asp Met Trp Asp Gln Val Lys Leu
210 215 220

Pro Glu Pro Asp Val Leu Tyr Gln Lys Leu Leu Asp Gln Gly Leu Lys
225 230 235 240

Pro Thr Gly Ala Asp Pro Asn Leu Ile Lys Lys Gln Pro Gln Gln Lys
245 250 255

Glu Lys Lys Gln Lys Lys Ala Arg Arg Gly Lys Ile Thr Asn Thr His
260 265 270

Met Lys Gly Ile Leu Lys Asp Tyr Ser Gln Leu Val
275 280

<210> 8
<211> 291
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: NP_002086

<220>
<221> misc_feature

<223> Corresponds to SEQ ID NO: 81

<400> 8

Met Asp Pro Ser Leu Leu Arg Glu Arg Glu Leu Phe Lys Lys Arg Ala
1 5 10 15

Leu Ser Thr Pro Val Val Glu Lys Arg Ser Ala Ser Ser Glu Ser Ser
20 25 30

Ser Ser Ser Ser Lys Lys Lys Lys Thr Lys Val Glu His Gly Gly Ser
35 40 45

Ser Gly Ser Lys Gln Asn Ser Asp His Ser Asn Gly Ser Phe Asn Leu
50 55 60

Lys Ala Leu Ser Gly Ser Ser Gly Tyr Lys Phe Gly Val Leu Ala Lys
65 70 75 80

Ile Val Asn Tyr Met Lys Thr Arg His Gln Arg Gly Asp Thr His Pro
85 90 95

Leu Thr Leu Asp Glu Ile Leu Asp Glu Thr Gln His Leu Asp Ile Gly
100 105 110

Leu Lys Gln Lys Gln Trp Leu Met Thr Glu Ala Leu Val Asn Asn Pro
115 120 125

Lys Ile Glu Val Ile Asp Gly Lys Tyr Ala Phe Lys Pro Lys Tyr Asn
130 135 140

Val Arg Asp Lys Lys Ala Leu Leu Arg Leu Leu Asp Gln His Asp Gln
145 150 155 160

Arg Gly Leu Gly Gly Ile Leu Leu Glu Asp Ile Glu Glu Ala Leu Pro
165 170 175

Asn Ser Gln Lys Ala Val Lys Ala Leu Gly Asp Gln Ile Leu Phe Val
180 185 190

Asn Arg Pro Asp Lys Lys Lys Ile Leu Phe Phe Asn Asp Lys Ser Cys
195 200 205

Gln Phe Ser Val Asp Glu Glu Phe Gln Lys Leu Trp Arg Ser Val Thr
210 215 220

Val Asp Ser Met Asp Glu Glu Lys Ile Glu Glu Tyr Leu Lys Arg Gln
225 230 235 240

Gly Ile Ser Ser Met Gln Glu Ser Gly Pro Lys Lys Val Ala Pro Ile
245 250 255

Gln Arg Arg Lys Lys Pro Ala Ser Gln Lys Lys Arg Arg Phe Lys Thr
260 265 270

His Asn Glu His Leu Ala Gly Val Leu Lys Asp Tyr Ser Asp Ile Thr
275 280 285

Ser Ser Lys
290

<210> 9
<211> 480
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 82

<400> 9

Met Ser Gln Glu Gln Tyr Thr Glu Asn Leu Lys Val Ile Val Ala Glu
1 5 10 15

Lys Leu Ala Gly Ile Pro Asn Phe Asn Glu Asp Ile Lys Tyr Val Ala

20 25 30

Glu Tyr Ile Val Leu Leu Ile Val Asn Gly Gly Thr Val Glu Ser Val
35 40 45

Val Asp Glu Leu Ala Ser Leu Phe Asp Ser Val Ser Arg Asp Thr Leu
50 55 60

Ala Asn Val Val Gln Thr Ala Phe Phe Ala Leu Glu Ala Leu Gln Gln
65 70 75 80

Gly Glu Ser Ala Glu Asn Ile Val Ser Lys Ile Arg Met Met Asn Ala
85 90 95

Gln Ser Leu Gly Gln Ser Asp Ile Ala Gln Gln Gln Gln Gln Gln Gln
100 105 110

Gln Gln Gln Gln Pro Asp Ile Ala Gln Gln Gln Pro Gln Gln Gln Pro
115 120 125

Gln Leu Gln Pro Leu Gln Pro Gln Leu Gly Thr Gln Asn Ala Met Gln
130 135 140

Thr Asp Ala Pro Ala Thr Pro Ser Pro Ile Ser Ala Phe Ser Gly Val
145 150 155 160

Val Asn Ala Ala Ala Pro Pro Gln Phe Ala Pro Val Asp Asn Ser Gln
165 170 175

Arg Phe Thr Gln Arg Gly Gly Gly Ala Val Gly Lys Asn Arg Arg Gly
180 185 190

Gly Arg Gly Gly Asn Arg Gly Gly Arg Asn Asn Asn Ser Thr Arg Phe
195 200 205

Asn Pro Leu Ala Lys Ala Leu Gly Met Ala Gly Glu Ser Asn Met Asn
210 215 220

Phe Thr Pro Thr Lys Lys Glu Gly Arg Cys Arg Leu Phe Pro His Cys
225 230 235 240

Pro Leu Gly Arg Ser Cys Pro His Ala His Pro Thr Lys Val Cys Asn
245 250 255

Glu Tyr Pro Asn Cys Pro Lys Pro Pro Gly Thr Cys Glu Phe Leu His
260 265 270

Pro Asn Glu Asp Glu Glu Leu Met Lys Glu Met Glu Arg Thr Arg Glu
275 280 285

Glu Phe Gln Lys Arg Lys Ala Asp Leu Leu Ala Ala Lys Arg Lys Pro
290 295 300

Val Gln Thr Gly Ile Val Leu Cys Lys Phe Gly Ala Leu Cys Ser Asn
305 310 315 320

Pro Ser Cys Pro Phe Gly His Pro Thr Pro Ala Asn Glu Asp Ala Lys
325 330 335

Val Ile Asp Leu Met Trp Cys Asp Lys Asn Leu Thr Cys Asp Asn Pro
340 345 350

Glu Cys Arg Lys Ala His Ser Ser Leu Ser Lys Ile Lys Glu Val Lys
355 360 365

Pro Ile Ser Gln Lys Lys Ala Ala Pro Pro Pro Val Glu Lys Ser Leu
370 375 380

Glu Gln Cys Lys Phe Gly Thr His Cys Thr Asn Lys Arg Cys Lys Tyr
385 390 395 400

Arg His Ala Arg Ser His Ile Met Cys Arg Glu Gly Ala Asn Cys Thr
405 410 415

Arg Ile Asp Cys Leu Phe Gly His Pro Ile Asn Glu Asp Cys Arg Phe
420 425 430

Gly Val Asn Cys Lys Asn Ile Tyr Cys Leu Phe Arg His Pro Pro Gly
435 440 445

Arg Val Leu Pro Glu Lys Lys Gly Ala Ala Pro Asn Ser Asn Val Pro
450 455 460

Thr Asn Glu Arg Pro Phe Ala Leu Pro Glu Asn Ala Ile Ile Glu Asn
465 470 475 480

<210> 10
<211> 418
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 83

<400> 10

Met Gln Phe Ala Pro Asp Asn Gln Ile Gly Lys Glu Leu Gln Gln Asn
1 5 10 15

Leu Ile Gln Glu Ile Gln Arg Arg Phe Asn Lys Pro Ala Asp Asp Ala
20 25 30

Val Asp Ile Ala Asp Tyr Ile Ile Tyr Leu Ile Val Ala Lys Lys Ser
35 40 45

Glu Gln Glu Ile Val Ala Glu Val Lys Asp Ile Ala Asp Ile Ser Ile
50 55 60

Asp Val Gly Phe Ile Gly Asp Val Tyr Leu Glu Ile Arg Lys Leu Glu
65 70 75 80

Val Lys Tyr Asn Gln Pro Pro Ala Ala Val Glu Glu Ala Ser Gln Pro

85 90 95

Gln Gln Glu Gln Gln Gln Gln Ser Gln Ala Ser Val Val Ala Pro Gln
100 105 110

Ile Pro Ile Gly Pro Lys Lys Gln Leu Thr Glu Glu Glu Lys Ile Ala
115 120 125

Leu Arg Ser Gln Arg Phe Gly Thr Thr Thr Arg Leu Ser Gly Arg Gly
130 135 140

Gly Arg Gly Gly Ile Thr Lys Thr Arg Thr Asp Phe Arg Asn Gly His
145 150 155 160

Asn Asn Lys Asn Phe Leu Asp Pro Lys Lys Leu Asp Gln Ile Ile Ser
165 170 175

Gly Ala Asn Asn Gly Ala Ile Lys Phe Val Pro Leu Pro Pro Lys Gly
180 185 190

Arg Cys Pro Asp Phe Pro Tyr Cys Lys Asn Gln Asn Cys Glu Lys Ala
195 200 205

His Pro Thr Lys Asn Cys Phe Asn Tyr Pro Asp Cys Pro Asn Pro Pro
210 215 220

Gly Thr Cys Asn Phe Leu His Pro Asp Gln Asp Gln Glu Leu Ile Ala
225 230 235 240

Lys Leu Glu Thr Ser Lys Lys Glu Phe Glu Glu Lys Lys Lys Asn Gln
245 250 255

Leu Met Val Lys Gln Gly Ser Cys Lys Tyr Gly Leu Lys Cys Ala Lys
260 265 270

Glu Asn Cys Pro Phe Ala His Pro Thr Pro Ala Asn Pro Glu Ser Gly
275 280 285

Lys Ile Glu Thr Leu Glu Trp Cys Pro Gln Gly Lys Asn Cys Gln Asp
290 295 300

Arg Asn Cys Thr Lys Ser His Pro Pro Pro Pro Thr Ala Asn Ser Glu
305 310 315 320

Lys Leu Leu Ser Ala Ala Asp Leu Ala Leu Glu Gln Cys Lys Phe Gly
325 330 335

Ser Gln Cys Thr Asn Leu Lys Cys Pro Arg Arg His Ala Thr Ser Ala
340 345 350

Val Pro Cys Arg Ala Gly Ala Glu Cys Arg Arg Val Asp Cys Thr Phe
355 360 365

Ser His Pro Leu Lys Glu Pro Cys Arg Phe Gly Thr Lys Cys Thr Asn
370 375 380

Lys Val Cys Met Tyr Gln His Pro Glu Gly Arg Thr Ile Ala Ser His
385 390 395 400

Thr Trp Thr Arg Asp Gly Ser Gly Asn Asn Asn Ser Thr Ser Asn Arg
405 410 415

Ser Phe

<210> 11
<211> 156
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: AAD42873

<220>
<221> misc_feature

<223> Corresponds to SEQ ID NO: 84

<400> 11

Pro Gln Gln Leu His Leu Leu Ser Arg Gln Leu Glu Asp Pro Asn Gly
1 5 10 15

Ser Phe Ser Asn Ala Glu Met Ser Glu Leu Ser Val Ala Gln Lys Pro
20 25 30

Glu Lys Leu Leu Glu Arg Cys Lys Tyr Trp Pro Ala Cys Lys Asn Gly
35 40 45

Asp Glu Cys Ala Tyr His His Pro Ile Ser Pro Cys Lys Ala Phe Pro
50 55 60

Asn Cys Lys Phe Ala Glu Lys Cys Leu Phe Val His Pro Asn Cys Lys
65 70 75 80

Tyr Asp Ala Lys Cys Thr Lys Pro Asp Cys Pro Phe Thr His Val Ser
85 90 95

Arg Arg Ile Gln Leu Cys Arg Tyr Phe Pro Ala Cys Lys Lys Met Glu
100 105 110

Cys Pro Phe Tyr His Pro Lys His Cys Arg Phe Asn Thr Gln Cys Thr
115 120 125

Arg Pro Asp Cys Thr Phe Tyr His Pro Thr Ile Asn Val Pro Pro Arg
130 135 140

His Ala Leu Lys Trp Ile Arg Pro Gln Thr Ser Glu
145 150 155

<210> 12
<211> 360
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 85

<400> 12

Met Ala Asn Ser Pro Lys Lys Pro Ser Asp Gly Thr Gly Val Ser Ala
1 5 10 15

Ser Asp Thr Pro Lys Tyr Gln His Thr Val Pro Glu Thr Lys Pro Ala
20 25 30

Phe Asn Leu Ser Pro Gly Lys Ala Ser Glu Leu Ser His Ser Leu Pro
35 40 45

Ser Pro Ser Gln Ile Lys Ser Thr Ala His Val Ser Ser Thr His Asn
50 55 60

Asp Ala Ala Gly Asn Thr Asp Asp Ser Val Leu Pro Lys Asn Val Ser
65 70 75 80

Pro Thr Thr Asn Leu Arg Val Glu Ser Asn Gly Asp Thr Asn Asn Met
85 90 95

Phe Ser Ser Pro Ala Gly Leu Ala Leu Pro Lys Lys Asp Asp Lys Lys
100 105 110

Lys Asn Lys Gly Thr Ser Lys Ala Asp Ser Lys Asp Gly Lys Ala Ser
115 120 125

Asn Ser Ser Gly Gln Asn Ala Gln Gln Gln Ser Asp Pro Asn Lys Met
130 135 140

Gln Asp Val Leu Phe Ser Ala Gly Ile Asp Val Arg Glu Glu Glu Ala
145 150 155 160

Leu Leu Asn Ser Ser Ile Asn Ala Ser Lys Ser Gln Val Gln Thr Asn
165 170 175

Asn Val Lys Ile Pro Asn His Leu Pro Phe Leu His Pro Glu Gln Val
180 185 190

Ser Asn Tyr Met Arg Lys Val Gly Lys Glu Gln Asn Phe Asn Leu Thr
195 200 205

Pro Thr Lys Asn Pro Glu Ile Leu Asp Met Met Ser Ser Ala Cys Glu
210 215 220

Asn Tyr Met Arg Asp Ile Leu Thr Asn Ala Ile Val Ile Ser Arg His
225 230 235 240

Arg Arg Lys Ala Val Lys Ile Asn Ser Gly Arg Arg Ser Glu Val Ser
245 250 255

Ala Ala Leu Arg Ala Ile Ala Leu Ile Gln Lys Lys Glu Glu Glu Arg
260 265 270

Arg Val Lys Lys Arg Ile Ala Leu Gly Leu Glu Lys Glu Asp Tyr Glu
275 280 285

Asn Lys Ile Asp Ser Glu Glu Thr Leu His Arg Ala Ser Asn Val Thr
290 295 300

Ala Gly Leu Arg Ala Gly Ser Lys Lys Gln Tyr Gly Trp Leu Thr Ser
305 310 315 320

Ser Val Asn Lys Pro Thr Ser Leu Gly Ala Lys Ser Ser Gly Lys Val
325 330 335

Ala Ser Asp Ile Thr Ala Arg Gly Glu Ser Gly Leu Lys Phe Arg Glu
340 345 350

Ala Arg Glu Glu Pro Gly Ile Val
355 360

<210> 13
<211> 358
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 86

<400> 13

Met Ser His Lys Ser Met Thr Ser Thr Pro Gln Glu Ser Ser Asn Leu
1 5 10 15

Lys Arg Gln Leu Glu Asn Ser Glu Asp Ser Ser Ser Pro Asn Lys Arg
20 25 30

Ser Lys Thr Glu Thr Thr Thr Glu Asn Gln Ser Ser Trp Glu Ser Asp
35 40 45

Phe Asn Ser Leu Pro Val Glu Leu Leu Gln Thr Glu Thr Asn Gly Thr
50 55 60

Ser Pro Ala Pro Ala Pro Ala Thr Pro Ile Asp Thr Thr Asn Ala Ser
65 70 75 80

Ser Thr Lys Glu Arg Asp Gln Asp Thr Ser Lys Leu Asn Asp Ala Ile
85 90 95

Ala Ala Ala Gly Val Asp Ile Gln Gln Glu Glu Glu Ile Leu Leu Gln
100 105 110

Gln Gln Leu Asn Arg Lys Ser Ala Glu Gly Met Ala Ser Asn Leu Lys
115 120 125

Ser Val Ile Arg Ser Ser Lys Leu Pro Pro Phe Leu His Asn Tyr His
130 135 140

Leu Ala Ala Phe Ile Asp Lys Val Ala Lys Gln Asn Gly Ile Gln Gln

145 150 155 160

Asn Phe Leu Met Asp Gly Glu Met Leu Glu Leu Ile Ser Ala Ala Cys
165 170 175

Glu Thr Trp Leu Ser Asn Leu Ala Thr Lys Thr Ile Ile Leu Ser Arg
180 185 190

His Arg Arg Arg Gly Ile Pro Val Ile Asn Lys Lys Ser Gly Ser Ser
195 200 205

Ser Val Pro Arg Ser Glu Ile Ser Lys Glu Leu Arg Ser Leu Ala Leu
210 215 220

Lys Gln Lys Glu Met Glu Glu Lys Arg Val Asn Lys Arg Val Met Leu
225 230 235 240

Gly Leu Glu Lys Ser Thr Lys Asp Ala Ser Lys Asn Asp Glu Asn Gly
245 250 255

Glu Ser Lys Ala Gly Ala Glu Glu Thr Leu His Arg Ala Ala Asn Ala
260 265 270

Thr Ala Ala Met Met Thr Met Asn Pro Gly Arg Lys Lys Tyr Ser Trp
275 280 285

Met Thr Ser Ser Ala Thr Ala Gly Gly Gly Ser Asp Phe Gly Lys Ser
290 295 300

Ser Gly Gly Ser Ser Lys Asp Ser Gly Lys His Gln Ser Pro Ile Ile
305 310 315 320

Ser Val Arg Gly Asp Asn Gly Leu Arg Phe Arg Glu Ile Arg Ser Gly
325 330 335

Asn Ser Ile Ile Met Lys Asp Leu Leu Gly Ala Ile Glu Asp Glu Lys
340 345 350

Met Gly Thr Arg Asn Ala
355

<210> 14
<211> 1023
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: CAA72189

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 87

<400> 14

Met Ala Ala Gly Ser Asp Leu Leu Asp Glu Val Phe Phe Asn Ser Glu
1 5 10 15

Val Asp Glu Lys Val Val Ser Asp Leu Val Gly Ser Leu Glu Ser Gln
20 25 30

Leu Ala Ala Ser Ala Ala His His His His Leu Ala Pro Arg Thr Pro
35 40 45

Glu Val Arg Ala Ala Ala Ala Gly Ala Leu Gly Asn His Val Val Ser
50 55 60

Gly Ser Pro Ala Gly Ala Ala Gly Ala Gly Pro Ala Ala Pro Ala Glu
65 70 75 80

Gly Ala Pro Gly Ala Ala Pro Glu Pro Pro Pro Ala Gly Arg Ala Arg
85 90 95

Pro Gly Gly Gly Gly Pro Gln Arg Pro Gly Pro Pro Ser Pro Arg Arg
100 105 110

Pro Leu Val Pro Ala Gly Pro Ala Pro Pro Ala Ala Lys Leu Arg Pro
115 120 125

Pro Pro Glu Gly Ser Ala Gly Ala Cys Ala Pro Val Pro Ala Ala Ala
130 135 140

Ala Val Ala Ala Gly Pro Glu Pro Ala Pro Ala Gly Pro Ala Lys Pro
145 150 155 160

Ala Gly Pro Ala Ala Leu Ala Ala Arg Ala Gly Pro Gly Pro Gly Pro
165 170 175

Gly Pro Gly Pro Gly Pro Gly Pro Gly Lys Pro Ala Gly Pro Gly Ala
180 185 190

Ala Gln Thr Leu Asn Gly Ser Ala Ala Leu Leu Asn Ser His His Ala
195 200 205

Ala Ala Pro Ala Val Ser Leu Val Asn Asn Gly Pro Ala Ala Leu Leu
210 215 220

Pro Leu Pro Lys Pro Ala Ala Pro Gly Thr Val Ile Gln Thr Pro Pro
225 230 235 240

Phe Val Gly Ala Ala Ala Pro Pro Ala Pro Ala Ala Pro Ser Pro Pro
245 250 255

Ala Ala Pro Ala Pro Ala Ala Pro Ala Ala Ala Pro Pro Pro Pro Pro
260 265 270

Pro Ala Pro Ala Thr Leu Ala Arg Pro Pro Gly His Pro Ala Gly Pro
275 280 285

Pro Thr Ala Ala Pro Ala Val Pro Pro Pro Ala Ala Ala Gln Asn Gly
290 295 300

Gly Ser Ala Gly Ala Ala Pro Ala Pro Ala Pro Ala Ala Gly Gly Pro

305 310 315 320

Ala Gly Val Ser Gly Gln Pro Gly Pro Gly Ala Ala Ala Ala Ala Pro
325 330 335

Ala Pro Gly Val Lys Ala Glu Ser Pro Lys Arg Val Val Gln Ala Ala
340 345 350

Pro Pro Ala Ala Gln Thr Leu Ala Ala Ser Gly Pro Ala Ser Thr Ala
355 360 365

Ala Ser Met Val Ile Gly Pro Thr Met Gln Gly Ala Leu Pro Ser Pro
370 375 380

Ala Ala Val Pro Pro Pro Ala Pro Gly Thr Pro Thr Gly Leu Pro Lys
385 390 395 400

Gly Ala Ala Gly Ala Val Thr Gln Ser Leu Ser Arg Thr Pro Thr Ala
405 410 415

Thr Thr Ser Gly Ile Arg Ala Thr Leu Thr Pro Thr Val Leu Ala Pro
420 425 430

Arg Leu Pro Gln Pro Pro Gln Asn Pro Thr Asn Ile Gln Asn Phe Gln
435 440 445

Leu Pro Pro Gly Met Val Leu Val Arg Ser Glu Asn Gly Gln Leu Leu
450 455 460

Met Ile Pro Gln Gln Ala Leu Ala Gln Met Gln Ala Gln Ala His Ala
465 470 475 480

Gln Pro Gln Thr Thr Met Ala Pro Arg Pro Ala Thr Pro Thr Ser Ala
485 490 495

Pro Pro Val Gln Ile Ser Thr Val Gln Ala Pro Gly Thr Pro Ile Ile
500 505 510

Ala Arg Gln Val Thr Pro Thr Thr Ile Ile Lys Gln Val Ser Gln Ala
515 520 525

Gln Thr Thr Val Gln Pro Ser Ala Thr Leu Gln Arg Ser Pro Gly Val
530 535 540

Gln Pro Gln Leu Val Leu Gly Gly Ala Ala Gln Thr Ala Ser Leu Gly
545 550 555 560

Thr Ala Thr Ala Val Gln Thr Gly Thr Pro Gln Arg Thr Val Pro Gly
565 570 575

Ala Thr Thr Thr Ser Ser Ala Ala Thr Glu Thr Met Glu Asn Val Lys
580 585 590

Lys Cys Lys Asn Phe Leu Ser Thr Leu Ile Lys Leu Ala Ser Ser Gly
595 600 605

Lys Gln Ser Thr Glu Thr Ala Ala Asn Val Lys Glu Leu Val Gln Asn
610 615 620

Leu Leu Asp Gly Lys Ile Glu Ala Glu Asp Phe Thr Ser Arg Leu Tyr
625 630 635 640

Arg Glu Leu Asn Ser Ser Pro Gln Pro Tyr Leu Val Pro Phe Leu Lys
645 650 655

Arg Ser Leu Pro Ala Leu Arg Gln Leu Thr Pro Asp Ser Ala Ala Phe
660 665 670

Ile Gln Gln Ser Gln Gln Gln Pro Pro Pro Pro Thr Ser Gln Ala Thr
675 680 685

Thr Ala Leu Thr Ala Val Val Leu Ser Ser Ser Val Gln Arg Thr Ala
690 695 700

Gly Lys Thr Ala Ala Thr Val Thr Ser Ala Leu Gln Pro Pro Val Leu
705 710 715 720

Ser Leu Thr Gln Pro Thr Gln Val Gly Val Gly Lys Gln Gly Gln Pro
725 730 735

Thr Pro Leu Val Ile Gln Gln Pro Pro Lys Pro Gly Ala Leu Ile Arg
740 745 750

Pro Pro Gln Val Thr Leu Thr Gln Thr Pro Met Val Ala Leu Arg Gln
755 760 765

Pro His Asn Arg Ile Met Leu Thr Thr Pro Gln Gln Val Asn Leu Ser
770 775 780

Glu Glu Ser Ala Arg Ile Leu Ala Thr Asn Ser Glu Leu Val Gly Thr
785 790 795 800

Leu Thr Arg Ser Cys Lys Asp Glu Thr Phe Leu Leu Gln Ala Pro Leu
805 810 815

Gln Arg Arg Ile Leu Glu Ile Gly Lys Lys His Gly Ile Thr Glu Leu
820 825 830

His Pro Asp Val Val Ser Tyr Val Ser His Ala Thr Gln Gln Arg Leu
835 840 845

Gln Asn Leu Val Glu Lys Ile Ser Glu Thr Ala Gln Gln Lys Asn Phe
850 855 860

Ser Tyr Lys Asp Asp Asp Arg Tyr Glu Gln Ala Ser Asp Val Arg Ala
865 870 875 880

Gln Leu Lys Phe Phe Glu Gln Leu Asp Gln Ile Glu Lys Gln Arg Lys
885 890 895

Asp Glu Gln Glu Arg Glu Ile Leu Met Arg Ala Ala Lys Ser Arg Ser

900 905 910

Arg Gln Glu Asp Pro Glu Gln Leu Arg Leu Lys Gln Lys Ala Lys Glu
915 920 925

Met Gln Gln Gln Glu Leu Ala Gln Met Arg Gln Arg Asp Ala Asn Leu
930 935 940

Thr Ala Leu Ala Ala Ile Gly Pro Arg Lys Lys Arg Lys Val Asp Cys
945 950 955 960

Pro Gly Pro Gly Ser Gly Ala Glu Gly Ser Gly Pro Gly Ser Val Val
965 970 975

Pro Gly Ser Ser Gly Val Gly Thr Pro Arg Gln Phe Thr Arg Gln Arg
980 985 990

Ile Thr Arg Val Asn Leu Arg Asp Leu Ile Phe Cys Leu Glu Asn Glu
995 1000 1005

Arg Glu Thr Ser His Ser Leu Leu Leu Tyr Lys Ala Phe Leu Lys
1010 1015 1020

<210> 15
<211> 184
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 88

<400> 15

Met Asn Thr Asn Ser Asn Thr Met Val Met Asn Asp Ala Asn Gln Ala
1 5 10 15

Gln Ile Thr Ala Thr Phe Thr Lys Lys Ile Leu Ala His Leu Asp Asp
20 25 30

Pro Asp Ser Asn Lys Leu Ala Gln Phe Val Gln Leu Phe Asn Pro Asn
35 40 45

Asn Cys Arg Ile Ile Phe Asn Ala Thr Pro Phe Ala Gln Ala Thr Val
50 55 60

Phe Leu Gln Met Trp Gln Asn Gln Val Val Gln Thr Gln His Ala Leu
65 70 75 80

Thr Gly Val Asp Tyr His Ala Ile Pro Gly Ser Gly Thr Leu Ile Cys
85 90 95

Asn Val Asn Cys Lys Val Arg Phe Asp Glu Ser Gly Arg Asp Lys Met
100 105 110

Gly Gln Asp Ala Thr Val Pro Ile Gln Pro Asn Asn Thr Gly Asn Arg
115 120 125

Asn Arg Pro Asn Asp Met Asn Lys Pro Arg Pro Leu Trp Gly Pro Tyr
130 135 140

Phe Gly Ile Ser Leu Gln Leu Ile Ile Asp Asp Arg Ile Phe Arg Asn
145 150 155 160

Asp Phe Asn Gly Val Ile Ser Gly Phe Asn Tyr Asn Met Val Tyr Lys
165 170 175

Pro Glu Asp Ser Leu Leu Lys Ile
180

<210> 16
<211> 181
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 89

<400> 16

Met Asn Gln Asp Pro Thr Gln Gln Leu Glu Pro Phe Leu Lys Arg Phe
1 5 10 15

Leu Ala Ser Leu Asp Leu Leu Tyr Thr Gln Pro Thr Ser Gln Pro Phe
20 25 30

Pro Asn Val Glu Ser Tyr Ala Thr Gln Leu Gly Ser Asn Leu Lys Arg
35 40 45

Ser Ser Ala Ile Ile Val Asn Gly Gln Pro Ile Ile Pro Ser Pro Gln
50 55 60

Glu Asp Cys Lys Leu Gln Phe Gln Lys Lys Trp Leu Gln Thr Pro Leu
65 70 75 80

Ser Ser His Gln Leu Thr Ser Tyr Asp Gly His Leu Ile Pro Gly Thr
85 90 95

Gly Thr Phe Val Val His Phe Ser Ala Lys Val Arg Phe Asp Gln Ser
100 105 110

Gly Arg Asn Arg Leu Gly Glu Ser Ala Asp Leu Phe Gln Glu Asn Asn
115 120 125

Ser Ile Val Ser Lys Thr Asn Gln Arg Pro Ile Trp Gly Ser Trp Phe
130 135 140

Gly Val Asp Val Asn Leu Val Val Asp Glu Asn Val Met Gln Asp Gly
145 150 155 160

Glu Ile Ile Asn Ser Met Asp Tyr Arg Phe Thr Tyr Val Pro Asn Asp
165 170 175

Ser Ile Ile Lys Val
180

<210> 17
<211> 244
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 90

<400> 17

Met Asn Ala Leu Tyr Asn His Ala Val Lys Gln Lys Asn Gln Leu Gln
1 5 10 15

Gln Glu Leu Ala Arg Phe Glu Lys Asn Ser Val Thr Ala Pro Ile Ser
20 25 30

Leu Gln Gly Ser Ile Ser Ala Thr Leu Val Ser Leu Glu Lys Thr Val
35 40 45

Lys Gln Tyr Ala Glu His Leu Asn Arg Tyr Lys Glu Asp Thr Asn Ala
50 55 60

Glu Glu Ile Asp Pro Lys Phe Ala Asn Arg Leu Ala Thr Leu Thr Gln
65 70 75 80

Asp Leu His Asp Phe Thr Ala Lys Phe Lys Asp Leu Lys Gln Ser Tyr
85 90 95

Asn Glu Asn Asn Ser Arg Thr Gln Leu Phe Gly Ser Gly Ala Ser His
100 105 110

Val Met Asp Ser Asp Asn Pro Phe Ser Thr Ser Glu Thr Ile Met Asn
115 120 125

Lys Arg Asn Val Gly Gly Ala Ser Ala Asn Gly Lys Glu Gly Ser Ser
130 135 140

Asn Gly Gly Gly Leu Pro Leu Tyr Gln Gly Leu Gln Lys Glu Gln Ser
145 150 155 160

Val Phe Glu Arg Gly Asn Ala Gln Leu Asp Tyr Ile Leu Glu Met Gly
165 170 175

Gln Gln Ser Phe Glu Asn Ile Val Glu Gln Asn Lys Ile Leu Ser Lys
180 185 190

Val Gln Asp Arg Met Ser Asn Gly Leu Arg Thr Leu Gly Val Ser Glu
195 200 205

Gln Thr Ile Thr Ser Ile Asn Lys Arg Val Phe Lys Asp Lys Leu Val
210 215 220

Phe Trp Ile Ala Leu Ile Leu Leu Ile Ile Gly Ile Tyr Tyr Val Leu
225 230 235 240

Lys Trp Leu Arg

<210> 18
<211> 238
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 91

<400> 18

Met Asn Ser Ile Tyr Asn His Gly Leu Lys Gln Thr Gln Thr Ile Thr
1 5 10 15

Lys Asp Leu Thr Gln Phe Glu Lys Asn Leu Ser Thr Ser Pro Leu Ser
20 25 30

Leu Gln Gly Ala Ile Thr Thr Ser Leu Thr Ala Phe Arg Lys Thr Ile

35 40 45

Lys Glu Tyr Ser Asp Leu Leu Glu Lys Asn Val Asn Asp Thr Ser Tyr
50 55 60

Thr Lys His Glu Asn Arg Leu Asn Lys Phe Asn Gln Asp Leu Asn Glu
65 70 75 80

Phe Thr Leu Lys Phe Asp Thr Leu Lys Lys Gln Arg Asp Ile Gln Val
85 90 95

Gln Glu Ala Asn Lys Gln Glu Leu Leu Gly Arg Arg His Ile Ser Thr
100 105 110

Thr Ala Thr Ala Ala Leu Gly Ser Thr Ser Ser Asp Asn Pro Tyr Glu
115 120 125

Ser Ser Ser Asn Pro Ser Gln Gln Gln Gln Gln Gln Leu Gln Asp Glu
130 135 140

Gln Asn Thr Met Ser Tyr Arg Glu Gly Leu Tyr His Glu Lys Asn Ser
145 150 155 160

Leu Glu Arg Gly Ser Glu Gln Leu Asp Arg Ile Leu Glu Met Gly Gln
165 170 175

Gln Ala Phe Glu Asp Ile Val Glu Gln Asn Glu Ile Leu Arg Lys Val
180 185 190

Gln Thr Lys Phe Glu Glu Ser Leu Ile Thr Leu Gly Val Ser Gln Gly
195 200 205

Thr Ile Arg Ser Val Glu Arg Arg Ala Lys Gln Asp Lys Trp Leu Phe
210 215 220

Trp Phe Cys Val Val Val Met Leu Val Val Phe Tyr Tyr Ile
225 230 235

<210> 19
<211> 261
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: NP_003560

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 92

<400> 19

Met Ser Tyr Thr Pro Gly Val Gly Gly Asp Pro Thr Gln Leu Ala Gln
1 5 10 15

Arg Ile Ser Ser Asn Ile Gln Lys Ile Thr Gln Cys Ser Val Glu Ile
20 25 30

Gln Arg Thr Leu Asn Gln Leu Gly Thr Pro Gln Asp Ser Pro Glu Leu
35 40 45

Arg Gln Gln Leu Gln Gln Lys Gln Gln Tyr Thr Asn Gln Leu Ala Lys
50 55 60

Glu Thr Asp Lys Tyr Ile Lys Glu Phe Gly Ser Leu Pro Thr Thr Pro
65 70 75 80

Ser Glu Gln Arg Gln Arg Lys Ile Gln Lys Asp Arg Leu Val Ala Glu
85 90 95

Phe Thr Thr Ser Leu Thr Asn Phe Gln Lys Val Gln Arg Gln Ala Ala
100 105 110

Glu Arg Glu Lys Glu Phe Val Ala Arg Val Arg Ala Ser Ser Arg Val
115 120 125

Ser Gly Ser Phe Pro Glu Asp Ser Ser Lys Glu Arg Asn Leu Val Ser
130 135 140

Trp Glu Ser Gln Thr Gln Pro Gln Val Gln Val Gln Asp Glu Glu Ile
145 150 155 160

Thr Glu Asp Asp Leu Arg Leu Ile His Glu Arg Glu Ser Ser Ile Arg
165 170 175

Gln Leu Glu Ala Asp Ile Met Asp Ile Asn Glu Ile Phe Lys Asp Leu
180 185 190

Gly Met Met Ile His Glu Gln Gly Asp Val Ile Asp Ser Ile Glu Ala
195 200 205

Asn Val Glu Asn Ala Glu Val His Val Gln Gln Ala Asn Gln Gln Leu
210 215 220

Ser Arg Ala Ala Asp Tyr Gln Arg Lys Ser Arg Lys Thr Leu Cys Ile
225 230 235 240

Ile Ile Leu Ile Leu Val Ile Gly Val Ala Ile Ile Ser Leu Ile Ile
245 250 255

Trp Gly Leu Asn His
260

<210> 20
<211> 258
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 93

<300>
<301> Bauer and Burgers
<302> Molecular cloning, structure and expression of the yeast proliferating cell nuclear

antigen gene.
<303> Nucleic Acids Research
<304> 18
<305> 2
<306> 261-265
<307> 1990
<308> X16676
<309> 1993-09-30

<400> 20

Met Leu Glu Ala Lys Phe Glu Glu Ala Ser Leu Phe Lys Arg Ile Ile
1 5 10 15

Asp Gly Phe Lys Asp Cys Val Gln Leu Val Asn Phe Gln Cys Lys Glu
20 25 30

Asp Gly Ile Ile Ala Gln Ala Val Asp Asp Ser Arg Val Leu Leu Val
35 40 45

Ser Leu Glu Ile Gly Val Glu Ala Phe Gln Glu Tyr Arg Cys Asp His
50 55 60

Pro Val Thr Leu Gly Met Asp Leu Thr Ser Leu Ser Lys Ile Leu Arg
65 70 75 80

Cys Gly Asn Asn Thr Asp Thr Leu Thr Leu Ile Ala Asp Asn Thr Pro
85 90 95

Asp Ser Ile Ile Leu Leu Phe Glu Asp Thr Lys Lys Asp Arg Ile Ala
100 105 110

Glu Tyr Ser Leu Lys Leu Met Asp Ile Asp Ala Asp Phe Leu Lys Ile
115 120 125

Glu Glu Leu Gln Tyr Asp Ser Thr Leu Ser Leu Pro Ser Ser Glu Phe
130 135 140

Ser Lys Ile Val Arg Asp Leu Ser Gln Leu Ser Asp Ser Ile Asn Ile
145 150 155 160

Met Ile Thr Lys Glu Thr Ile Lys Phe Val Ala Asp Gly Asp Ile Gly
165 170 175

Ser Gly Ser Val Ile Ile Lys Pro Phe Val Asp Met Glu His Pro Glu
180 185 190

Thr Ser Ile Lys Leu Glu Met Asp Gln Pro Val Asp Leu Thr Phe Gly
195 200 205

Ala Lys Tyr Leu Leu Asp Ile Ile Lys Gly Ser Ser Leu Ser Asp Arg
210 215 220

Val Gly Ile Arg Leu Ser Ser Glu Ala Pro Ala Leu Phe Gln Phe Asp
225 230 235 240

Leu Lys Ser Gly Phe Leu Gln Phe Phe Leu Ala Pro Lys Phe Asn Asp
245 250 255

Glu Glu

<210> 21
<211> 259
<212> PRT
<213> Canidia albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 94

<400> 21

Met Leu Glu Gly Lys Phe Glu Glu Ala Ala Leu Leu Lys Lys Val Val
1 5 10 15

Glu Ala Ile Lys Asp Cys Val Lys Lys Cys Asn Phe Asn Cys Ser Glu
20 25 30

His Gly Ile Thr Val Gln Ala Val Asp Asp Ser Arg Val Leu Leu Val
35 40 45

Ser Leu Leu Ile Gly Gln Thr Ser Phe Ser Glu Arg Cys Asp Arg Asp
50 55 60

Val Thr Leu Gly Ile Asp Leu Glu Ser Phe Ser Lys Ile Ile Lys Ser
65 70 75 80

Ala Asn Asn Glu Asp Phe Leu Thr Leu Leu Ala Glu Asp Ser Pro Asp
85 90 95

Gln Ile Met Ala Ile Leu Glu Glu Lys Gln Lys Glu Lys Ile Ser Glu
100 105 110

Tyr Ser Leu Lys Leu Met Asp Ile Asp Ser Glu Phe Leu Gln Ile Asp
115 120 125

Asp Met Glu Tyr Asp Ala Val Val Asn Met Pro Ser Ser Asp Phe Ala
130 135 140

Lys Leu Val Arg Asp Leu Lys Asn Leu Ser Glu Ser Leu Arg Val Val
145 150 155 160

Val Thr Lys Asp Ser Val Lys Phe Thr Ser Glu Gly Asp Ser Gly Ser
165 170 175

Gly Ser Val Ile Leu Lys Pro Tyr Thr Asn Leu Lys Asn Glu Arg Glu
180 185 190

Ser Val Thr Ile Ser Leu Asp Asp Pro Val Asp Leu Thr Phe Gly Leu
195 200 205

Lys Tyr Leu Asn Asp Ile Val Lys Ala Ala Thr Leu Ser Asp Val Ile
210 215 220

Thr Ile Lys Leu Ala Asp Lys Thr Pro Ala Leu Phe Glu Phe Lys Met

225 230 235 240

Gln Ser Gly Gly Tyr Leu Arg Phe Tyr Leu Ala Pro Lys Phe Asp Asp
245 250 255

Asp Glu Tyr

<210> 22
<211> 261
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 95

<300>
<301> Almendral, Huebsch, Blundell, MacDonald-Bravo, and Bravo
<302> Cloning and sequence of the human nuclear protein cyclin: Homology with DNA-binding proteins
<303> Proc. Natl. Acad. Sci. U.S.A.
<304> 84
<305> 6
<306> 1575-1579
<307> 1987
<308> m15796
<309> 1993-04-27

<400> 22

Met Phe Glu Ala Arg Leu Val Gln Gly Ser Ile Leu Lys Lys Val Leu
1 5 10 15

Glu Ala Leu Lys Asp Leu Ile Asn Glu Ala Cys Trp Asp Ile Ser Ser
20 25 30

Ser Gly Val Asn Leu Gln Ser Met Asp Ser Ser His Val Ser Leu Val
35 40 45

Gln Leu Thr Leu Arg Ser Glu Gly Phe Asp Thr Tyr Arg Cys Asp Arg
50 55 60

Asn Leu Ala Met Gly Val Asn Leu Thr Ser Met Ser Lys Ile Leu Lys
65 70 75 80

Cys Ala Gly Asn Glu Asp Ile Ile Thr Leu Arg Ala Glu Asp Asn Ala
85 90 95

Asp Thr Leu Ala Leu Val Phe Glu Ala Pro Asn Gln Glu Lys Val Ser
100 105 110

Asp Tyr Glu Met Lys Leu Met Asp Leu Asp Val Glu Gln Leu Gly Ile
115 120 125

Pro Glu Gln Glu Tyr Ser Cys Val Val Lys Met Pro Ser Gly Glu Phe
130 135 140

Ala Arg Ile Cys Arg Asp Leu Ser His Ile Gly Asp Ala Val Val Ile
145 150 155 160

Ser Cys Ala Lys Asp Gly Val Lys Phe Ser Ala Ser Gly Glu Leu Gly
165 170 175

Asn Gly Asn Ile Lys Leu Ser Gln Thr Ser Asn Val Asp Lys Glu Glu
180 185 190

Glu Ala Val Thr Ile Glu Met Asn Glu Pro Val Gln Leu Thr Phe Ala
195 200 205

Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala Thr Pro Leu Ser Ser Thr
210 215 220

Val Thr Leu Ser Met Ser Ala Asp Val Pro Leu Val Val Glu Tyr Lys
225 230 235 240

Ile Ala Asp Met Gly His Leu Lys Tyr Tyr Leu Ala Pro Lys Ile Glu
245 250 255

Asp Glu Glu Gly Ser
260

<210> 23
<211> 511
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 96

<400> 23

Met Ser Lys Arg Ser Ile Glu Val Asn Glu Glu Gln Asp Arg Val Val
1 5 10 15

Ser Ala Lys Thr Glu Ser His Ser Val Pro Ala Ile Pro Ala Ser Glu
20 25 30

Glu Gln Asp Ala Pro Lys Asn Asp Leu Glu Glu Gln Leu Ser Asp Glu
35 40 45

Phe Asp Ser Asp Gly Glu Ile Ile Glu Ile Asp Gly Asp Asp Glu Ile
50 55 60

Asn Asp Glu Asp Asp Leu Arg Lys Lys Gln Glu Glu Ala Glu Thr Leu
65 70 75 80

Val Gln Lys Asp Gln Ser Glu Gly Asn Lys Glu Lys Ile Gln Glu Leu
85 90 95

Tyr Leu Pro His Met Ser Arg Pro Leu Gly Pro Asp Glu Val Leu Glu
100 105 110

Ala Asp Pro Thr Val Tyr Glu Met Leu His Asn Val Asn Met Pro Trp
115 120 125

Pro Cys Leu Thr Leu Asp Val Ile Pro Asp Thr Leu Gly Ser Glu Arg

130 135 140

Arg Asn Tyr Pro Gln Ser Ile Leu Leu Thr Thr Ala Thr Gln Ser Ser
145 150 155 160

Arg Lys Lys Glu Asn Glu Leu Met Val Leu Ala Leu Ser Asn Leu Ala
165 170 175

Lys Thr Leu Leu Lys Asp Asp Asn Glu Gly Glu Asp Asp Glu Glu Asp
180 185 190

Asp Glu Asp Asp Val Asp Pro Val Ile Glu Asn Glu Asn Ile Pro Leu
195 200 205

Arg Asp Thr Thr Asn Arg Leu Lys Val Ser Pro Phe Ala Ile Ser Asn
210 215 220

Gln Glu Val Leu Thr Ala Thr Met Ser Glu Asn Gly Asp Val Tyr Ile
225 230 235 240

Tyr Asn Leu Ala Pro Gln Ser Lys Ala Phe Ser Thr Pro Gly Tyr Gln
245 250 255

Ile Pro Lys Ser Ala Lys Arg Pro Ile His Thr Val Lys Asn His Gly
260 265 270

Asn Val Glu Gly Tyr Gly Leu Asp Trp Ser Pro Leu Ile Lys Thr Gly
275 280 285

Ala Leu Leu Ser Gly Asp Cys Ser Gly Gln Ile Tyr Phe Thr Gln Arg
290 295 300

His Thr Ser Arg Trp Val Thr Asp Lys Gln Pro Phe Thr Val Ser Asn
305 310 315 320

Asn Lys Ser Ile Glu Asp Ile Gln Trp Ser Arg Thr Glu Ser Thr Val
325 330 335

Phe Ala Thr Ala Gly Cys Asp Gly Tyr Ile Arg Ile Trp Asp Thr Arg
340 345 350

Ser Lys Lys His Lys Pro Ala Ile Ser Val Lys Ala Ser Asn Thr Asp
355 360 365

Val Asn Val Ile Ser Trp Ser Asp Lys Ile Gly Tyr Leu Leu Ala Ser
370 375 380

Gly Asp Asp Asn Gly Thr Trp Gly Val Trp Asp Leu Arg Gln Phe Thr
385 390 395 400

Pro Ser Asn Ala Asp Ala Val Gln Pro Val Ala Gln Tyr Asp Phe His
405 410 415

Lys Gly Ala Ile Thr Ser Ile Ala Phe Asn Pro Leu Asp Glu Ser Ile
420 425 430

Val Ala Val Gly Ser Glu Asp Asn Thr Val Thr Leu Trp Asp Leu Ser
435 440 445

Val Glu Ala Asp Asp Glu Glu Ile Lys Gln Gln Ala Ala Glu Thr Lys
450 455 460

Glu Leu Gln Glu Ile Pro Pro Gln Leu Leu Phe Val His Trp Gln Lys
465 470 475 480

Glu Val Lys Asp Val Lys Trp His Lys Gln Ile Pro Gly Cys Leu Val
485 490 495

Ser Thr Gly Thr Asp Gly Leu Asn Val Trp Lys Thr Ile Ser Val
500 505 510

<210> 24
<211> 420
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 97

<400> 24

Met Ser Lys Arg Ser Ala Glu Asp Asp Leu Ser Gly Asn Gly Ser Thr
1 5 10 15

Ser His Thr Ala Val Lys Thr Asn Lys Asp Ser Leu Pro Thr Thr Thr
20 25 30

Asn Gly Lys Glu Glu Glu Pro Asp Asn Met Asp Ile Gly Glu Phe Glu
35 40 45

Asp Pro Tyr Gly Asp Glu Phe Glu Ser Asp Glu Ile Ile Glu Leu Asp
50 55 60

Asp Asn Asn Asp Glu Glu Asp Asp Glu Met Ile Asp Glu Asn Ser Thr
65 70 75 80

Gln Ala Lys Ile Glu Glu Leu Glu Ala Lys Glu Gln Glu Gln Glu Gln
85 90 95

Gln Ser Ser Ile Tyr Leu Pro His Lys Ser Lys Pro Leu Gly Pro Asp
100 105 110

Glu Val Leu Glu Ala Asp Pro Thr Val Tyr Glu Met Leu His Asn Ile
115 120 125

Asn Leu Pro Trp Pro Cys Leu Thr Val Asp Ile Leu Pro Asp Ser Leu
130 135 140

Gly Asn Glu Arg Arg Ser Tyr Pro Ala Thr Val Tyr Leu Ala Thr Ala
145 150 155 160

Thr Gln Ala Ala Lys Ala Lys Asp Asn Glu Leu Leu Ala Met Lys Ala
165 170 175

Ser Ser Leu Ala Lys Thr Leu Val Lys Asp Glu Asn Glu Glu Asp Glu
180 185 190

Glu Asp Glu Asp Asp Asp Asp Asp Val Asp Ser Asp Pro Ile Leu Asp
195 200 205

Ser Glu Ser Ile Pro Leu Arg His Thr Thr Asn Arg Ile Arg Val Ser
210 215 220

Pro His Ala Gln Gln Thr Gly Glu Tyr Leu Thr Ala Ser Met Ser Glu
225 230 235 240

Asn Gly Glu Val Tyr Ile Phe Asp Leu Leu Ala Gln Tyr Lys Ala Phe
245 250 255

Asp Thr Pro Gly Tyr Met Ile Pro Lys Ser Ser Lys Arg Pro Ile His
260 265 270

Thr Ile Arg Ala His Gly Asn Val Glu Gly Tyr Gly Leu Asp Trp Ser
275 280 285

Pro Leu Val Asn Thr Gly Ala Leu Leu Ser Gly Asp Met Ser Gly Arg
290 295 300

Ile Tyr Leu Thr Asn Arg Thr Thr Ser Ser Trp Thr Thr Asp Lys Thr
305 310 315 320

Pro Phe Phe Ala Ser Gln Ser Ser Ile Glu Asp Ile Gln Trp Ser Thr
325 330 335

Gly Glu Thr Thr Val Phe Ala Thr Gly Gly Cys Asp Gly Tyr Ile Cys
340 345 350

Ile Trp Asp Thr Arg Ser Lys Lys His Lys Pro Ala Leu Ser Val Ile
355 360 365

Ala Ser Lys Ser Asp Val Asn Val Ile Ser Trp Ser Ser Lys Ile Asn
370 375 380

His Leu Leu Ala Ser Gly His Asp Asp Gly Ser Trp Gly Val Trp Asp
385 390 395 400

Leu Arg Asn Phe Thr Asn Asn Thr Thr Ser Asn Pro Ser Pro Val Ala
405 410 415

Asn Tyr Asp Phe
420

<210> 25
<211> 425
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: NP_005601

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 98

<400> 25

Met Ala Asp Lys Glu Ala Ala Phe Asp Asp Ala Val Glu Glu Arg Val
1 5 10 15

Ile Asn Glu Glu Tyr Lys Ile Trp Lys Lys Asn Thr Pro Phe Leu Tyr
20 25 30

Asp Leu Val Met Thr His Ala Leu Glu Trp Pro Ser Leu Thr Ala Gln
35 40 45

Trp Leu Pro Asp Val Thr Arg Pro Glu Gly Lys Asp Phe Ser Ile His
50 55 60

Arg Leu Val Leu Gly Thr His Thr Ser Asp Glu Gln Asn His Leu Val
65 70 75 80

Ile Ala Ser Val Gln Leu Pro Asn Asp Asp Ala Gln Phe Asp Ala Ser
85 90 95

His Tyr Asp Ser Glu Lys Gly Glu Phe Gly Gly Phe Gly Ser Val Ser
100 105 110

Gly Lys Ile Glu Ile Glu Ile Lys Ile Asn His Glu Gly Glu Val Asn
115 120 125

Arg Ala Arg Tyr Met Pro Gln Asn Pro Cys Ile Ile Ala Thr Lys Thr
130 135 140

Pro Ser Ser Asp Val Leu Val Phe Asp Tyr Thr Lys His Pro Ser Lys
145 150 155 160

Pro Asp Pro Ser Gly Glu Cys Asn Pro Asp Leu Arg Leu Arg Gly His
165 170 175

Gln Lys Glu Gly Tyr Gly Leu Ser Trp Asn Pro Asn Leu Ser Gly His
180 185 190

Leu Leu Ser Ala Ser Asp Asp His Thr Ile Cys Leu Trp Asp Ile Ser
195 200 205

Ala Val Pro Lys Glu Gly Lys Val Val Asp Ala Lys Thr Ile Phe Thr
210 215 220

Gly His Thr Ala Val Val Glu Asp Val Ser Trp His Leu Leu His Glu
225 230 235 240

Ser Leu Phe Gly Ser Val Ala Asp Asp Gln Lys Leu Met Ile Trp Asp
245 250 255

Thr Arg Ser Asn Asn Thr Ser Lys Pro Ser His Ser Val Asp Ala His

260 265 270

Thr Ala Glu Val Asn Cys Leu Ser Phe Asn Pro Tyr Ser Glu Phe Ile
275 280 285

Leu Ala Thr Gly Ser Ala Asp Lys Thr Val Ala Leu Trp Asp Leu Arg
290 295 300

Asn Leu Lys Leu Lys Leu His Ser Phe Glu Ser His Lys Asp Glu Ile
305 310 315 320

Phe Gln Val Gln Trp Ser Pro His Asn Glu Thr Ile Leu Ala Ser Ser
325 330 335

Gly Thr Asp Arg Arg Leu Asn Val Trp Asp Leu Ser Lys Ile Gly Glu
340 345 350

Glu Gln Ser Pro Glu Asp Ala Glu Asp Gly Pro Pro Glu Leu Leu Phe
355 360 365

Ile His Gly Gly His Thr Ala Lys Ile Ser Asp Phe Ser Trp Asn Pro
370 375 380

Asn Glu Pro Trp Val Ile Cys Ser Val Ser Glu Asp Asn Ile Met Gln
385 390 395 400

Val Trp Gln Met Ala Glu Asn Ile Tyr Asn Asp Glu Asp Pro Glu Gly
405 410 415

Ser Val Asp Pro Glu Gly Gln Gly Ser
420 425

<210> 26
<211> 431
<212> PRT
<213> Saccharomyces cerevisiae

<220>

<221> misc_feature
<223> Corresponds to SEQ ID NO: 99

<400> 26

Met Glu Pro Gln Glu Glu Phe Ile Thr Thr Glu Glu Val Glu Gln Glu
1 5 10 15

Ile Val Pro Thr Val Glu Val Glu Gln Asp Val Pro Val Asp Ile Glu
20 25 30

Gly Glu Asn Asp Asp Asp Asp Glu Met Met Asn Asp Asp Glu Glu Ala
35 40 45

Leu Glu Val Asp Met Ser Asn Asn Ser Leu Thr Tyr Phe Asp Lys His
50 55 60

Thr Asp Ser Val Phe Ala Ile Gly His His Pro Asn Leu Pro Leu Val
65 70 75 80

Cys Thr Gly Gly Gly Asp Asn Leu Ala His Leu Trp Thr Ser His Ser
85 90 95

Gln Pro Pro Lys Phe Ala Gly Thr Leu Thr Gly Tyr Gly Glu Ser Val
100 105 110

Ile Ser Cys Ser Phe Thr Ser Glu Gly Gly Phe Leu Val Thr Ala Asp
115 120 125

Met Ser Gly Lys Val Leu Val His Met Gly Gln Lys Gly Gly Ala Gln
130 135 140

Trp Lys Leu Ala Ser Gln Met Gln Glu Val Glu Glu Ile Val Trp Leu
145 150 155 160

Lys Thr His Pro Thr Ile Ala Arg Thr Phe Ala Phe Gly Ala Thr Asp
165 170 175

Gly Ser Val Trp Cys Tyr Gln Ile Asn Glu Gln Asp Gly Ser Leu Glu
180 185 190

Gln Leu Met Ser Gly Phe Val His Gln Gln Asp Cys Ser Met Gly Glu
195 200 205

Phe Ile Asn Thr Asp Lys Gly Glu Asn Thr Leu Glu Leu Val Thr Cys
210 215 220

Ser Leu Asp Ser Thr Ile Val Ala Trp Asn Cys Phe Thr Gly Gln Gln
225 230 235 240

Leu Phe Lys Ile Thr Gln Ala Glu Ile Lys Gly Leu Glu Ala Pro Trp
245 250 255

Ile Ser Leu Ser Leu Ala Pro Glu Thr Leu Thr Lys Gly Asn Ser Gly
260 265 270

Val Val Ala Cys Gly Ser Asn Asn Gly Leu Leu Ala Val Ile Asn Cys
275 280 285

Asn Asn Gly Gly Ala Ile Leu His Leu Ser Thr Val Ile Glu Leu Lys
290 295 300

Pro Glu Gln Asp Glu Leu Asp Ala Ser Ile Glu Ser Ile Ser Trp Ser
305 310 315 320

Ser Lys Phe Ser Leu Met Ala Ile Gly Leu Val Cys Gly Glu Ile Leu
325 330 335

Leu Tyr Asp Thr Ser Ala Trp Arg Val Arg His Lys Phe Val Leu Glu
340 345 350

Asp Ser Val Thr Lys Leu Met Phe Asp Asn Asp Asp Leu Phe Ala Ser
355 360 365

Cys Ile Asn Gly Lys Val Tyr Gln Phe Asn Ala Arg Thr Gly Gln Glu

370 375 380

Lys Phe Val Cys Val Gly His Asn Met Gly Val Leu Asp Phe Ile Leu
385 390 395 400

Leu His Pro Val Ala Asn Thr Gly Thr Glu Gln Lys Arg Lys Val Ile
405 410 415

Thr Ala Gly Asp Glu Gly Val Ser Leu Val Phe Glu Val Pro Asn
420 425 430

<210> 27
<211> 417
<212> PRT
<213> Candida albicans

<220>
<221> MISC_FEATURE
<222> (326)..(326)
<223> X can be any amino acid

<220>
<221> MISC_FEATURE
<222> (367)..(367)
<223> X can be any amino acid

<220>
<221> MISC_FEATURE
<222> (378)..(378)
<223> X can be any amino acid

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 100

<400> 27

Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr
1 5 10 15

Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala
20 25 30

Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu
35 40 45

Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys
50 55 60

His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met
65 70 75 80

Val Leu Thr Glu Gly Gly Asp Asn Thr Ala Tyr Leu Trp Thr Thr His
85 90 95

Thr Gln Pro Pro Arg Phe Val Gly Glu Ile Thr Gly His Lys Glu Ser
100 105 110

Val Ile Ser Gly Gly Phe Thr Ala Asp Gly Lys Phe Val Val Thr Ala
115 120 125

Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu
130 135 140

Gln Trp Val Lys Phe Gly Glu Leu Asp Glu Val Glu Glu Val Leu Phe
145 150 155 160

Val Thr Val His Pro Thr Leu Pro Phe Phe Ala Phe Gly Ala Thr Asp
165 170 175

Gly Ser Ile Trp Val Tyr Gln Ile Asp Glu Ser Ser Lys Leu Leu Val
180 185 190

Gln Ile Met Ser Gly Phe Ser His Thr Leu Lys Cys Asn Gly Ala Val
195 200 205

Phe Ile Gln Gly Lys Asp Glu Asn Asp Leu Thr Leu Val Ser Ile Ser

210 215 220

Glu Asp Gly Thr Val Val Asn Trp Asn Cys Phe Thr Gly Gln Val Asn
225 230 235 240

Tyr Lys Leu Gln Pro His Asp Asp Phe Lys Gly Val Glu Ser Pro Trp
245 250 255

Val Thr Val Lys Val His Gly Asn Leu Val Ala Ile Gly Gly Arg Asp
260 265 270

Gly Gln Leu Ser Ile Val Asn Asn Asp Thr Gly Lys Ile Val His Thr
275 280 285

Leu Lys Thr Leu Asp Asn Val Asp Asp Ile Ala Glu Leu Ser Ile Glu
290 295 300

Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly
305 310 315 320

Leu Val Ser Gly Asp Xaa Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu
325 330 335

Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val
340 345 350

Gly Glu Thr Pro Ile Leu Val Gly Asn Ser Met Asp Gly Lys Xaa Tyr
355 360 365

Lys Trp Glu Pro Arg Thr Gly Glu Lys Xaa Phe Ala Gly Val Gly Thr
370 375 380

Asn Met Gly Ser Tyr Gly Leu Cys Tyr Phe Lys Ile Glu Val Lys Asn
385 390 395 400

Trp Leu Leu Leu Val Asp Glu Arg Cys Phe His Trp Ser Leu Phe Met
405 410 415

Lys

<210> 28
<211> 611
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: NP_001078

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 101

<400> 28

Met Asp Ser Gly Arg Arg Leu Gly Pro Glu Lys Trp Ile Arg Arg Leu
1 5 10 15

Arg Arg Met Glu Ser Glu Ser Glu Ser Gly Ala Ala Ala Asp Thr Pro
20 25 30

Pro Leu Glu Thr Leu Ser Phe His Gly Asp Glu Glu Ile Ile Glu Val
35 40 45

Val Glu Leu Asp Pro Gly Pro Pro Asp Pro Asp Asp Leu Ala Gln Glu
50 55 60

Met Glu Asp Val Asp Phe Glu Glu Glu Glu Glu Glu Glu Gly Asn Glu
65 70 75 80

Glu Gly Trp Val Leu Glu Pro Gln Glu Gly Val Val Gly Ser Met Glu
85 90 95

Gly Pro Asp Asp Ser Glu Val Thr Phe Ala Leu His Ser Ala Ser Val
100 105 110

Phe Cys Val Ser Leu Asp Pro Lys Thr Asn Thr Leu Ala Val Thr Gly
115 120 125

Gly Glu Asp Asp Lys Ala Phe Val Trp Arg Leu Ser Asp Gly Glu Leu
130 135 140

Leu Phe Glu Cys Ala Gly His Lys Asp Ser Val Thr Cys Ala Gly Phe
145 150 155 160

Ser His Asp Ser Thr Leu Val Ala Thr Gly Asp Met Ser Gly Leu Leu
165 170 175

Lys Val Trp Gln Val Asp Thr Lys Glu Glu Val Trp Ser Phe Glu Ala
180 185 190

Gly Asp Leu Glu Trp Met Glu Trp His Pro Arg Ala Pro Val Leu Leu
195 200 205

Ala Gly Thr Ala Asp Gly Asn Thr Trp Met Trp Lys Val Pro Asn Gly
210 215 220

Asp Cys Lys Thr Phe Gln Gly Pro Asn Cys Pro Ala Thr Cys Gly Arg
225 230 235 240

Val Leu Pro Asp Gly Lys Arg Ala Val Val Gly Tyr Glu Asp Gly Thr
245 250 255

Ile Arg Ile Trp Asp Leu Lys Gln Gly Ser Pro Ile His Val Leu Lys
260 265 270

Gly Thr Glu Gly His Gln Gly Pro Leu Thr Cys Val Ala Ala Asn Gln
275 280 285

Asp Gly Ser Leu Ile Leu Thr Gly Ser Val Asp Cys Gln Ala Lys Leu
290 295 300

Val Ser Ala Thr Thr Gly Lys Val Val Gly Val Phe Arg Pro Glu Thr

305 310 315 320

Val Ala Ser Gln Pro Ser Leu Gly Glu Gly Glu Glu Ser Glu Ser Asn
325 330 335

Ser Val Glu Ser Leu Gly Phe Cys Ser Val Met Pro Leu Ala Ala Val
340 345 350

Gly Tyr Leu Asp Gly Thr Leu Ala Ile Tyr Asp Leu Ala Thr Gln Thr
355 360 365

Leu Arg His Gln Cys Gln His Gln Ser Gly Ile Val Gln Leu Leu Trp
370 375 380

Glu Ala Gly Thr Ala Val Val Tyr Thr Cys Ser Leu Asp Gly Ile Val
385 390 395 400

Arg Leu Trp Asp Ala Arg Thr Gly Arg Leu Leu Thr Asp Tyr Arg Gly
405 410 415

His Thr Ala Glu Ile Leu Asp Phe Ala Leu Ser Lys Asp Ala Ser Leu
420 425 430

Val Val Thr Thr Ser Gly Asp His Lys Ala Lys Val Phe Cys Val Gln
435 440 445

Arg Pro Asp Arg Asp Phe Ser Pro Asp Gly Ala Leu Leu Ala Thr Ala
450 455 460

Ser Tyr Asp Thr Arg Val Tyr Ile Trp Asp Pro His Asn Gly Asp Ile
465 470 475 480

Leu Met Glu Phe Gly His Leu Phe Pro Pro Pro Thr Pro Ile Phe Ala
485 490 495

Gly Gly Ala Asn Asp Arg Trp Val Arg Ser Val Ser Phe Ser His Asp
500 505 510

Gly Leu His Val Ala Ser Leu Ala Asp Asp Lys Met Val Arg Phe Trp
515 520 525

Arg Ile Asp Glu Asp Tyr Pro Val Gln Val Ala Pro Leu Ser Asn Gly
530 535 540

Leu Cys Cys Ala Phe Ser Thr Asp Gly Ser Val Leu Ala Ala Gly Thr
545 550 555 560

His Asp Gly Ser Val Tyr Phe Trp Ala Thr Pro Arg Gln Val Pro Ser
565 570 575

Leu Gln His Leu Cys Arg Met Ser Ile Arg Arg Val Met Pro Thr Gln
580 585 590

Glu Val Gln Glu Leu Pro Ile Pro Ser Lys Leu Leu Glu Phe Leu Ser
595 600 605

Tyr Arg Ile
610

<210> 29
<211> 240
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 102

<400> 29

Met Ser Ala Pro Thr Met Arg Ser Thr Ser Ile Leu Thr Glu His Leu
1 5 10 15

Gly Tyr Pro Pro Ile Ser Leu Val Asp Asp Ile Ile Asn Ala Val Asn
20 25 30

Glu Ile Met Tyr Lys Cys Thr Ala Ala Met Glu Lys Tyr Leu Leu Ser
35 40 45

Lys Ser Lys Ile Gly Glu Glu Asp Tyr Gly Glu Glu Ile Lys Ser Gly
50 55 60

Val Ala Lys Leu Glu Ser Leu Leu Glu Asn Ser Val Asp Lys Asn Phe
65 70 75 80

Asp Lys Leu Glu Leu Tyr Val Leu Arg Asn Val Leu Arg Ile Pro Glu
85 90 95

Glu Tyr Leu Asp Ala Asn Val Phe Arg Leu Glu Asn Gln Lys Asp Leu
100 105 110

Val Ile Val Asp Glu Asn Glu Leu Lys Lys Ser Glu Glu Lys Leu Arg
115 120 125

Glu Lys Val Asn Asp Val Glu Leu Ala Phe Lys Lys Asn Glu Met Leu
130 135 140

Leu Lys Arg Val Thr Lys Val Lys Arg Leu Leu Phe Thr Ile Arg Gly
145 150 155 160

Phe Lys Gln Lys Leu Asn Glu Leu Leu Lys Cys Lys Asp Asp Val Gln
165 170 175

Leu Gln Lys Ile Leu Glu Ser Leu Lys Pro Ile Asp Asp Thr Met Thr
180 185 190

Leu Leu Thr Asp Ser Leu Arg Lys Leu Tyr Val Asp Ser Glu Ser Thr
195 200 205

Ser Ser Thr Glu Glu Val Glu Ala Leu Leu Gln Arg Leu Lys Thr Asn
210 215 220

Gly Lys Gln Asn Asn Lys Asp Phe Arg Thr Arg Tyr Ile Asp Ile Arg

225 230 235 240

<210> 30
<211> 314
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 103

<400> 30

Met Ser Asp Lys Thr Leu Asp Glu Arg Thr Thr Ala Ile Leu Thr Glu
1 5 10 15

His Leu Glu Phe Ala Pro Leu Thr Leu Ile Asp Asp Val Ile Asn Ala
20 25 30

Val Asn Glu Ile Met Tyr Lys Gly Thr Thr Ala Ile Glu Thr Tyr Leu
35 40 45

Lys Glu Gln Lys Gln Leu Met Lys Asn Gly Ile Thr Lys Val Thr Glu
50 55 60

Asp Glu Ile Glu Ile Gly Met Gly Lys Leu Glu Ser Leu Leu Glu Ser
65 70 75 80

Thr Ile Asp Lys Asn Phe Asp Lys Phe Glu Leu Tyr Cys Leu Arg Asn
85 90 95

Ile Phe Asn Ile Pro Lys Asp Leu Ile Pro Tyr Ile Gln Leu Ser His
100 105 110

Gln Gln Gly Ile Glu Phe Lys Ser Asp Asn Val Glu Gln Lys Arg Glu
115 120 125

Phe Asp Gln Gln Ile Lys Asn Leu Gln Leu Lys Ile Met Gln Glu Leu
130 135 140

Gln Leu Arg Lys Ile Leu Lys Leu Gln Leu Val Lys Val Gln Lys Leu
145 150 155 160

Ile Lys Val Leu Ile Ala Ile Asp Asn Asp Phe Lys Lys Ile Asp Phe
165 170 175

Ala Ser Gly Gly Gly Gly Asn Glu Glu Ser Ile Arg Ile Leu Lys Asn
180 185 190

Leu Gln Pro Ile Asp Glu Thr Leu Tyr Phe Leu Ile Ser Gln Ile Lys
195 200 205

Asn Leu Ile Asn Gln Ile Glu Gln Leu Ser Asn Lys Val Asn Thr Asn
210 215 220

Leu Lys Thr Gln Lys Phe Ile Pro Asn Leu Arg Asp Lys Phe Ile Asp
225 230 235 240

Gly Arg Thr Phe Arg Val Leu Gln Gln Thr Gly Ile Trp Lys Asp Leu
245 250 255

Glu Lys Asn Asp Ile Lys Ile Leu Val Gln Gly Asn Asp Asn Asn Asn
260 265 270

Asn Asn Asn Asn Asn Asn Asn Asn Thr Leu Thr Asp Leu Gln Asn Gln
275 280 285

Asp Asp Ile Asp Met Ile Ile Pro Glu Gln Asp Asp Ile Asp Val Asp
290 295 300

Ala Ile Lys Asn Ile Asn Ala Gln Ile Phe
305 310

<210> 31
<211> 600
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 104

<400> 31

Met Ser His Ser Gly Ala Ala Ile Phe Glu Lys Val Ser Gly Ile Ile
1 5 10 15

Ala Ile Asn Glu Asp Val Ser Pro Ala Glu Leu Thr Trp Arg Ser Thr
20 25 30

Asp Gly Asp Lys Val His Thr Val Val Leu Ser Thr Ile Asp Lys Leu
35 40 45

Gln Ala Thr Pro Ala Ser Ser Glu Lys Met Met Leu Arg Leu Ile Gly
50 55 60

Lys Val Asp Glu Ser Lys Lys Arg Lys Asp Asn Glu Gly Asn Glu Val
65 70 75 80

Val Pro Lys Pro Gln Arg His Met Phe Ser Phe Asn Asn Arg Thr Val
85 90 95

Met Asp Asn Ile Lys Met Thr Leu Gln Gln Ile Ile Ser Arg Tyr Lys
100 105 110

Asp Ala Asp Ile Tyr Glu Glu Lys Arg Arg Arg Glu Glu Ser Ala Gln
115 120 125

His Thr Glu Thr Pro Met Ser Ser Ser Ser Val Thr Ala Gly Thr Pro
130 135 140

Thr Pro His Leu Asp Thr Pro Gln Leu Asn Asn Gly Ala Pro Leu Ile
145 150 155 160

Asn Thr Ala Lys Leu Asp Asp Ser Leu Ser Lys Glu Lys Leu Leu Thr
165 170 175

Asn Leu Lys Leu Gln Gln Ser Leu Leu Lys Gly Asn Lys Val Leu Met
180 185 190

Lys Val Phe Gln Glu Thr Val Ile Asn Ala Gly Leu Pro Pro Ser Glu
195 200 205

Phe Trp Ser Thr Arg Ile Pro Leu Leu Arg Ala Phe Ala Leu Ser Thr
210 215 220

Ser Gln Lys Val Gly Pro Tyr Asn Val Leu Ser Thr Ile Lys Pro Val
225 230 235 240

Ala Ser Ser Glu Asn Lys Val Asn Val Asn Leu Ser Arg Glu Lys Ile
245 250 255

Leu Asn Ile Phe Glu Asn Tyr Pro Ile Val Lys Lys Ala Tyr Thr Asp
260 265 270

Asn Val Pro Lys Asn Phe Lys Glu Pro Glu Phe Trp Ala Arg Phe Phe
275 280 285

Ser Ser Lys Leu Phe Arg Lys Leu Arg Gly Glu Lys Ile Met Gln Asn
290 295 300

Asp Arg Gly Asp Val Ile Ile Asp Arg Tyr Leu Thr Leu Asp Gln Glu
305 310 315 320

Phe Asp Arg Lys Asp Asp Asp Met Leu Leu His Pro Val Lys Lys Ile
325 330 335

Ile Asp Leu Asp Gly Asn Ile Gln Asp Asp Pro Val Val Arg Gly Asn
340 345 350

Arg Pro Asp Phe Thr Met Gln Pro Gly Val Asp Ile Asn Gly Asn Ser
355 360 365

Asp Gly Thr Val Asp Ile Leu Lys Gly Met Asn Arg Leu Ser Glu Lys
370 375 380

Met Ile Met Ala Leu Lys Asn Glu Tyr Ser Arg Thr Asn Leu Gln Asn
385 390 395 400

Lys Ser Asn Ile Thr Asn Asp Glu Glu Asp Glu Asp Asn Asp Glu Arg
405 410 415

Asn Glu Leu Lys Ile Asp Asp Leu Asn Glu Ser Tyr Lys Thr Asn Tyr
420 425 430

Ala Ile Ile His Leu Lys Arg Asn Ala His Glu Lys Thr Thr Asp Asn
435 440 445

Asp Ala Lys Ser Ser Ala Asp Ser Ile Lys Asn Ala Asp Leu Lys Val
450 455 460

Ser Asn Gln Gln Met Leu Gln Gln Leu Ser Leu Val Met Asp Asn Leu
465 470 475 480

Ile Asn Lys Leu Asp Leu Asn Gln Val Val Pro Asn Asn Glu Val Ser
485 490 495

Asn Lys Ile Asn Lys Arg Val Ile Thr Ala Ile Lys Ile Asn Ala Lys
500 505 510

Gln Ala Lys His Asn Asn Val Asn Ser Ala Leu Gly Ser Phe Val Asp
515 520 525

Asn Thr Ser Gln Ala Asn Glu Leu Glu Val Lys Ser Thr Leu Pro Ile
530 535 540

Asp Leu Leu Glu Ser Cys Arg Met Leu His Thr Thr Cys Cys Glu Phe
545 550 555 560

Leu Lys His Phe Tyr Ile His Phe Gln Ser Gly Glu Gln Lys Gln Ala

565 570 575

Ser Thr Val Lys Lys Leu Tyr Asn His Leu Lys Asp Cys Ile Glu Lys
580 585 590

Leu Asn Glu Leu Phe Gln Asp Val
595 600

<210> 32
<211> 670
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 105

<400> 32

Met Asp Ile Ile Arg Gly Ala Cys Ser Val Asp Lys Ile Gly Gly Met
1 5 10 15

Val Tyr Ile Arg Glu Asp Leu Ala Pro Leu Met Leu Glu Trp Lys Pro
20 25 30

Ile Asp Glu Gln Glu Glu Asp Arg Ala Ile Ser Ile Pro Leu Asn Ser
35 40 45

Leu Thr Thr Leu Gln Ser Thr Lys Glu Thr Ser Pro Lys Met Ile Leu
50 55 60

Lys Ile Val Tyr Lys Leu Thr Ser Gly Pro Pro Asn Thr Asn Ala Asp
65 70 75 80

Gly Thr Asp Asn Gly Gly Gly Gly Gly Gly Glu Gln Lys Ser Phe Lys
85 90 95

Leu Thr Phe Thr Asn Arg Pro Thr Met Asn Thr Ile Lys Asp Ser Leu
100 105 110

Gln Thr Ile Val Ala Arg Ser Arg Thr Lys Gly Gly Leu Lys Val Pro
115 120 125

Val Leu Gln Leu Gln Leu Gln His Gln Leu Gln His Leu Gly Ser Ala
130 135 140

Pro Gln Ala Asp Ser Thr Arg Asp Ser Thr Ser Ser Ser Thr Pro Ile
145 150 155 160

Pro Pro Thr Thr Ser Gly Thr Ser Thr Ser Ser Ser Leu Leu Ser Leu
165 170 175

Ala Ala Ser Gln Ser Leu Ser Asp Ala Asn Leu Leu Lys Asn Phe Glu
180 185 190

Leu Gln Gln Lys Leu Leu Leu Glu Asp Arg Gln Leu Arg Asp Val Phe
195 200 205

Thr Lys Ser Val Met Gln Phe Lys Leu Ser Pro Gln Val Phe Trp Ser
210 215 220

Ser Arg Leu Asn Gln Leu Arg Thr Phe Ala Leu Thr Ile Ser Gln His
225 230 235 240

Lys Gly Pro Tyr Asn Val Leu Ser Thr Ile Lys Pro Val Ala Thr Ser
245 250 255

Asp Asn Gln Val Asn Val Asn Val Thr Arg Asp Thr Ile Asn Glu Ile
260 265 270

Phe Thr Ile Tyr Pro Ile Ile Lys Lys Ala Phe Asp Asp Leu Val Pro
275 280 285

Asn Lys Phe Asn Glu Gly Glu Phe Trp Ser Arg Phe Phe Asn Ser Lys
290 295 300

Leu Phe Arg Arg Leu Arg Gly Asp Lys Ile Ser Ile Ser Asn Ser Arg
305 310 315 320

Gly Asp Val Val Leu Asp Lys Tyr Leu Tyr Ile Asp Gln Asn Tyr Gln
325 330 335

Glu Lys Leu Gln Lys Ser Ser Thr Leu Glu Asn Asn Gly Ser Gly Gly
340 345 350

Gly Gly Gly Gly Ala Gly Gly Gly Ser Gly Asn Ser Glu Gln Gly Ile
355 360 365

Gln Thr Leu Glu Ser Pro His Val Lys Lys Phe Leu Asp Leu Met Gly
370 375 380

Asn Gln Gln Asp Asn Ser Gln Lys Leu Gly Asn Arg Pro Asp Phe Thr
385 390 395 400

Met Arg Tyr Asp Glu Asp Asn Val Asp Asp Asp Asn Lys Lys Pro Thr
405 410 415

Leu Gly Asn Glu Asn Glu Met Ile Ile Leu Met Lys Asn Met Asn Arg
420 425 430

Leu Ser Ser Lys Met Met Ser Met Ser Ser Thr Asn Gly Pro Glu Lys
435 440 445

Pro Ser Glu Thr Thr Ile Asp Gly Leu Ser Ala Ala Glu Leu Asn Glu
450 455 460

Tyr Glu Glu Glu Leu Asp Leu His Asp Leu Asn Asp Ser Glu Asn Leu
465 470 475 480

Gln Tyr Ile Lys Leu Asn Ile Asn Thr Asp Ile Ala Lys Gly Thr Lys
485 490 495

Leu Asp Ser Tyr Glu Gly Ser Asn Thr Asn Asn Lys Ile Ser Gln Asp

500 505 510

Glu Leu His Lys Tyr Leu Gln Ser Gln Thr Phe Gln Gly Gln Ile Glu
515 520 525

Leu Thr Glu Thr Tyr Thr Cys Lys Ser Glu Glu Ile Glu Lys Thr Ser
530 535 540

Met Glu Ile Ala Met Leu Ile Lys Gln Asn Phe Arg Thr Phe Lys Leu
545 550 555 560

Ile Asn Lys Glu Asn Asp Ile Ala Gly Thr Asn Ile Val Pro Asn Ser
565 570 575

Leu Ile Gln Glu Ile Ile Thr Tyr Asn Ile Thr Ile Val Glu Phe Leu
580 585 590

Ser His Phe Trp Lys Ile Phe Leu His Gly Asn Asn Pro Gly Gln Leu
595 600 605

Lys Lys Ile Phe Thr Ser Leu Lys Asn Cys Gln Ser Gly Leu Ile Glu
610 615 620

Leu Glu Asn Lys Ala Ile Asp Gln Phe Lys Ser Met Asp Ile Leu Gln
625 630 635 640

Lys Asn Gln Lys Leu Gln Asp Lys Val Leu Lys Asp Phe Ala Ser Cys
645 650 655

Leu Gln Pro Met Lys Ile Ala Leu Asp Lys Ala Cys Asn Glu
660 665 670

<210> 33
<211> 498
<212> PRT
<213> Homo sapiens

<220>

<221> misc_feature
<223> human genbank accession #: W19128

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 106

<400> 33

Met Ala Thr Ser Ser Glu Glu Val Leu Leu Ile Val Lys Lys Val Arg
1 5 10 15

Gln Lys Lys Gln Asp Gly Ala Leu Tyr Leu Met Ala Glu Arg Ile Ala
20 25 30

Trp Ala Pro Glu Gly Lys Asp Arg Phe Thr Ile Ser His Met Tyr Ala
35 40 45

Asp Ile Lys Cys Gln Lys Ile Ser Pro Glu Gly Lys Ala Lys Ile Gln
50 55 60

Leu Gln Leu Val Leu His Ala Gly Asp Thr Thr Asn Phe His Phe Ser
65 70 75 80

Asn Glu Ser Thr Ala Val Lys Glu Arg Asp Ala Val Lys Asp Leu Leu
85 90 95

Gln Gln Leu Leu Pro Phe Lys Arg Ala Asn Lys Glu Leu Glu Lys Asn
100 105 110

Arg Cys Cys Lys Ile Leu Phe Cys Phe Ser Phe Ile Lys Leu Arg Thr
115 120 125

Gly Glu Glu Gln Met Leu Glu Asp Pro Val Leu Phe Gln Leu Tyr Lys
130 135 140

Asp Val Ser Gln Val Ile Ser Ala Glu Glu Phe Trp Asn Arg Leu Asn
145 150 155 160

Val Asn Ala Thr Asp Ser Ser Thr Ser Asn His Lys Gln Asp Val Gly
165 170 175

Ile Ser Ala Ala Phe Leu Ala Asp Val Arg Pro Gln Thr Asp Gly Cys
180 185 190

Asn Gly Leu Arg Tyr Asn Leu Thr Ser Asp Ile Ile Glu Ser Ile Phe
195 200 205

Arg Thr Tyr Pro Ala Val Lys Met Lys Tyr Ala Glu Asn Val Pro His
210 215 220

Asn Met Thr Glu Lys Glu Phe Trp Thr Arg Phe Phe Gln Ser His Tyr
225 230 235 240

Phe His Arg Asp Arg Leu Asn Thr Gly Ser Lys Asp Leu Phe Ala Glu
245 250 255

Cys Ala Lys Ile Asp Glu Lys Gly Leu Lys Thr Met Val Ser Leu Gly
260 265 270

Val Lys Asn Pro Leu Leu Asp Leu Thr Ala Leu Glu Asp Lys Pro Leu
275 280 285

Asp Glu Gly Tyr Gly Ile Ser Ser Val Pro Ser Ser Asn Ser Lys Ser
290 295 300

Ile Lys Glu Asn Ser Asn Ala Ala Ile Ile Lys Arg Phe Asn His His
305 310 315 320

Ser Ala Met Val Leu Ala Ala Gly Leu Arg Lys Gln Glu Ala Gln Asn
325 330 335

Glu Gln Thr Ser Glu Pro Ser Asn Met Asp Gly Asn Ser Gly Asp Ala
340 345 350

Asp Cys Phe Gln Pro Ala Val Lys Arg Ala Lys Leu Gln Glu Ser Ile
355 360 365

Glu Tyr Glu Asp Leu Gly Lys Asn Asn Ser Val Lys Thr Ile Ala Leu
370 375 380

Asn Leu Lys Lys Ser Asp Arg Tyr Tyr His Gly Pro Thr Pro Ile Gln
385 390 395 400

Ser Leu Gln Tyr Ala Thr Ser Gln Asp Ile Ile Asn Ser Phe Gln Ser
405 410 415

Ile Arg Gln Glu Met Glu Ala Tyr Thr Pro Lys Leu Thr Gln Val Leu
420 425 430

Ser Ser Ser Ala Ala Ser Ser Thr Ile Thr Ala Leu Ser Pro Gly Gly
435 440 445

Ala Leu Met Gln Gly Gly Thr Gln Gln Ala Ile Asn Gln Met Val Pro
450 455 460

Asn Asp Ile Gln Thr Asn Leu Val Ser His Ile Glu Glu Met Leu Gln
465 470 475 480

Thr Ala Tyr Asn Lys Leu His Thr Trp Gln Ser Arg Arg Leu Met Lys
485 490 495

Lys Thr

<210> 34
<211> 846
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 107

<400> 34

Met Glu Leu Glu Pro Thr Leu Phe Gly Ile Ile Glu Ala Leu Ala Pro
1 5 10 15

Gln Leu Leu Ser Gln Ser His Leu Gln Thr Phe Val Ser Asp Val Val
20 25 30

Asn Leu Leu Arg Ser Ser Thr Lys Ser Ala Thr Gln Leu Gly Pro Leu
35 40 45

Ile Asp Phe Tyr Lys Leu Gln Ser Leu Asp Ser Pro Glu Thr Thr Ile
50 55 60

Met Trp His Lys Ile Glu Lys Phe Leu Asp Ala Leu Phe Gly Ile Gln
65 70 75 80

Asn Thr Asp Asp Met Val Lys Tyr Leu Ser Val Phe Gln Ser Leu Leu
85 90 95

Pro Ser Asn Tyr Arg Ala Lys Ile Val Gln Lys Ser Ser Gly Leu Asn
100 105 110

Met Glu Asn Leu Ala Asn His Glu His Leu Leu Ser Pro Val Arg Ala
115 120 125

Pro Ser Ile Tyr Thr Glu Ala Ser Phe Glu Asn Met Asp Arg Phe Ser
130 135 140

Glu Arg Arg Ser Met Val Ser Ser Pro Asn Arg Tyr Val Pro Ser Ser
145 150 155 160

Thr Tyr Ser Ser Val Thr Leu Arg Gln Leu Ser Asn Pro Tyr Tyr Val
165 170 175

Asn Thr Ile Pro Glu Glu Asp Ile Leu Lys Tyr Val Ser Tyr Thr Leu
180 185 190

Leu Ala Thr Thr Ser Ala Leu Phe Pro Phe Asp His Glu Gln Ile Gln
195 200 205

Ile Pro Ser Lys Ile Pro Asn Phe Glu Ser Gly Leu Leu His Leu Ile
210 215 220

Phe Glu Ala Gly Leu Leu Tyr Gln Ser Leu Gly Tyr Lys Val Glu Lys
225 230 235 240

Phe Arg Met Leu Asn Ile Ser Pro Met Lys Lys Ala Leu Ile Ile Glu
245 250 255

Ile Ser Glu Glu Leu Gln Asn Tyr Thr Ala Phe Val Asn Asn Leu Val
260 265 270

Ser Ser Gly Thr Val Val Ser Leu Lys Ser Leu Tyr Arg Glu Ile Tyr
275 280 285

Glu Asn Ile Ile Arg Leu Arg Ile Tyr Cys Arg Phe Thr Glu His Leu
290 295 300

Glu Glu Leu Ser Gly Asp Thr Phe Leu Ile Glu Leu Asn Ile Phe Lys
305 310 315 320

Ser His Gly Asp Leu Thr Ile Arg Lys Ile Ala Thr Asn Leu Phe Asn
325 330 335

Ser Met Ile Ser Leu Tyr Tyr Glu Tyr Leu Met Asn Trp Leu Thr Lys
340 345 350

Gly Leu Leu Arg Ala Thr Tyr Gly Glu Phe Phe Ile Ala Glu Asn Thr
355 360 365

Asp Thr Asn Gly Thr Asp Asp Asp Phe Ile Tyr His Ile Pro Ile Glu
370 375 380

Phe Asn Gln Glu Arg Val Pro Ala Phe Ile Pro Lys Glu Leu Ala Tyr

385 390 395 400

Lys Ile Phe Met Ile Gly Lys Ser Tyr Ile Phe Leu Glu Lys Tyr Cys
405 410 415

Lys Glu Val Gln Trp Thr Asn Glu Phe Ser Lys Lys Tyr His Val Leu
420 425 430

Tyr Gln Ser Asn Ser Tyr Arg Gly Ile Ser Thr Asn Phe Phe Glu Ile
435 440 445

Ile Asn Asp Gln Tyr Ser Glu Ile Val Asn His Thr Asn Gln Ile Leu
450 455 460

Asn Gln Lys Phe His Tyr Arg Asp Val Val Phe Ala Leu Lys Asn Ile
465 470 475 480

Leu Leu Met Gly Lys Ser Asp Phe Met Asp Ala Leu Ile Glu Lys Ala
485 490 495

Asn Asp Ile Leu Ala Thr Pro Ser Asp Ser Leu Pro Asn Tyr Lys Leu
500 505 510

Thr Arg Val Leu Gln Glu Ala Val Gln Leu Ser Ser Leu Arg His Leu
515 520 525

Met Asn Ser Pro Arg Asn Ser Ser Val Ile Asn Gly Leu Asp Ala Arg
530 535 540

Val Leu Asp Leu Gly His Gly Ser Val Gly Trp Asp Val Phe Thr Leu
545 550 555 560

Asp Tyr Ile Leu Tyr Pro Pro Leu Ser Leu Val Leu Asn Val Asn Arg
565 570 575

Pro Phe Gly Arg Lys Glu Tyr Leu Arg Ile Phe Asn Phe Leu Trp Arg
580 585 590

Phe Lys Lys Asn Asn Tyr Phe Tyr Gln Lys Glu Met Leu Lys Ser Asn
595 600 605

Asp Ile Ile Arg Ser Phe Lys Lys Ile Arg Gly Tyr Asn Pro Leu Ile
610 615 620

Arg Asp Ile Ile Asn Lys Leu Ser Arg Ile Ser Ile Leu Arg Thr Gln
625 630 635 640

Phe Gln Gln Phe Asn Ser Lys Met Glu Ser Tyr Tyr Leu Asn Cys Ile
645 650 655

Ile Glu Glu Asn Phe Lys Glu Met Thr Arg Lys Leu Gln Arg Thr Glu
660 665 670

Asn Lys Ser Gln Asn Gln Phe Asp Leu Ile Arg Leu Asn Asn Gly Thr
675 680 685

Ile Glu Leu Asn Gly Ile Leu Thr Pro Lys Ala Glu Val Leu Thr Lys
690 695 700

Ser Ser Ser Ser Lys Pro Gln Lys His Ala Ile Glu Lys Thr Leu Asn
705 710 715 720

Ile Asp Glu Leu Glu Ser Val His Asn Thr Phe Leu Thr Asn Ile Leu
725 730 735

Ser His Lys Leu Phe Ala Thr Asn Thr Ser Glu Ile Ser Val Gly Asp
740 745 750

Tyr Ser Gly Gln Pro Tyr Pro Thr Ser Leu Val Leu Leu Leu Asn Ser
755 760 765

Val Tyr Glu Phe Val Lys Val Tyr Cys Asn Leu Asn Asp Ile Gly Tyr
770 775 780

Glu Ile Phe Ile Lys Met Asn Leu Asn Asp His Glu Ala Ser Asn Gly
785 790 795 800

Leu Leu Gly Lys Phe Asn Thr Asn Leu Lys Glu Ile Val Ser Gln Tyr
805 810 815

Lys Asn Phe Lys Asp Arg Leu Tyr Ile Phe Arg Ala Asp Leu Lys Asn
820 825 830

Asp Gly Asp Glu Glu Leu Phe Leu Leu Ser Lys Ser Leu Arg
835 840 845

<210> 35
<211> 712
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 108

<400> 35

Met Ala Leu Asn Lys Val Gln Leu Ile Lys Leu Tyr Ser Asn Arg Leu
1 5 10 15

Val Lys Ser Leu Val Pro Val Glu Phe Gly Glu Ala Phe Ile Gln Ser
20 25 30

Ile Ile Asn Asp Leu Gln Thr Thr Leu Leu Asn Thr Ser Ser Glu Glu
35 40 45

Gln Asn Leu Ser Ile Ile Ile Asn Lys Leu Lys Met Gln Phe Leu Ser
50 55 60

Asn Asn Leu Lys Asn Glu Trp Val Glu Phe Gln Asn Ile Val Asn Ser
65 70 75 80

Leu Ser Lys Phe Lys Ser Leu Asp Gln Ile Cys Asn Tyr Leu Ala Phe

85 90 95

Leu Asp Ala Leu Arg Asp Glu Lys Pro Glu Asp Ile Leu Ser Thr Ser
100 105 110

Thr Ala Ser Leu Ser Pro Gly Lys Gln Asn Val Met Ile Asn Thr Val
115 120 125

Asn Thr Ala Leu Thr Leu Ser Gln Leu Ile Glu Pro Tyr Tyr Asp Thr
130 135 140

Leu Ser Glu Gln Thr Ile Leu Thr Tyr Leu Pro Tyr Thr Met Leu Gly
145 150 155 160

Leu Asp Ser Lys Ile Phe Thr Phe Ser Asn Asn Tyr Thr Arg Leu Glu
165 170 175

Ile Pro Lys Asp Ile Asn Asn Ser Phe Ser Ser Leu Leu Arg Glu Val
180 185 190

Phe Glu Phe Ala Ile Leu Tyr Lys Gln Leu Ala Ile Val Val Asp Arg
195 200 205

Tyr Lys Gly Thr Leu Val Leu Ala Ile Lys Thr Ala Tyr Ile Ala Ile
210 215 220

Leu Glu Ala Gln Leu Asn Lys Tyr Val Asn Asp Ile Asn Asn Ile Phe
225 230 235 240

Asn Asn Lys Pro Asn Ser Ile Leu Val Val Tyr Asn Ser Ile Phe Pro
245 250 255

Trp Ile Ser Ile Leu Arg Phe Leu Tyr Arg Val Ser Asn Arg Leu Asn
260 265 270

Arg Leu Asp Gly Tyr Glu Phe Leu Thr Phe Ile Tyr Ser Phe Thr Asn
275 280 285

His Gly Asp Pro Lys Ile Arg Gly Ile Ala Val Thr Ala Phe Thr Glu
290 295 300

Val Val Lys Pro Tyr Tyr Asn Ile Val Glu His Trp Ile Val Lys Gly
305 310 315 320

Glu Leu Ile Asp Asn Asn Asn Glu Phe Phe Ile Ile Phe Asp Gln Glu
325 330 335

Gln Asn Glu Phe Asn Ser Ile Ile Lys Leu Leu Pro Lys Lys Ile Pro
340 345 350

Ala Phe Ile Lys Ser Ser Asp Lys Ile Phe Gln Ile Gly Thr Thr Leu
355 360 365

Ile Phe Leu Asn Lys Tyr Cys Arg Glu Leu Lys Trp Val Asn Gln Tyr
370 375 380

Asn Val Lys Tyr Ser Ala Ile Leu Phe Asn Asn His Gln Gly Leu Ala
385 390 395 400

Ser Met Thr Thr Asn Glu Met Ile Lys Leu Ile Asp Leu Gln Tyr Asn
405 410 415

Glu Ile Leu Thr Phe Leu Thr Gln Ile Ile Gln Gly Asn Asn Lys Leu
420 425 430

Leu Thr His Val Tyr Asn Ile Lys Arg Tyr Tyr Phe Met Glu Thr Asn
435 440 445

Asp Phe Ile Asp Ala Ile Met Val Lys Gly Lys Asp Val Phe Asn Glu
450 455 460

Ser Ser Val Asn Ile Ser Ser Thr Tyr Leu Arg Lys Val Leu Gln Asp
465 470 475 480

Ala Ile Gln Ile Ser Ser Val Lys Asn Phe Glu Tyr Val Asp Arg Leu
485 490 495

Asp Ser Arg Val Leu Asn Pro Gln His Gly Asn Leu Gly Trp Glu Ser
500 505 510

Phe Thr Ile Glu Tyr Lys Ile Asp Asp Leu Pro Met Ser Tyr Leu Phe
515 520 525

Glu Gly His Gln His Leu Gln Tyr Leu Lys Met Phe His Phe Leu Trp
530 535 540

Lys Leu Arg Gln Leu Asn Asn Leu Leu Asn Trp His Phe Glu Met Phe
545 550 555 560

Asn Glu Leu Asn His Asn Val Val Thr Lys Leu Ser Ser Arg Asn Arg
565 570 575

Arg Pro Leu Ala Lys Ser Leu Ser Ile Ile Thr Ser Ile Arg Phe His
580 585 590

Phe Thr Gln Phe Leu Asn Glu Leu Ile Ala Tyr Leu Ser Tyr Asp Val
595 600 605

Ile Glu Glu Asn Phe Gln Gln His Ile Val Arg Lys Leu Phe Tyr Asn
610 615 620

Lys Asn Asp Gln Asp Leu Leu Leu Asn Lys Leu Phe Met Asn Leu Leu
625 630 635 640

Glu Ile Asp Pro Asn Asn Asp Leu Pro Lys Phe Asn Val Asn Leu Leu
645 650 655

Thr Ile Asp Glu Leu Val Glu Leu His Gly Thr Tyr Ile Asp Ser Ile
660 665 670

Ile Asn Ser Ser Leu Leu Asn Glu Lys Leu Lys Gly Asn Glu Thr Asn

675 680 685

Ile Ser Tyr Ile Asp Gln Ile Phe Asp Ile Leu Gln Thr Ile Phe Asn
690 695 700

Phe Ile Ile Gln Val Arg Asn Ser
705 710

<210> 36
<211> 880
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: AAC39727

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 109

<400> 36

Met Ala Thr Pro Asp Gln Lys Ser Pro Asn Val Leu Leu Gln Asn Leu
1 5 10 15

Cys Cys Arg Ile Leu Gly Arg Ser Glu Ala Asp Val Ala Gln Gln Phe
20 25 30

Gln Tyr Ala Val Arg Val Ile Gly Ser Asn Phe Ala Pro Thr Val Glu
35 40 45

Arg Asp Glu Phe Leu Val Ala Glu Lys Ile Lys Lys Glu Leu Ile Arg
50 55 60

Gln Arg Arg Glu Ala Asp Ala Ala Leu Phe Ser Glu Leu His Arg Lys
65 70 75 80

Leu His Ser Gln Gly Val Leu Lys Asn Lys Trp Ser Ile Leu Tyr Leu

85 90 95

Leu Leu Ser Leu Ser Glu Asp Pro Arg Arg Gln Pro Ser Lys Val Ser
100 105 110

Ser Tyr Ala Thr Leu Phe Ala Gln Ala Leu Pro Arg Asp Ala His Ser
115 120 125

Thr Pro Tyr Tyr Tyr Ala Arg Pro Gln Thr Leu Pro Leu Ser Tyr Gln
130 135 140

Asp Arg Ser Ala Gln Ser Ala Gln Ser Ser Gly Ser Val Gly Ser Ser
145 150 155 160

Gly Ile Ser Ser Ile Gly Leu Cys Ala Leu Ser Gly Pro Ala Pro Ala
165 170 175

Pro Gln Ser Leu Leu Pro Gly Gln Ser Asn Gln Ala Pro Gly Val Gly
180 185 190

Asp Cys Leu Arg Gln Gln Leu Gly Ser Arg Leu Ala Trp Thr Leu Thr
195 200 205

Ala Asn Gln Pro Ser Ser Gln Ala Thr Thr Ser Lys Gly Val Pro Ser
210 215 220

Ala Val Ser Arg Asn Met Thr Arg Ser Arg Arg Glu Gly Asp Thr Gly
225 230 235 240

Gly Thr Met Glu Ile Thr Glu Ala Ala Leu Val Arg Asp Ile Leu Tyr
245 250 255

Val Phe Gln Gly Ile Asp Gly Lys Asn Ile Lys Met Asn Asn Thr Glu
260 265 270

Asn Cys Tyr Lys Val Glu Gly Lys Ala Asn Leu Ser Arg Ser Leu Arg
275 280 285

Asp Thr Ala Val Arg Leu Ser Glu Leu Gly Trp Leu His Asn Lys Ile
290 295 300

Arg Arg Tyr Thr Asp Gln Arg Ser Leu Asp Arg Ser Phe Gly Leu Val
305 310 315 320

Gly Gln Ser Phe Cys Ala Ala Leu His Gln Glu Leu Arg Glu Tyr Tyr
325 330 335

Arg Leu Leu Ser Val Leu His Ser Gln Leu Gln Leu Glu Asp Asp Gln
340 345 350

Gly Val Asn Leu Gly Leu Glu Ser Ser Leu Thr Leu Arg Arg Leu Leu
355 360 365

Val Trp Thr Tyr Asp Pro Lys Ile Arg Leu Lys Thr Leu Ala Ala Leu
370 375 380

Val Asp His Cys Gln Gly Arg Lys Gly Gly Glu Leu Ala Ser Ala Val
385 390 395 400

His Ala Tyr Thr Lys Thr Gly Asp Pro Tyr Met Arg Ser Leu Val Gln
405 410 415

His Ile Leu Ser Leu Val Ser His Pro Val Leu Ser Phe Leu Tyr Arg
420 425 430

Trp Ile Tyr Asp Gly Glu Leu Glu Asp Thr Tyr His Glu Phe Phe Val
435 440 445

Ala Ser Asp Pro Thr Val Lys Thr Asp Arg Leu Trp His Asp Lys Tyr
450 455 460

Thr Leu Arg Lys Ser Met Ile Pro Ser Phe Met Thr Met Asp Gln Ser
465 470 475 480

Arg Lys Val Leu Leu Ile Gly Lys Ser Ile Asn Phe Leu His Gln Val
485 490 495

Cys His Asp Gln Thr Pro Thr Thr Lys Met Ile Ala Val Thr Lys Ser
500 505 510

Ala Glu Ser Pro Gln Asp Ala Ala Asp Leu Phe Thr Asp Leu Glu Asn
515 520 525

Ala Phe Gln Gly Lys Ile Asp Ala Ala Tyr Phe Glu Thr Ser Lys Tyr
530 535 540

Leu Leu Asp Val Leu Asn Lys Lys Tyr Ser Leu Leu Asp His Met Gln
545 550 555 560

Ala Met Arg Arg Tyr Leu Leu Leu Gly Gln Gly Asp Phe Ile Arg His
565 570 575

Leu Met Asp Leu Leu Lys Pro Glu Leu Val Arg Pro Ala Thr Thr Leu
580 585 590

Tyr Gln His Asn Leu Thr Gly Ile Leu Glu Thr Ala Val Arg Ala Thr
595 600 605

Asn Ala Gln Phe Asp Ser Pro Glu Ile Leu Arg Arg Leu Asp Val Arg
610 615 620

Leu Leu Glu Val Ser Pro Gly Asp Thr Gly Trp Asp Val Phe Ser Leu
625 630 635 640

Asp Tyr His Val Asp Gly Pro Ile Ala Thr Val Phe Thr Arg Glu Cys
645 650 655

Met Ser His Tyr Leu Arg Val Phe Asn Phe Leu Trp Arg Ala Lys Arg
660 665 670

Met Glu Tyr Ile Leu Thr Asp Ile Arg Lys Gly His Met Cys Asn Ala

675 680 685

Lys Leu Leu Arg Asn Met Pro Glu Phe Ser Gly Val Leu His Gln Cys
690 695 700

His Ile Leu Ala Ser Glu Met Val His Phe Ile His Gln Met Gln Tyr
705 710 715 720

Tyr Ile Thr Phe Glu Val Leu Glu Cys Ser Trp Asp Glu Leu Trp Asn
725 730 735

Lys Val Gln Gln Ala Gln Asp Leu Asp His Ile Ile Ala Ala His Glu
740 745 750

Val Phe Leu Asp Thr Ile Ile Ser Arg Cys Leu Leu Asp Ser Asp Ser
755 760 765

Arg Ala Leu Leu Asn Gln Leu Arg Ala Val Phe Asp Gln Ile Ile Glu
770 775 780

Leu Gln Asn Ala Gln Asp Ala Ile Tyr Arg Ala Ala Leu Glu Glu Leu
785 790 795 800

Gln Arg Arg Leu Gln Phe Glu Glu Lys Lys Lys Gln Arg Glu Ile Glu
805 810 815

Gly Gln Trp Gly Val Thr Ala Ala Glu Glu Glu Glu Glu Asn Lys Arg
820 825 830

Ile Gly Glu Phe Lys Glu Ser Ile Pro Lys Met Cys Ser Gln Leu Arg
835 840 845

Ile Leu Thr His Phe Tyr Gln Gly Ile Val Gln Gln Phe Leu Val Leu
850 855 860

Leu Thr Thr Ser Ser Asp Glu Ser Leu Arg Phe Leu Ser Phe Arg Leu
865 870 875 880

<210> 37
<211> 534
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 110

<400> 37

Met Glu Lys Ser Leu Ala Asp Gln Ile Ser Asp Ile Ala Ile Lys Pro
1 5 10 15

Val Asn Lys Asp Phe Asp Ile Glu Asp Glu Glu Asn Ala Ser Leu Phe
20 25 30

Gln His Asn Glu Lys Asn Gly Glu Ser Asp Leu Ser Asp Tyr Gly Asn
35 40 45

Ser Asn Thr Glu Glu Thr Lys Lys Ala His Tyr Leu Glu Val Glu Lys
50 55 60

Ser Lys Leu Arg Ala Glu Lys Gly Leu Glu Leu Asn Asp Pro Lys Tyr
65 70 75 80

Thr Gly Val Lys Gly Ser Arg Gln Ala Leu Tyr Glu Glu Val Ser Glu
85 90 95

Asn Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Lys Glu Glu
100 105 110

Asp Ala Leu Ser Phe Arg Thr Asp Ser Glu Asp Glu Glu Val Glu Ile
115 120 125

Asp Glu Glu Glu Ser Asp Ala Asp Gly Gly Glu Thr Glu Glu Ala Gln
130 135 140

Gln Lys Arg His Ala Leu Ser Lys Leu Ile Gln Gln Glu Thr Lys Gln
145 150 155 160

Ala Ile Asn Lys Leu Ser Gln Ser Val Gln Arg Asp Ala Ser Lys Gly
165 170 175

Tyr Ser Ile Leu Gln Gln Thr Lys Leu Phe Asp Asn Ile Ile Asp Leu
180 185 190

Arg Ile Lys Leu Gln Lys Ala Val Ile Ala Ala Asn Lys Leu Pro Leu
195 200 205

Thr Thr Glu Ser Trp Glu Glu Ala Lys Met Asp Asp Ser Glu Glu Thr
210 215 220

Lys Arg Leu Leu Lys Glu Asn Glu Lys Leu Phe Asn Asn Leu Phe Asn
225 230 235 240

Arg Leu Ile Asn Phe Arg Ile Lys Phe Gln Leu Gly Asp His Ile Thr
245 250 255

Gln Asn Glu Glu Val Ala Lys His Lys Leu Ser Lys Lys Arg Ser Leu
260 265 270

Lys Glu Leu Tyr Gln Glu Thr Asn Ser Leu Asp Ser Glu Leu Lys Glu
275 280 285

Tyr Arg Thr Ala Val Leu Asn Lys Trp Ser Thr Lys Val Ser Ser Ala
290 295 300

Ser Gly Asn Ala Ala Leu Ser Ser Asn Lys Phe Lys Ala Ile Asn Leu
305 310 315 320

Pro Ala Asp Val Gln Val Glu Asn Gln Leu Ser Asp Met Ser Arg Leu
325 330 335

Met Lys Arg Thr Lys Leu Asn Arg Arg Asn Ile Thr Pro Leu Tyr Phe

340 345 350

Gln Lys Asp Cys Ala Asn Gly Arg Leu Pro Glu Leu Ile Ser Pro Val
355 360 365

Val Lys Asp Ser Val Asp Asp Asn Glu Asn Ser Asp Asp Gly Leu Asp
370 375 380

Ile Pro Lys Asn Tyr Asp Pro Arg Arg Lys Asp Asn Asn Ala Ile Asp
385 390 395 400

Ile Thr Glu Asn Pro Tyr Val Phe Asp Asp Glu Asp Phe Tyr Arg Val
405 410 415

Leu Asn Asp Leu Ile Asp Lys Lys Ile Ser Asn Ala His Asn Ser
420 425 430

Glu Ser Ala Ala Ile Thr Ile Thr Ser Thr Asn Ala Arg Ser Asn Asn
435 440 445

Lys Leu Lys Lys Asn Ile Asp Thr Lys Ala Ser Lys Gly Arg Lys Leu
450 455 460

Asn Tyr Ser Val Gln Asp Pro Ile Ala Asn Tyr Glu Ala Pro Ile Thr
465 470 475 480

Ser Gly Tyr Lys Trp Ser Asp Asp Gln Ile Asp Glu Phe Phe Ala Gly
485 490 495

Leu Leu Gly Gln Arg Val Asn Phe Asn Glu Asn Glu Asp Glu Glu Gln
500 505 510

His Ala Arg Ile Glu Asn Asp Glu Glu Leu Glu Ala Val Lys Asn Asp
515 520 525

Asp Ile Gln Ile Phe Gly
530

<210> 38
<211> 480
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 111

<400> 38

Met Ser Phe Phe Gly Leu His Phe Gln Leu Asn Ser Leu Thr Leu Asn
1 5 10 15

Ile Ser Asn Met Ala Lys Lys Ser Leu Ser Glu Gln Ile Ser Ser Leu
20 25 30

Tyr Thr Pro Lys Thr Asp Tyr Asp Ile Glu Asp His Asp Leu Asp Val
35 40 45

Ser Lys Asp Asn Gly Ile Phe Gln His His Asp Gly Gly Ser Glu Asn
50 55 60

Glu Ser Glu Asp Glu Asp Thr Gly Leu Arg Asn Glu His Tyr Val Glu
65 70 75 80

Ser Ser Lys Ser Lys Leu Arg Gln Gln Asn Glu Gly Val Asn Leu Gly
85 90 95

Glu Lys Tyr Val Gly Asn Val Thr Ser Arg Ser Lys Leu Tyr Asp Asp
100 105 110

Glu Asp Asp Lys Gln Pro Thr Glu Ala Ser Ser Gly Glu Glu Leu Asp
115 120 125

Ala Glu Ser Ala Glu Glu Glu Glu Asp Glu Glu Ser Glu Asp Val Ala
130 135 140

Asp Asp Asp Glu Asp Asp Gln Glu Ser Asp Arg Ser Ser Ser Ser Asp

145 150 155 160

Ala Glu Asn Asp Glu Asp Glu Asn Ile Ser His Lys Arg Glu Leu Leu
165 170 175

Lys Gln Leu Met Ser Lys Glu Arg Ser His Ile Val Asn Arg Leu Ser
180 185 190

Gln Ser Ala Thr Asn Asp Ala Leu Lys Gly Tyr Ser Ile Gln Gln Gln
195 200 205

Asn Lys Thr Phe Glu Lys Ile Ile Asp Val Arg Leu Lys Phe Gln Lys
210 215 220

Ser Val Thr Ser Ser Asn Met Leu Pro Ile Asn Thr Ser Thr Tyr Ser
225 230 235 240

Glu Thr Lys Ser Glu Asp Ser Asp Glu Leu Val Thr Lys Ala Lys Lys
245 250 255

Gln Leu Tyr Ser Leu Leu Asp His Leu Phe Thr Leu Arg Asn Glu Leu
260 265 270

Asp Glu Ser Thr Ser Val Lys Thr Pro Lys Lys Arg Ser Phe Ala Lys
275 280 285

Tyr Ser Glu Val Thr Ser Ala Ala Asp Ala Gln Leu Asn Ser Arg Arg
290 295 300

Asn Gln Ile Leu Thr Lys Trp Ser Ala Lys Val Ala Asn Ser Ser Gly
305 310 315 320

Arg Asn Ala Met Asn Ala Asn Lys Phe Lys Thr Ile Asn Gln Ser Phe
325 330 335

Glu Gln Gln Val Asn Asn Asn Leu Ser Asp Met Asp Arg Leu Ile Lys
340 345 350

Arg Thr Lys Leu Asn Arg Arg Asn Val Thr Pro Ile Gly Tyr Thr Thr
355 360 365

Lys Glu Glu Asp Asp His Glu Asn Gly Asn Lys Asn Lys Ser Ile Asp
370 375 380

Glu Asp Asp Asp Asp Ile Pro Glu Asp Thr Ser Val Arg Lys Lys Thr
385 390 395 400

Gln Gly Leu Glu Asn Asp Tyr Ile Phe Asp Asp Glu Asp Phe Tyr Arg
405 410 415

Val Leu Leu Asn Asp Leu Val Asp Lys Lys Val Gln Thr Ser Asp Pro
420 425 430

Thr Ser Gly Ile Thr Ile Ser Leu Arg Ala Ala Gln Lys Ser Asn Lys
435 440 445

Leu Lys Asn Asn Val Asp Thr Lys Ala Ser Lys Gly Arg Lys Leu Arg
450 455 460

Tyr His Val Gln Glu Pro Ile Ala Asn Phe Glu Thr Ser Arg Gly Ser
465 470 475 480

<210> 39
<211> 558
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: NM_000055

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 112

<400> 39

Met Gly Arg Pro Leu Ala Leu Gln Leu Glu Gln Leu Leu Asn Pro Arg
1 5 10 15

Pro Ser Glu Ala Asp Pro Glu Ala Asp Pro Glu Glu Ala Thr Ala Ala
20 25 30

Arg Val Ile Asp Arg Phe Asp Glu Gly Glu Asp Gly Glu Gly Asp Phe
35 40 45

Leu Val Val Gly Ser Ile Arg Lys Leu Ala Ser Ala Ser Leu Leu Asp
50 55 60

Thr Asp Lys Arg Tyr Cys Gly Lys Thr Thr Ser Arg Lys Ala Trp Asn
65 70 75 80

Glu Asp His Trp Glu Gln Thr Leu Pro Gly Ser Ser Asp Glu Glu Ile
85 90 95

Ser Asp Glu Glu Gly Ser Gly Asp Glu Asp Ser Glu Gly Leu Gly Leu
100 105 110

Glu Glu Tyr Asp Glu Asp Asp Leu Gly Ala Ala Glu Glu Gln Glu Cys
115 120 125

Gly Asp His Arg Glu Ser Lys Lys Thr Arg Ser His Ser Ala Lys Thr
130 135 140

Pro Gly Phe Ser Val Gln Ser Ile Ser Asp Phe Glu Lys Phe Thr Lys
145 150 155 160

Gly Met Asp Asp Leu Gly Ser Ser Glu Glu Glu Glu Asp Glu Glu Ser
165 170 175

Gly Met Glu Glu Gly Asp Asp Ala Glu Asp Ser Gln Gly Glu Ser Glu
180 185 190

Glu Asp Arg Ala Gly Asp Arg Asn Ser Glu Asp Asp Gly Val Val Met

195 200 205

Thr Phe Ser Ser Val Lys Val Ser Glu Glu Val Glu Lys Gly Arg Ala
210 215 220

Val Lys Asn Gln Ile Ala Leu Trp Asp Gln Leu Leu Glu Gly Arg Ile
225 230 235 240

Lys Leu Gln Lys Ala Leu Leu Thr Thr Asn Gln Leu Pro Gln Pro Asp
245 250 255

Val Phe Pro Val Phe Lys Asp Lys Gly Gly Pro Glu Phe Ala Ser Ala
260 265 270

Leu Lys Asn Ser His Lys Ala Leu Lys Ala Leu Leu Arg Ser Leu Val
275 280 285

Gly Leu Gln Glu Glu Leu Leu Phe Gln Tyr Pro Asp Thr Arg Tyr Val
290 295 300

Val Asp Gly Thr Lys Pro Asn Ala Gly Ser Glu Glu Ile Ser Ser Glu
305 310 315 320

Asp Asp Glu Leu Val Glu Glu Lys Lys Gln Gln Arg Arg Arg Val Pro
325 330 335

Ala Lys Arg Lys Leu Glu Met Glu Asp Tyr Pro Ser Phe Met Ala Lys
340 345 350

Ala Leu Pro Thr Leu Gln Ser Thr Gly Thr Thr Leu Gln Lys Trp His
355 360 365

Asp Lys Thr Lys Leu Ala Ser Gly Lys Leu Gly Lys Gly Phe Gly Ala
370 375 380

Phe Glu Arg Ser Ile Leu Thr Gln Ile Asp His Ile Leu Met Cys Lys
385 390 395 400

Glu Arg Leu Leu Arg Arg Thr Gln Thr Lys Arg Ser Val Tyr Arg Val
405 410 415

Leu Gly Lys Pro Glu Pro Ala Ala Gln Pro Val Pro Glu Ser Leu Pro
420 425 430

Gly Glu Pro Glu Ile Leu Pro Gln Ala Pro Ala Asn Ala His Leu Lys
435 440 445

Asp Leu Asp Glu Glu Ile Phe Asp Asp Asp Asp Phe Tyr His Gln Leu
450 455 460

Leu Arg Glu Leu Ile Glu Arg Lys Thr Ser Ser Leu Asp Pro Asn Asp
465 470 475 480

Gln Val Ala His Gly Lys Ala Val Ala Cys Asn Pro Glu Val Thr Glu
485 490 495

Ala Lys Ser Thr Lys Lys Val Asp Arg Lys Ala Ser Lys Gly Arg Lys
500 505 510

Leu Arg Phe His Val Leu Ser Lys Leu Leu Ser Phe Met Ala Pro Ile
515 520 525

Asp His Thr Thr Met Asn Asp Asp Ala Arg Thr Glu Leu Tyr Arg Ser
530 535 540

Leu Phe Gly Gln Leu His Pro Pro Asp Glu Gly His Gly Asp
545 550 555

<210> 40
<211> 300
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 113

<400> 40

Met Ala Thr Leu His Phe Val Pro Gln His Glu Glu Glu Gln Val Tyr
1 5 10 15

Ser Ile Ser Gly Lys Ala Leu Lys Leu Thr Thr Ser Asp Asp Ile Lys
20 25 30

Pro Tyr Leu Glu Glu Leu Ala Ala Leu Lys Thr Cys Thr Lys Leu Asp
35 40 45

Leu Ser Gly Asn Thr Ile Gly Thr Glu Ala Ser Glu Ala Leu Ala Lys
50 55 60

Cys Ile Ala Glu Asn Thr Gln Val Arg Glu Ser Leu Val Glu Val Asn
65 70 75 80

Phe Ala Asp Leu Tyr Thr Ser Arg Leu Val Asp Glu Val Val Asp Ser
85 90 95

Leu Lys Phe Leu Leu Pro Val Leu Leu Lys Cys Pro His Leu Glu Ile
100 105 110

Val Asn Leu Ser Asp Asn Ala Phe Gly Leu Arg Thr Ile Glu Leu Leu
115 120 125

Glu Asp Tyr Ile Ala His Ala Val Asn Ile Lys His Leu Ile Leu Ser
130 135 140

Asn Asn Gly Met Gly Pro Phe Ala Gly Glu Arg Ile Gly Lys Ala Leu
145 150 155 160

Phe His Leu Ala Gln Asn Lys Lys Ala Ala Ser Lys Pro Phe Leu Glu
165 170 175

Thr Phe Ile Cys Asn Thr Phe Thr Lys His Ala Ser Leu Ile Leu Ala
180 185 190

Lys Ala Leu Pro Thr Trp Lys Asp Ser Leu Phe Glu Leu Asn Leu Asn
195 200 205

Asp Cys Leu Leu Lys Thr Ala Gly Ser Asp Glu Val Phe Lys Val Phe
210 215 220

Thr Glu Val Lys Phe Pro Asn Leu His Val Leu Lys Phe Glu Tyr Asn
225 230 235 240

Glu Met Ala Gln Glu Thr Ile Glu Val Ser Phe Leu Pro Ala Met Glu
245 250 255

Lys Gly Asn Leu Pro Glu Leu Glu Lys Leu Glu Ile Asn Gly Asn Arg
260 265 270

Leu Asp Glu Asp Ser Asp Ala Leu Asp Leu Leu Gln Ser Lys Phe Asp
275 280 285

Asp Leu Glu Val Asp Asp Phe Glu Glu Val Asp Ser
290 295 300

<210> 41
<211> 415
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 114

<400> 41

Met Ala Ser Val Glu Val Glu Leu Gly Val Thr Pro Glu Thr Thr Tyr
1 5 10 15

Ser Ile Ser Gly Lys Gln Leu Lys Phe Asp Ser Glu Ser Asp Ile Ala
20 25 30

Pro Tyr Ile Lys Glu Leu Thr Glu Lys Glu Asn Val Lys Lys Val Asp
35 40 45

Phe Ser Gly Asn Thr Ile Gly Ile Glu Ala Ser Lys Ala Leu Ser Glu
50 55 60

Ala Leu Leu Lys His Lys Asp Thr Ile Val Glu Ile Asn Phe Ser Asp
65 70 75 80

Leu Tyr Thr Gly Arg Leu Asn Thr Glu Ile Pro Gln Ser Leu Glu Tyr
85 90 95

Leu Leu Pro Ala Leu Ser Lys Leu Pro Asn Leu Lys Leu Ile Asn Leu
100 105 110

Ser Asp Asn Ala Phe Gly Leu Gln Thr Ile Asp Pro Ile Glu Ala Tyr
115 120 125

Leu Ala Lys Ala Val Ser Ile Glu His Leu Ile Leu Ser Asn Asn Gly
130 135 140

Met Gly Pro Phe Ala Gly Ser Arg Ile Gly Gly Ser Leu Phe Lys Leu
145 150 155 160

Ala Lys Ala Lys Lys Ala Glu Gly Lys Glu Ser Leu Lys Thr Phe Ile
165 170 175

Cys Gly Arg Asn Arg Leu Glu Asn Gly Ser Val Asn Tyr Leu Ser Val
180 185 190

Gly Leu Arg Asn His Lys Asp Leu Glu Val Val Arg Leu Tyr Gln Asn
195 200 205

Gly Ile Arg Pro Ala Gly Ile Ser Lys Leu Val Glu Gln Gly Leu Ser
210 215 220

Asn Asn Lys Lys Leu Lys Val Leu Asp Leu Gln Asp Asn Thr Ile Thr

225 230 235 240

Thr Arg Gly Ala Ile His Ile Ala Glu Ser Leu Ser Asn Trp Pro Leu
245 250 255

Leu Val Glu Leu Asn Leu Asn Asp Ser Leu Leu Lys Asn Lys Gly Ser
260 265 270

Leu Lys Leu Val Glu Ala Phe His Ala Gly Asp Glu Lys Pro Gln Leu
275 280 285

Ile Thr Leu Lys Leu Gln Tyr Asn Glu Leu Glu Thr Asp Ser Leu Arg
290 295 300

Val Leu Ala Asp Ala Ile Ala Ser Lys Leu Pro Gln Leu Lys Phe Leu
305 310 315 320

Glu Leu Asn Gly Asn Arg Phe Glu Glu Asp Ser Glu His Ile Asp Lys
325 330 335

Ile Asn Gly Ile Phe Glu Glu Arg Gly Tyr Gly Glu Ile Asp Glu Leu
340 345 350

Asp Glu Leu Glu Glu Leu Asp Ser Glu Glu Glu Glu Asp Asp Glu Asp
355 360 365

Asp Glu Gly Glu Asp Asp Thr Leu Glu Glu Asp Leu Asp Leu Thr Gln
370 375 380

Leu Glu Glu Glu Leu Ala Gly Val Ser Leu Glu Asp Lys Asp Gly Asn
385 390 395 400

Val Asp Glu Ile Ala Glu Glu Leu Ser Lys Thr His Ile Lys Glx
405 410 415

<210> 42
<211> 587

<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: CAA57714

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 115

<400> 42

Met Ala Ser Glu Asp Ile Ala Lys Leu Ala Glu Thr Leu Ala Lys Thr
1 5 10 15

Gln Val Ala Gly Gly Gln Leu Ser Phe Lys Gly Lys Ser Leu Lys Leu
20 25 30

Asn Thr Ala Glu Asp Ala Lys Asp Val Ile Lys Glu Ile Glu Asp Phe
35 40 45

Asp Ser Leu Glu Ala Leu Arg Leu Glu Gly Asn Thr Val Gly Val Glu
50 55 60

Ala Ala Arg Val Ile Ala Lys Ala Leu Glu Lys Lys Ser Glu Leu Lys
65 70 75 80

Arg Cys His Trp Ser Asp Met Phe Thr Gly Arg Leu Arg Thr Glu Ile
85 90 95

Pro Pro Ala Leu Ile Ser Leu Gly Glu Gly Leu Ile Thr Ala Gly Ala
100 105 110

Gln Leu Val Glu Leu Asp Leu Ser Asp Asn Ala Phe Gly Pro Asp Gly
115 120 125

Val Gln Gly Phe Glu Ala Leu Leu Lys Ser Ser Ala Cys Phe Thr Leu
130 135 140

Gln Glu Leu Lys Leu Asn Asn Cys Gly Met Gly Ile Gly Gly Gly Lys
145 150 155 160

Ile Leu Ala Ala Ala Leu Thr Glu Cys His Arg Lys Ser Ser Ala Gln
165 170 175

Gly Lys Pro Leu Ala Leu Lys Val Phe Val Ala Gly Arg Asn Arg Leu
180 185 190

Glu Asn Asp Gly Ala Thr Ala Leu Ala Glu Ala Phe Arg Val Ile Gly
195 200 205

Thr Leu Glu Glu Val His Met Pro Gln Asn Gly Ile Asn His Pro Gly
210 215 220

Ile Thr Ala Leu Ala Gln Ala Phe Ala Val Asn Pro Leu Leu Arg Val
225 230 235 240

Ile Asn Leu Asn Asp Asn Thr Phe Thr Glu Lys Gly Ala Val Ala Met
245 250 255

Ala Glu Thr Leu Lys Thr Leu Arg Gln Val Glu Val Ile Asn Phe Gly
260 265 270

Asp Cys Leu Val Arg Ser Lys Gly Ala Val Ala Ile Ala Asp Ala Ile
275 280 285

Arg Gly Gly Leu Pro Lys Leu Lys Glu Leu Asn Leu Ser Phe Cys Glu
290 295 300

Ile Lys Arg Asp Ala Ala Leu Ala Val Ala Glu Ala Met Ala Asp Lys
305 310 315 320

Ala Glu Leu Glu Lys Leu Asp Leu Asn Gly Asn Thr Leu Gly Glu Glu
325 330 335

Gly Cys Glu Gln Leu Gln Glu Val Leu Glu Gly Phe Asn Met Ala Lys
340 345 350

Val Leu Ala Ser Leu Ser Asp Asp Glu Asp Glu Glu Glu Glu Glu Glu
355 360 365

Gly Glu Glu Glu Glu Glu Glu Ala Glu Glu Glu Glu Glu Glu Asp Glu
370 375 380

Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Pro Gln Gln
385 390 395 400

Arg Gly Gln Gly Glu Lys Ser Ala Thr Pro Ser Arg Lys Ile Leu Asp
405 410 415

Pro Asn Thr Gly Glu Pro Ala Pro Val Leu Ser Ser Pro Pro Pro Ala
420 425 430

Asp Val Ser Thr Phe Leu Ala Phe Pro Ser Pro Glu Lys Leu Leu Arg
435 440 445

Leu Gly Pro Lys Ser Ser Val Leu Ile Ala Gln Gln Thr Asp Thr Ser
450 455 460

Asp Pro Glu Lys Val Val Ser Ala Phe Leu Lys Val Ser Ser Val Phe
465 470 475 480

Lys Asp Glu Ala Thr Val Arg Met Ala Val Gln Asp Ala Val Asp Ala
485 490 495

Leu Met Gln Lys Ala Phe Asn Ser Ser Ser Phe Asn Ser Asn Thr Phe
500 505 510

Leu Thr Arg Leu Leu Val His Met Gly Leu Leu Lys Ser Glu Asp Lys
515 520 525

Val Lys Ala Ile Ala Asn Leu Tyr Gly Pro Leu Met Ala Leu Asn His

530 535 540

Met Val Gln Gln Asp Tyr Phe Pro Lys Ala Leu Ala Pro Leu Leu Leu
545 550 555 560

Ala Phe Val Thr Lys Pro Asn Ser Ala Leu Glu Ser Cys Ser Phe Ala
565 570 575

Arg His Ser Leu Leu Gln Thr Leu Tyr Lys Val
580 585

<210> 43
<211> 381
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 116

<400> 43

Met Ser Ser Gln Ala Phe Thr Ser Val His Pro Asn Ala Ala Thr Ser
1 5 10 15

Asp Val Asn Val Thr Ile Asp Thr Phe Val Ala Lys Leu Lys Arg Arg
20 25 30

Gln Val Gln Gly Ser Tyr Ala Ile Ala Leu Glu Thr Leu Gln Leu Leu
35 40 45

Met Arg Phe Ile Ser Ala Ala Arg Trp Asn His Val Asn Asp Leu Ile
50 55 60

Glu Gln Ile Arg Asp Leu Gly Asn Ser Leu Glu Lys Ala His Pro Thr
65 70 75 80

Ala Phe Ser Cys Gly Asn Val Ile Arg Arg Ile Leu Ala Val Leu Arg
85 90 95

Asp Glu Val Glu Glu Asp Thr Met Ser Thr Thr Val Thr Ser Thr Ser
100 105 110

Val Ala Glu Pro Leu Ile Ser Ser Met Phe Asn Leu Leu Gln Lys Pro
115 120 125

Glu Gln Pro His Gln Asn Arg Lys Asn Ser Ser Gly Ser Ser Ser Met
130 135 140

Lys Thr Lys Thr Asp Tyr Arg Gln Val Ala Ile Gln Gly Ile Lys Asp
145 150 155 160

Leu Ile Asp Glu Ile Lys Asn Ile Asp Glu Gly Ile Gln Gln Ile Ala
165 170 175

Ile Asp Leu Ile His Asp His Glu Ile Leu Leu Thr Pro Thr Pro Asp
180 185 190

Ser Lys Thr Val Leu Lys Phe Leu Ile Thr Ala Arg Glu Arg Ser Asn
195 200 205

Arg Thr Phe Thr Val Leu Val Thr Glu Gly Phe Pro Asn Asn Thr Lys
210 215 220

Asn Ala His Glu Phe Ala Lys Lys Leu Ala Gln His Asn Ile Glu Thr
225 230 235 240

Leu Val Val Pro Asp Ser Ala Val Phe Ala Leu Met Ser Arg Val Gly
245 250 255

Lys Val Ile Ile Gly Thr Lys Ala Val Phe Val Asn Gly Gly Thr Ile
260 265 270

Ser Ser Asn Ser Gly Val Ser Ser Val Cys Glu Cys Ala Arg Glu Phe
275 280 285

Arg Thr Pro Val Phe Ala Val Ala Gly Leu Tyr Lys Leu Ser Pro Leu
290 295 300

Tyr Pro Phe Asp Val Glu Lys Phe Val Glu Phe Gly Gly Ser Gln Arg
305 310 315 320

Ile Leu Pro Arg Met Asp Pro Arg Lys Arg Leu Asp Thr Val Asn Gln
325 330 335

Ile Thr Asp Tyr Val Pro Pro Glu Asn Ile Asp Ile Tyr Ile Thr Asn
340 345 350

Val Gly Gly Phe Asn Pro Ser Phe Ile Tyr Arg Ile Ala Trp Asp Asn
355 360 365

Tyr Lys Gln Ile Asp Val His Leu Asp Lys Asn Lys Ala
370 375 380

<210> 44
<211> 365
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 117

<400> 44

Met Ser Lys Leu Leu Thr Pro Glu Ile Leu Ala Leu Ile Asp Pro Val
1 5 10 15

Val Ser Ser Leu Lys Arg His Gln Leu Val Asp Asp Lys Glu Ile Ala
20 25 30

Leu Thr Ile Ala Gln Leu Leu Met Lys Val Ile Ser Ala Ala Arg Trp
35 40 45

Ser Asn Thr Tyr Asp Leu Ile Glu Leu Ile Arg Gln Val Gly Val Ile

50 55 60

Phe Thr Glu Ala Tyr Pro Arg Lys Val Ile Pro Gly Asn Ile Val Arg
65 70 75 80

Arg Val Leu Ala Leu Ile Arg Asp Glu Thr Glu Thr Glu Thr Glu Thr
85 90 95

Glu Thr Glu Gln Thr Asp Asn Ile Pro Met Met Ser Ser Met Phe Ser
100 105 110

Leu Leu Ala Thr His Asn Lys Asn Glu Thr Ile Lys Glu Gln Thr Gln
115 120 125

Leu Gln Leu Lys Lys Gln Thr Ser Asp Met Arg Ala Ile Ile Ile Gln
130 135 140

Gly Ile Arg Asp Leu Val Asp Glu Ile Ser Asn Val Asn Asp Gly Ile
145 150 155 160

Glu Thr Met Ala Val Asp Leu Ile His Asp Asp Glu Ile Leu Leu Thr
165 170 175

Pro Thr Pro Asn Ser Glu Thr Val Gln His Phe Leu Ile Lys Ala Arg
180 185 190

Leu Lys Arg Lys Phe Thr Val Val Val Thr Glu Asn Tyr Pro Asn Asp
195 200 205

Ile Lys Ala Ala His Lys Phe Val Lys Thr Leu Ala Glu His Asn Ile
210 215 220

Glu Thr Ile Leu Ile Pro Asp Thr Thr Ile Tyr Ala Val Met Ser Arg
225 230 235 240

Val Gly Lys Val Ile Ile Gly Thr Asn Ala Val Phe Ala Asn Gly Gly
245 250 255

Cys Leu Ser Asn Ser Gly Val Ala Asn Val Val Glu Cys Ala Lys Glu
260 265 270

His Arg Thr Pro Val Phe Ala Val Ala Gly Leu Phe Lys Leu Ser Pro
275 280 285

Leu Tyr Pro Phe Thr Arg Asn Asp Leu Ile Glu Val Gly Asn Ser Gly
290 295 300

Lys Val Leu Asn Tyr Asp Asp Phe Glu Leu Val Gln Asn Val Asp Val
305 310 315 320

Val Thr Asn Pro Leu Glu Asp Tyr Ile Pro Pro Gln His Ile Asp Ile
325 330 335

Phe Met Thr Asn Ile Gly Gly Phe Ser Pro Ser Phe Ile Tyr Arg Ile
340 345 350

Val Leu Asp Asn Tyr Lys Ala Glu Asp Asn Lys Leu Glu
355 360 365

<210> 45
<211> 349
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: AAC42002

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 118

<400> 45

Met Pro Gly Ser Ala Ala Lys Gly Ser Glu Leu Ser Glu Arg Ile Glu
1 5 10 15

Ser Phe Val Glu Thr Leu Lys Arg Gly Gly Gly Pro Arg Ser Ser Glu
20 25 30

Glu Met Ala Arg Glu Thr Leu Gly Leu Leu Arg Gln Ile Ile Thr Asp
35 40 45

His Arg Trp Ser Asn Ala Gly Glu Leu Met Glu Leu Ile Arg Arg Glu
50 55 60

Gly Arg Arg Met Thr Ala Ala Gln Pro Ser Glu Thr Thr Val Gly Asn
65 70 75 80

Met Val Arg Arg Val Leu Lys Ile Ile Arg Glu Glu Tyr Gly Arg Leu
85 90 95

His Gly Arg Ser Asp Glu Asp Gln Gln Glu Ser Leu His Lys Leu Leu
100 105 110

Thr Ser Gly Gly Leu Asn Glu Asp Phe Ser Phe His Tyr Ala Gln Leu
115 120 125

Gln Ser Asn Ile Ile Glu Ala Ile Asn Glu Leu Leu Val Glu Leu Glu
130 135 140

Gly Thr Met Glu Asn Ile Ala Ala Gln Ala Leu Glu His Ile His Ser
145 150 155 160

Asn Glu Val Ile Met Thr Ile Gly Phe Ser Arg Thr Val Glu Ala Phe
165 170 175

Leu Lys Glu Ala Ala Arg Lys Arg Lys Phe His Val Ile Val Ala Glu
180 185 190

Cys Ala Pro Phe Cys Gln Gly His Glu Met Ala Val Asn Leu Ser Lys
195 200 205

Ala Gly Ile Glu Thr Thr Val Met Thr Ala Ala Ile Phe Ala Val Met

210 215 220

Ser Arg Val Asn Lys Val Ile Ile Gly Thr Lys Thr Ile Leu Ala Asn
225 230 235 240

Gly Ala Leu Arg Ala Val Thr Gly Thr His Thr Leu Ala Leu Ala Ala
245 250 255

Lys His His Ser Thr Pro Leu Ile Val Cys Ala Pro Met Phe Lys Leu
260 265 270

Ser Pro Gln Phe Pro Asn Glu Glu Asp Ser Phe His Lys Phe Val Ala
275 280 285

Pro Glu Glu Val Leu Pro Phe Thr Glu Gly Asp Ile Leu Glu Lys Val
290 295 300

Ser Val His Cys Pro Val Phe Asp Tyr Val Pro Pro Glu Leu Ile Thr
305 310 315 320

Leu Phe Ile Ser Asn Ile Gly Gly Asn Ala Pro Ser Tyr Ile Tyr Arg
325 330 335

Leu Met Ser Glu Leu Tyr His Pro Asp Asp His Val Leu
340 345

<210> 46
<211> 246
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 119

<400> 46

Met Ser Arg Leu Glu Ile Tyr Ser Pro Glu Gly Leu Arg Leu Asp Gly
1 5 10 15

Arg Arg Trp Asn Glu Leu Arg Arg Phe Glu Ser Ser Ile Asn Thr His
20 25 30

Pro His Ala Ala Asp Gly Ser Ser Tyr Met Glu Gln Gly Asn Asn Lys
35 40 45

Ile Ile Thr Leu Val Lys Gly Pro Lys Glu Pro Arg Leu Lys Ser Gln
50 55 60

Met Asp Thr Ser Lys Ala Leu Leu Asn Val Ser Val Asn Ile Thr Lys
65 70 75 80

Phe Ser Lys Phe Glu Arg Ser Lys Ser Ser His Lys Asn Glu Arg Arg
85 90 95

Val Leu Glu Ile Gln Thr Ser Leu Val Arg Met Phe Glu Lys Asn Val
100 105 110

Met Leu Asn Ile Tyr Pro Arg Thr Val Ile Asp Ile Glu Ile His Val
115 120 125

Leu Glu Gln Asp Gly Gly Ile Met Gly Ser Leu Ile Asn Gly Ile Thr
130 135 140

Leu Ala Leu Ile Asp Ala Gly Ile Ser Met Phe Asp Tyr Ile Ser Gly
145 150 155 160

Ile Ser Val Gly Leu Tyr Asp Thr Thr Pro Leu Leu Asp Thr Asn Ser
165 170 175

Leu Glu Glu Asn Ala Met Ser Thr Val Thr Leu Gly Val Val Gly Lys
180 185 190

Ser Glu Lys Leu Ser Leu Leu Leu Val Glu Asp Lys Ile Pro Leu Asp
195 200 205

Arg Leu Glu Asn Val Leu Ala Ile Gly Ile Ala Gly Ala His Arg Val
210 215 220

Arg Asp Leu Met Asp Glu Glu Leu Arg Lys His Ala Gln Lys Arg Val
225 230 235 240

Ser Asn Ala Ser Ala Arg
245

<210> 47
<211> 180
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 120

<400> 47

Met Glu Leu Tyr Ser Pro Glu Gly Leu Arg Ile Asp Gly Arg Arg Trp
1 5 10 15

Asn Glu Leu Arg Arg Phe Glu Cys Arg Ile Asn Thr His Pro Asn Ser
20 25 30

Ser Asp Gly Ser Ser Tyr Val Glu Gln Gly Asn Thr Lys Val Met Cys
35 40 45

Thr Val Gln Gly Pro Ile Glu Pro Ala Leu Arg Ser Gln Gln His Ser
50 55 60

Glu Arg Ala Asn Ile Glu Val Asn Leu Asn Ile Ala Ser Phe Ser Thr
65 70 75 80

Phe Glu Arg Lys Lys Arg Ser Arg Asn Glu Arg Arg Leu Val Glu Leu
85 90 95

Lys Thr Thr Leu Glu Lys Thr Phe Glu Glu Ser Val Met Ile Asn Leu

100 105 110

Tyr Pro Arg Thr Asn Ile Val Ile Asn Val Gln Val Leu Cys Gln Asp
115 120 125

Gly Gly Met Leu Ala Ala Val Ile Asn Ser Ile Thr Leu Ala Leu Ile
130 135 140

Asp Ala Gly Ile Ser Met Tyr Asp Tyr Val Ser Gly Val Ser Cys Gly
145 150 155 160

Leu Tyr Asp Gln Thr Pro Leu Leu Asp Val Asn Asn Leu Glu Glu His
165 170 175

Asp Met Ser Cys
180

<210> 48
<211> 245
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: BAA91279

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 121

<400> 48

Met Ala Gly Leu Glu Leu Leu Ser Asp Gln Gly Tyr Arg Val Asp Gly
1 5 10 15

Arg Arg Ala Gly Glu Leu Arg Lys Ile Gln Ala Arg Met Gly Val Phe
20 25 30

Ala Gln Ala Asp Gly Ser Ala Tyr Ile Glu Gln Gly Asn Thr Lys Ala

35 40 45

Leu Ala Val Val Tyr Gly Pro His Glu Ile Arg Ser Arg Ala Arg Ala
50 55 60

Leu Pro Asp Arg Ala Leu Val Asn Cys Gln Tyr Ser Ser Ala Thr Phe
65 70 75 80

Ser Thr Gly Glu Arg Lys Arg Arg Pro His Gly Asp Arg Lys Ser Cys
85 90 95

Glu Met Gly Leu Gln Leu Arg Gln Thr Phe Glu Ala Ala Ile Leu Thr
100 105 110

Gln Leu His Pro Arg Ser Gln Ile Asp Ile Tyr Val Gln Val Leu Gln
115 120 125

Ala Asp Gly Gly Thr Tyr Ala Ala Cys Val Asn Ala Ala Thr Leu Ala
130 135 140

Val Leu Asp Ala Gly Ile Pro Met Arg Asp Phe Val Cys Ala Cys Ser
145 150 155 160

Ala Gly Phe Val Asp Gly Thr Ala Leu Ala Asp Leu Ser His Val Glu
165 170 175

Glu Ala Ala Gly Gly Pro Gln Leu Ala Leu Ala Leu Leu Pro Ala Ser
180 185 190

Gly Gln Ile Ala Leu Leu Glu Met Asp Ala Arg Leu His Glu Asp His
195 200 205

Leu Glu Arg Val Leu Glu Ala Ala Ala Gln Ala Ala Arg Asp Val His
210 215 220

Thr Leu Leu Asp Arg Val Val Arg Gln His Val Arg Glu Ala Ser Ile
225 230 235 240

Leu Leu Gly Asp Gly
245

<210> 49
<211> 720
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 122

<400> 49

Met Ser Arg Phe Phe Ser Ser Asn Tyr Glu Tyr Asp Val Ala Ser Ser
1 5 10 15

Ser Ser Glu Glu Asp Leu Leu Ser Ser Ser Glu Glu Asp Leu Leu Ser
20 25 30

Ser Ser Ser Ser Glu Ser Glu Leu Asp Gln Glu Ser Asp Asp Ser Phe
35 40 45

Phe Asn Glu Ser Glu Ser Glu Ser Glu Ala Asp Val Asp Ser Asp Asp
50 55 60

Ser Asp Ala Lys Pro Tyr Gly Pro Asp Trp Phe Lys Lys Ser Glu Phe
65 70 75 80

Arg Lys Gln Gly Gly Gly Ser Asn Lys Phe Leu Lys Ser Ser Asn Tyr
85 90 95

Asp Ser Ser Asp Glu Glu Ser Asp Glu Glu Asp Gly Lys Lys Val Val
100 105 110

Lys Ser Ala Lys Glu Lys Leu Leu Asp Glu Met Gln Asp Val Tyr Asn
115 120 125

Lys Ile Ser Gln Ala Glu Asn Ser Asp Asp Trp Leu Thr Ile Ser Asn
130 135 140

Glu Phe Asp Leu Ile Ser Arg Leu Leu Val Arg Ala Gln Gln Gln Asn
145 150 155 160

Trp Gly Thr Pro Asn Ile Phe Ile Lys Val Val Ala Gln Val Glu Asp
165 170 175

Ala Val Asn Asn Thr Gln Gln Ala Asp Leu Lys Asn Lys Ala Val Ala
180 185 190

Arg Ala Tyr Asn Thr Thr Lys Gln Arg Val Lys Lys Val Ser Arg Glu
195 200 205

Asn Glu Asp Ser Met Ala Lys Phe Arg Asn Asp Pro Glu Ser Phe Asp
210 215 220

Lys Glu Pro Thr Ala Asp Leu Asp Ile Ser Ala Asn Gly Phe Thr Ile
225 230 235 240

Ser Ser Ser Gln Gly Asn Asp Gln Ala Val Gln Glu Asp Phe Phe Thr
245 250 255

Arg Leu Gln Thr Ile Ile Asp Ser Arg Gly Lys Lys Thr Val Asn Gln
260 265 270

Gln Ser Leu Ile Ser Thr Leu Glu Glu Leu Leu Thr Val Ala Glu Lys
275 280 285

Pro Tyr Glu Phe Ile Met Ala Tyr Leu Thr Leu Ile Pro Ser Arg Phe
290 295 300

Asp Ala Ser Ala Asn Leu Ser Tyr Gln Pro Ile Asp Gln Trp Lys Ser
305 310 315 320

Ser Phe Asn Asp Ile Ser Lys Leu Leu Ser Ile Leu Asp Gln Thr Ile

325 330 335

Asp Thr Tyr Gln Val Asn Glu Phe Ala Asp Pro Ile Asp Phe Ile Glu
340 345 350

Asp Glu Pro Lys Glu Asp Ser Asp Gly Val Lys Arg Ile Leu Gly Ser
355 360 365

Ile Phe Ser Phe Val Glu Arg Leu Asp Asp Glu Phe Met Lys Ser Leu
370 375 380

Leu Asn Ile Asp Pro His Ser Ser Asp Tyr Leu Ile Arg Leu Arg Asp
385 390 395 400

Glu Gln Ser Ile Tyr Asn Leu Ile Leu Arg Thr Gln Leu Tyr Phe Glu
405 410 415

Ala Thr Leu Lys Asp Glu His Asp Leu Glu Arg Ala Leu Thr Arg Pro
420 425 430

Phe Val Lys Arg Leu Asp His Ile Tyr Tyr Lys Ser Glu Asn Leu Ile
435 440 445

Lys Ile Met Glu Thr Ala Ala Trp Asn Ile Ile Pro Ala Gln Phe Lys
450 455 460

Ser Lys Phe Thr Ser Lys Asp Gln Leu Asp Ser Ala Asp Tyr Val Asp
465 470 475 480

Asn Leu Ile Asp Gly Leu Ser Thr Ile Leu Ser Lys Gln Asn Asn Ile
485 490 495

Ala Val Gln Lys Arg Ala Ile Leu Tyr Asn Ile Tyr Tyr Thr Ala Leu
500 505 510

Asn Lys Asp Phe Gln Thr Ala Lys Asp Met Leu Leu Thr Ser Gln Val
515 520 525

Gln Thr Asn Ile Asn Gln Phe Asp Ser Ser Leu Gln Ile Leu Phe Asn
530 535 540

Arg Val Val Val Gln Leu Gly Leu Ser Ala Phe Lys Leu Cys Leu Ile
545 550 555 560

Glu Glu Cys His Gln Ile Leu Asn Asp Leu Leu Ser Ser Ser His Leu
565 570 575

Arg Glu Ile Leu Gly Gln Gln Ser Leu His Arg Ile Ser Leu Asn Ser
580 585 590

Ser Asn Asn Ala Ser Ala Asp Glu Arg Ala Arg Gln Cys Leu Pro Tyr
595 600 605

His Gln His Ile Asn Leu Asp Leu Ile Asp Val Val Phe Leu Thr Cys
610 615 620

Ser Leu Leu Ile Glu Ile Pro Arg Met Thr Ala Phe Tyr Ser Gly Ile
625 630 635 640

Lys Val Lys Arg Ile Pro Tyr Ser Pro Lys Ser Ile Arg Arg Ser Leu
645 650 655

Glu His Tyr Asp Ser Leu Lys Thr Tyr Phe Phe Ser Phe Lys Arg Phe
660 665 670

Tyr Ser Ser Phe Ser Val Ala Lys Leu Ala Glu Leu Phe Asp Leu Pro
675 680 685

Glu Asn Lys Val Val Glu Val Leu Gln Ser Val Ile Ala Glu Leu Glu
690 695 700

Ile Pro Ala Lys Leu Asn Asp Glu Lys Thr Ile Phe Val Val Glu Lys
705 710 715 720

<210> 50
<211> 874
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 123

<400> 50

Met Ser Arg Phe Phe Val Ser Gly Tyr Thr Ser Asp Ser Ser Ser Glu
1 5 10 15

Glu Glu Asp Leu Leu Ser Thr Ser Glu Glu Glu Leu Leu Ser Ser Ser
20 25 30

Asp Glu Gly Glu Asp Asn Glu Ser Asp Ser Ser Phe Phe Gly Glu Asp
35 40 45

Asp Asp Glu Ser Glu Glu Ser Ser Ser Asp Asp Glu Asp Gly Arg Pro
50 55 60

Ser Gly Pro Ala Tyr Phe Leu Lys Lys Ser Phe Leu Lys Gly Ala Gly
65 70 75 80

Gly Asp Asp Ser Asp Ser Asp Ser Asp Asp Glu Gly Arg Lys Val Val
85 90 95

Lys Ser Ala Lys Asp Lys Leu Leu Asp Asp Met Lys Ser Ser Ile Glu
100 105 110

Ile Ile Asn Ser Asn Lys Tyr Asn Asn Asn Trp Ser Ile Val Leu Gly
115 120 125

Glu Phe Asp Lys Phe Gly Arg Phe Leu Ile Arg Cys Asn Gln Thr Asn
130 135 140

Leu Gly Thr Pro Lys Phe Tyr Ile Lys Leu Leu Thr Ser Leu Asp Asn
145 150 155 160

Ser Ile Thr Glu Thr Ser Asn Asn Glu Arg Asp Asp Lys Thr Leu Lys
165 170 175

Ala Asp Glu Ala Arg Ala Phe Asn Thr Leu Arg Gln Arg Ile Lys Lys
180 185 190

Gln Ile Arg Glu Phe Gln Val Tyr Tyr Asp Leu Tyr Lys Glu Asn Pro
195 200 205

Glu Glu Phe Asp Glu Asn Glu Asp Glu Pro Leu Glu Ser Val Gln Ala
210 215 220

Gly Leu Asn Asp Asn Val Lys Asn Glu Ala Asp Asn Ser Asn Val Gly
225 230 235 240

Ala Leu Ala Ser Asn Arg Val Leu Ser Pro Ile Phe His Thr Leu Lys
245 250 255

Thr Ile Ser Glu Ser Arg Gly Lys Lys Asn Ile Asp Lys Leu Glu Gln
260 265 270

Ile Ala Thr Leu Glu Lys Leu Leu Glu Ala Asn Val Ser Lys Ser Ser
275 280 285

Pro Phe Glu Leu Ile Ser Ile Tyr Gln Met Leu Leu Ser Val Arg Phe
290 295 300

Asp Ala Ser Ser Asn Gln Ala Phe Met Pro Leu Glu Gln Trp Gln Lys
305 310 315 320

Asn Glu His Asp Leu Gly Lys Leu Leu Asp Leu Leu Glu Ala Asn Val
325 330 335

Asp Thr Tyr Gln Val Ser Glu Leu Gly Ser Thr Thr Asp Asp Ile Asp
340 345 350

Ile Glu Pro Val Ala Asn Ala Gln Gly Val Lys Val Ile Phe Gly Ser
355 360 365

Ile Thr Ser Ser Ile Asp Arg Leu Asp Asp Glu Leu Thr Lys Ser Leu
370 375 380

Gln His Thr Asp Pro His Ser Ile Glu Tyr Val Glu Arg Leu Lys Asp
385 390 395 400

Glu Ser Thr Ile Tyr Asn Leu Ile Val Arg Gly Gln Ala Tyr Val Glu
405 410 415

Ser Ile Thr Pro Glu Asp Val Lys Tyr Asn Ser Glu Gln Leu Ala Arg
420 425 430

Ile Val Leu Arg Arg Leu Glu His Ile Tyr Tyr Lys Pro Lys Gln Leu
435 440 445

Ile Lys Ala Asn Glu Glu Glu Ala Trp Arg Asn Ile Glu Tyr Asn Ser
450 455 460

Ser Ile Val Ser Lys Gly Ser Ser Val Asp Glu Val Ile Asp Gln Leu
465 470 475 480

Thr Glu Phe Leu Gln Lys Gln Gln Lys Asn Lys Thr Tyr Gly Lys His
485 490 495

Ala Ile Leu Phe Ser Ile Tyr Tyr Tyr Ala Val Asn Ser Gln Tyr Glu
500 505 510

Lys Ala Lys Glu Leu Phe Leu Arg Ser Gln Phe Tyr Ser Asn Ile Asn
515 520 525

Ser Ala Glu Ser Ser Leu Gln Val Gln Tyr Asn Arg Ala Leu Val Gln
530 535 540

Leu Gly Leu Ser Ala Phe Arg Ala Gly Ser Ile Glu Glu Ser His Lys

545 550 555 560

Ile Leu Asn Glu Ile Val Asn Ser Gln Arg Ser Lys Glu Leu Leu Gly
565 570 575

Gln Gly Phe Asn Ser Lys Phe Pro Asn Gln Ala Thr Val Leu Glu Arg
580 585 590

Gln Lys Leu Leu Pro Phe His Gln His Ile Asn Leu Glu Leu Leu Glu
595 600 605

Cys Val Phe Met Thr Cys Ser Leu Leu Ile Glu Ile Pro Thr Leu Ala
610 615 620

Ala Ile Ala Asn Asn His Lys Asp Ser Lys Arg Lys Asn Ala Ser Leu
625 630 635 640

Lys Ser Phe Lys Ser Lys Leu Asp Phe His Asp Arg Gln Phe Phe Thr
645 650 655

Gly Pro Pro Glu Ser Ile Lys Asp His Ile Val His Ala Ser Ile Ala
660 665 670

Leu Gln Lys Gly Asp Trp Leu Lys Ser Tyr Asn Leu Leu Ser Ser Ile
675 680 685

Lys Ile Trp Lys Leu Phe Pro Asp Asn Asp Lys Leu Leu Ala Met Met
690 695 700

Lys Asn Gln Leu Gln Ile Glu Gly Leu Arg Thr Tyr Ile Phe Thr Tyr
705 710 715 720

Lys Ser Val Phe Lys Lys Leu Ser Ile Glu Lys Leu Gln Gln Ile Phe
725 730 735

Gln Leu Ser Lys Asp Glu Val Val Ser Ile Leu Glu Lys Met Ile Thr
740 745 750

Thr Gly Asn Val Ser Gly Gly Glu Ile Ile Asp Asn Lys Phe Ile Ser
755 760 765

Phe Thr Ser Thr Thr Glu Pro Gln Arg Ser Lys Leu Gln Glu Leu Ala
770 775 780

Ile Val Leu Asn Glu Lys Ile Gln Leu Leu Thr Glu Lys Asn Glu Lys
785 790 795 800

Thr Gln Ser Asn Gly Tyr Gly Lys Lys Gln Gln Asn Lys Asp Gln Gln
805 810 815

Asn Gln Gln Gln Gln Asn Gln Asn Gln Asn Gln Gln Gln Gln Gln Asn
820 825 830

Gln Gln Gln Gln Gln Gln Gln Gln Ser Ser Gln Gln Gln Ser Asn Asn
835 840 845

Ile Leu Ser Glu Glu Ser Ala Asn Lys Phe Arg Tyr Ala Asn Val Asn
850 855 860

Ser Asn Asn Asp Glu Phe Gln Ala Thr Ala
865 870

<210> 51
<211> 853
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: AAD03462

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 124

<400> 51

Met Ser Arg Phe Phe Thr Thr Gly Ser Asp Ser Glu Ser Glu Ser Ser
1 5 10 15

Leu Ser Gly Glu Glu Leu Val Thr Lys Pro Val Gly Gly Asn Tyr Gly
20 25 30

Lys Gln Pro Leu Leu Leu Ser Glu Asp Glu Glu Asp Thr Lys Arg Val
35 40 45

Val Arg Ser Ala Lys Asp Lys Arg Phe Glu Glu Leu Thr Asn Leu Ile
50 55 60

Arg Thr Ile Arg Asn Ala Met Lys Ile Arg Asp Val Thr Lys Cys Leu
65 70 75 80

Glu Glu Phe Glu Leu Leu Gly Lys Ala Tyr Gly Lys Ala Lys Ser Ile
85 90 95

Val Asp Lys Glu Gly Val Pro Arg Phe Tyr Ile Arg Ile Leu Ala Asp
100 105 110

Leu Glu Asp Tyr Leu Asn Glu Leu Trp Glu Asp Lys Glu Gly Lys Lys
115 120 125

Lys Met Asn Lys Asn Asn Ala Lys Ala Leu Ser Thr Leu Arg Gln Lys
130 135 140

Ile Arg Lys Tyr Asn Arg Asp Phe Glu Ser His Ile Thr Ser Tyr Lys
145 150 155 160

Gln Asn Pro Glu Gln Ser Ala Asp Glu Asp Ala Glu Lys Asn Glu Glu
165 170 175

Asp Ser Glu Gly Ser Ser Asp Glu Asp Glu Asp Glu Asp Gly Val Ser
180 185 190

Ala Ala Thr Phe Leu Lys Lys Lys Ser Glu Ala Pro Ser Gly Glu Ser

195 200 205

Arg Lys Phe Leu Lys Lys Met Asp Asp Glu Asp Glu Asp Ser Glu Asp
210 215 220

Ser Glu Asp Asp Glu Asp Trp Asp Thr Gly Ser Thr Ser Ser Asp Ser
225 230 235 240

Asp Ser Glu Glu Glu Glu Gly Lys Gln Thr Ala Leu Ala Ser Arg Phe
245 250 255

Leu Lys Lys Ala Pro Thr Thr Asp Glu Asp Lys Lys Ala Ala Glu Lys
260 265 270

Lys Arg Glu Asp Lys Ala Lys Lys Lys His Asp Arg Lys Ser Lys Arg
275 280 285

Leu Asp Glu Glu Glu Glu Asp Asn Glu Gly Gly Glu Ala Ala Glu Asn
290 295 300

Asn Leu Gly Glu Gly Val Ile Val Lys Ile Lys Phe Asn Ile Ile Ala
305 310 315 320

Ser Leu Tyr Asp Tyr Asn Pro Asn Leu Ala Thr Tyr Met Lys Pro Glu
325 330 335

Met Trp Gly Lys Cys Leu Asp Cys Ile Asn Glu Leu Met Asp Ile Leu
340 345 350

Phe Ala Asn Pro Asn Ile Phe Val Gly Glu Asn Ile Leu Glu Glu Ser
355 360 365

Glu Asn Leu His Asn Ala Asp Gln Pro Leu Arg Val Arg Gly Cys Ile
370 375 380

Leu Thr Leu Val Glu Arg Met Asp Glu Glu Phe Thr Lys Ile Met Gln
385 390 395 400

Asn Thr Asp Pro His Ser Gln Glu Tyr Val Glu His Leu Lys Asp Glu
405 410 415

Ala Gln Val Cys Ala Ile Ile Glu Arg Val Gln Arg Tyr Leu Glu Glu
420 425 430

Lys Gly Thr Thr Glu Glu Val Cys Arg Ile Tyr Leu Leu Arg Ile Leu
435 440 445

His Thr Tyr Tyr Lys Phe Asp Tyr Lys Ala His Gln Arg Gln Leu Thr
450 455 460

Pro Pro Glu Gly Ser Ser Lys Ser Glu Gln Asp Gln Ala Glu Asn Glu
465 470 475 480

Gly Glu Asp Ser Ala Val Leu Met Glu Arg Leu Cys Lys Tyr Ile Tyr
485 490 495

Ala Lys Asp Arg Thr Asp Arg Ile Arg Thr Cys Ala Ile Leu Cys His
500 505 510

Ile Tyr His His Ala Leu His Ser Arg Trp Tyr Gln Ala Arg Asp Leu
515 520 525

Met Leu Met Ser His Leu Gln Asp Asn Ile Gln His Ala Asp Pro Pro
530 535 540

Val Gln Ile Leu Tyr Asn Arg Thr Met Val Gln Leu Gly Ile Cys Ala
545 550 555 560

Phe Arg Gln Gly Leu Thr Lys Asp Ala His Asn Ala Leu Leu Asp Ile
565 570 575

Gln Ser Ser Gly Arg Ala Lys Glu Leu Leu Gly Gln Gly Leu Leu Leu
580 585 590

Arg Ser Leu Gln Glu Arg Asn Gln Glu Gln Glu Lys Val Glu Arg Arg
595 600 605

Arg Gln Val Pro Phe His Leu His Ile Asn Leu Glu Leu Leu Glu Cys
610 615 620

Val Tyr Leu Val Ser Ala Met Leu Leu Glu Ile Pro Tyr Met Ala Ala
625 630 635 640

His Glu Ser Asp Ala Arg Arg Arg Met Ile Ser Lys Gln Phe His His
645 650 655

Gln Leu Arg Val Gly Glu Arg Gln Pro Leu Leu Gly Pro Pro Glu Ser
660 665 670

Met Arg Glu His Val Val Ala Ala Ser Lys Ala Met Lys Met Gly Asp
675 680 685

Trp Lys Thr Cys His Ser Phe Ile Ile Asn Glu Lys Met Asn Gly Lys
690 695 700

Val Trp Asp Leu Phe Pro Glu Ala Asp Lys Val Arg Thr Met Leu Val
705 710 715 720

Arg Lys Ile Gln Glu Glu Ser Leu Arg Thr Tyr Leu Phe Thr Tyr Ser
725 730 735

Ser Val Tyr Asp Ser Ile Ser Met Glu Thr Leu Ser Asp Met Phe Glu
740 745 750

Leu Asp Leu Pro Thr Val His Ser Ile Ile Ser Lys Met Ile Ile Asn
755 760 765

Glu Glu Leu Met Ala Ser Leu Asp Gln Pro Thr Gln Thr Val Val Met
770 775 780

His Arg Thr Glu Pro Thr Ala Gln Gln Asn Leu Ala Leu Gln Leu Ala

785 790 795 800

Glu Lys Leu Gly Ser Leu Val Glu Asn Asn Glu Arg Val Phe Asp His
805 810 815

Lys Gln Gly Thr Tyr Gly Gly Tyr Phe Arg Asp Gln Lys Asp Gly Tyr
820 825 830

Arg Lys Asn Glu Gly Tyr Met Arg Arg Gly Gly Tyr Arg Gln Gln Gln
835 840 845

Ser Gln Thr Ala Tyr
850

<210> 52
<211> 297
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 125

<400> 52

Met Ser Glu Leu Asn Ala Leu Leu Lys Asp Ile Asn Gly Ser Leu Thr
1 5 10 15

Ala Thr Ser Glu Ser Leu Glu Arg Leu Ser Gly Ile Tyr Ser Asn Ser
20 25 30

Ala Thr Asp Glu Ile Pro Glu Ser Asn Gln Leu His Glu His Leu Phe
35 40 45

Tyr Asp Ala Lys Lys Pro Ala Glu Lys Val Ser Leu Leu Ser Leu Lys
50 55 60

Asn Gly Ser Met Leu Gly Tyr Ile Asn Ser Leu Leu Met Leu Ile Gly
65 70 75 80

Asn Arg Leu Asp Asp Glu Cys Lys Asp Pro Ser Ala Met Asp Ala Arg
85 90 95

Glu Arg Ser Ile Gln His Arg Val Val Leu Glu Arg Gly Val Lys Pro
100 105 110

Leu Glu Lys Lys Leu Ala Tyr Gln Leu Asp Lys Leu Thr Arg Ala Tyr
115 120 125

Val Lys Met Glu Lys Glu Tyr Lys Asp Ala Glu Lys Arg Ala Leu Glu
130 135 140

Lys Ser Thr Leu Val Asn His Ser Gly Asn Asp Asp Ser Glu Asp Asp
145 150 155 160

Glu Ser Ser Glu Asp Glu Ile Ala Tyr Arg Pro Asn Thr Ser Gly Ile
165 170 175

Ile Asn Thr Asn Lys Lys Ser Ser Ala Tyr Arg Val Glu Glu Thr Ala
180 185 190

Lys Gln Glu Asn Gly Glu Glu Asn Asp Asp Asn Glu Thr Gly Val Tyr
195 200 205

Lys Pro Pro Lys Ile Thr Ala Val Leu Pro Pro Gln Gln Thr His Phe
210 215 220

Glu Asp Arg Phe Asp Ala Arg Glu His Lys Asp Arg Ser Asn Lys Ser
225 230 235 240

Asn Lys Ala Glu Lys Arg Lys Gln Lys Gln Arg Glu Arg Asn Ala Arg
245 250 255

Met Asn Val Ile Gly Gly Glu Asp Phe Gly Ile Phe Ser Ser Lys Arg
260 265 270

Lys Leu Glu Asp Ser Thr Ser Arg Arg Gly Ala Lys Lys Thr Arg Ser
275 280 285

Ala Trp Asp Arg Ala Gln Arg Arg Leu
290 295

<210> 53
<211> 300
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 126

<400> 53

Met Ser Lys Val Asp Thr Val Leu Lys Glu Ile Ile Ser Ser Thr Lys
1 5 10 15

Ser Thr Glu Ala Ser Val Lys Glu Leu Ile Ala Phe Val Lys Asp Ser
20 25 30

Ser Ser Gln His Pro Glu Leu Val Arg Asn Leu Leu Ala Lys Ser Asn
35 40 45

Ser Ser Leu Glu Gly Val Ser Leu Leu Gly Leu Lys Asn Glu Ser Leu
50 55 60

Val Ser Tyr Ile Asn Asn Ile Val Leu Val Val Leu Ser His Leu Glu
65 70 75 80

Arg Leu Glu Ser Asp Ser Glu Thr Gly Ser Ser Ala Val Glu Arg Ser
85 90 95

Ile Ile Gln Arg Val Thr Leu Glu Lys Gly Val Lys Pro Leu Glu Lys
100 105 110

Lys Leu Ser Tyr Gln Leu Asp Lys Met Ile Arg Ala Tyr Gly Arg Met

115 120 125

Glu Gln Asp Glu Ile Lys Ala Glu Gln Lys Leu Asn Asp Arg Gly Ser
130 135 140

Gly Glu Asn Asp Glu Asn Asp Glu Asn Asp Ser Glu Glu Asp Ser Glu
145 150 155 160

Glu Asp Ser Glu Asp Asp Ser Glu Asp Asp Glu Leu Ala Tyr Arg Pro
165 170 175

Asp Ala Ser Ser Phe Ala Lys Leu Thr Ser Ala Lys Thr Lys Ser Lys
180 185 190

Pro Thr Ser Ser Ala Val Ser Thr Ser Asn Glu Lys Tyr Arg Pro Pro
195 200 205

Lys Ile Ser Ala Met Ala Pro Pro Thr Ala Val Lys Ser His Asp Leu
210 215 220

Asp Ala Asn Thr Thr Ser Ser Lys Asn Arg Lys Leu Gln Ser Met Glu
225 230 235 240

Glu Tyr Leu Gln Glu Gln Ser Asp Met Pro Met Val Glu Ala Ser Val
245 250 255

Gly Ser Thr Ile Val Glu His Gly Arg Gly Gly Val Lys Thr Gln His
260 265 270

Asp Arg Lys Lys Glu Arg Glu Ile Gln Thr Tyr Glu Glu Asp Asn Phe
275 280 285

Val Arg Leu Pro Thr Ser Gln Thr Lys Lys Ser Phe
290 295 300

<210> 54
<211> 311

<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: AL050003

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 127

<400> 54

Met Ala Ala Leu Gly Val Leu Glu Ser Asp Leu Pro Ser Ala Val Thr
1 5 10 15

Leu Leu Lys Asn Leu Gln Glu Gln Val Met Ala Val Thr Ala Gln Val
20 25 30

Lys Ser Leu Thr Gln Lys Val Gln Ala Gly Ala Tyr Pro Thr Glu Lys
35 40 45

Gly Leu Ser Phe Leu Glu Val Lys Asp Gln Leu Leu Leu Met Tyr Leu
50 55 60

Met Asp Leu Thr His Leu Ile Leu Asp Lys Ala Ser Gly Gly Ser Leu
65 70 75 80

Gln Gly His Asp Ala Val Leu Arg Leu Val Glu Ile Arg Thr Val Leu
85 90 95

Glu Lys Leu Arg Pro Leu Asp Gln Lys Leu Lys Tyr Gln Ile Asp Lys
100 105 110

Leu Ile Lys Thr Ala Val Thr Gly Ser Leu Ser Glu Asn Asp Pro Leu
115 120 125

Arg Phe Lys Pro His Pro Ser Asn Met Met Ser Lys Leu Ser Ser Glu
130 135 140

Asp Glu Glu Glu Asp Glu Ala Glu Asp Asp Gln Ser Glu Ala Ser Gly
145 150 155 160

Lys Lys Ser Val Lys Gly Val Ser Lys Lys Tyr Val Pro Pro Arg Leu
165 170 175

Val Pro Val His Tyr Asp Glu Thr Glu Ala Glu Arg Glu Lys Lys Arg
180 185 190

Leu Glu Arg Ala Lys Arg Arg Ala Leu Ser Ser Ser Val Ile Arg Glu
195 200 205

Leu Lys Glu Gln Tyr Ser Asp Ala Pro Glu Glu Ile Arg Asp Ala Arg
210 215 220

His Pro His Val Thr Arg Gln Ser Gln Glu Asp Gln His Arg Ile Asn
225 230 235 240

Tyr Glu Glu Ser Met Met Val Arg Leu Ser Val Ser Lys Arg Glu Lys
245 250 255

Gly Arg Arg Lys Arg Ala Asn Val Met Ser Ser Gln Leu His Ser Leu
260 265 270

Thr His Phe Ser Asp Ile Ser Ala Leu Thr Gly Gly Thr Val His Leu
275 280 285

Asp Glu Asp Gln Asn Pro Ile Lys Lys Arg Lys Lys Ile Pro Gln Lys
290 295 300

Gly Arg Lys Lys Lys Gly Gln
305 310

<210> 55
<211> 221
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 128

<400> 55

Met Ser Ala Thr Glu Ser Ser Ser Ile Phe Thr Leu Ser His Asn Ser
1 5 10 15

Asn Leu Gln Asp Ile Leu Ala Ala Asn Ala Lys Trp Ala Ser Gln Met
20 25 30

Asn Asn Ile Gln Pro Thr Leu Phe Pro Asp His Asn Ala Lys Gly Gln
35 40 45

Ser Pro His Thr Leu Phe Ile Gly Cys Ser Asp Ser Arg Tyr Asn Glu
50 55 60

Asn Cys Leu Gly Val Leu Pro Gly Glu Val Phe Thr Trp Lys Asn Val
65 70 75 80

Ala Asn Ile Cys His Ser Glu Asp Leu Thr Leu Lys Ala Thr Leu Glu
85 90 95

Phe Ala Ile Ile Cys Leu Lys Val Asn Lys Val Ile Ile Cys Gly His
100 105 110

Thr Asp Cys Gly Gly Ile Lys Thr Cys Leu Thr Asn Gln Arg Glu Ala
115 120 125

Leu Pro Lys Val Asn Cys Ser His Leu Tyr Lys Tyr Leu Asp Asp Ile
130 135 140

Asp Thr Met Tyr His Glu Glu Ser Gln Asn Leu Ile His Leu Lys Thr
145 150 155 160

Gln Arg Glu Lys Ser His Tyr Leu Ser His Cys Asn Val Lys Arg Gln
165 170 175

Phe Asn Arg Ile Ile Glu Asn Pro Thr Val Gln Thr Ala Val Gln Asn
180 185 190

Gly Glu Leu Gln Val Tyr Gly Leu Leu Tyr Asn Val Glu Asp Gly Leu
195 200 205

Leu Gln Thr Val Ser Thr Tyr Thr Lys Val Thr Pro Lys
210 215 220

<210> 56
<211> 281
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 129

<400> 56

Met Gly Arg Glu Asn Ile Leu Lys Tyr Gln Leu Glu His Asp His Glu
1 5 10 15

Ser Asp Leu Val Thr Glu Lys Asp Gln Ser Leu Leu Leu Asp Asn Asn
20 25 30

Asn Asn Leu Asn Gly Met Asn Asn Thr Ile Lys Thr His Pro Val Arg
35 40 45

Val Ser Ser Gly Asn His Asn Asn Phe Pro Phe Thr Leu Ser Ser Glu
50 55 60

Ser Thr Leu Gln Asp Phe Leu Asn Asn Asn Lys Phe Phe Val Asp Ser
65 70 75 80

Ile Lys His Asn His Gly Asn Gln Ile Phe Asp Leu Asn Gly Gln Gly
85 90 95

Gln Ser Pro His Thr Leu Trp Ile Gly Cys Ser Asp Ser Arg Ala Gly
100 105 110

Asp Gln Cys Leu Ala Thr Leu Pro Gly Glu Ile Phe Val His Arg Asn
115 120 125

Ile Ala Asn Ile Val Asn Ala Asn Asp Ile Ser Ser Gln Gly Val Ile
130 135 140

Gln Phe Ala Ile Asp Val Leu Lys Val Lys Lys Ile Ile Val Cys Gly
145 150 155 160

His Thr Asp Cys Gly Gly Ile Trp Ala Ser Leu Ser Lys Lys Lys Ile
165 170 175

Gly Gly Val Leu Asp Leu Trp Leu Asn Pro Val Arg His Ile Arg Ala
180 185 190

Ala Asn Leu Lys Leu Leu Glu Glu Tyr Asn Gln Asp Pro Lys Leu Lys
195 200 205

Ala Lys Lys Leu Ala Glu Leu Asn Val Ile Ser Ser Val Thr Ala Leu
210 215 220

Lys Arg His Pro Ser Ala Ser Val Ala Leu Lys Lys Asn Glu Ile Glu
225 230 235 240

Val Trp Gly Met Leu Tyr Asp Val Ala Thr Gly Tyr Leu Ser Gln Val
245 250 255

Glu Ile Pro Gln Asp Glu Phe Glu Asp Leu Phe His Val His Asp Glu
260 265 270

His Asp Glu Glu Glu Tyr Asn Pro His
275 280

<210> 57

<211> 281
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 130

<400> 57

Met Lys Ala Arg Lys Ser Gln Arg Lys Ala Gly Ser Lys Pro Asn Leu
1 5 10 15

Ile Gln Ser Lys Leu Gln Val Asn Asn Gly Ser Lys Ser Asn Lys Ile
20 25 30

Val Lys Cys Asp Lys Cys Glu Met Ser Tyr Ser Ser Thr Ser Ile Glu
35 40 45

Asp Arg Ala Ile His Glu Lys Tyr His Thr Leu Gln Leu His Gly Arg
50 55 60

Lys Trp Ser Pro Asn Trp Gly Ser Ile Val Tyr Thr Glu Arg Asn His
65 70 75 80

Ser Arg Thr Val His Leu Ser Arg Ser Thr Gly Thr Ile Thr Pro Leu
85 90 95

Asn Ser Ser Pro Leu Lys Lys Ser Ser Pro Ser Ile Thr His Gln Glu
100 105 110

Glu Lys Ile Val Tyr Val Arg Pro Asp Lys Ser Asn Gly Glu Val Arg
115 120 125

Ala Met Thr Glu Ile Met Thr Leu Val Asn Asn Glu Leu Asn Ala Pro
130 135 140

His Asp Glu Asn Val Ile Trp Asn Ser Thr Thr Glu Glu Lys Gly Lys
145 150 155 160

Ala Phe Val Tyr Ile Arg Asn Asp Arg Ala Val Gly Ile Ile Ile Ile
165 170 175

Glu Asn Leu Tyr Gly Gly Asn Gly Lys Thr Ser Ser Arg Gly Arg Trp
180 185 190

Met Val Tyr Asp Ser Arg Arg Leu Val Gln Asn Val Tyr Pro Asp Phe
195 200 205

Lys Ile Gly Ile Ser Arg Ile Trp Val Cys Arg Thr Ala Arg Lys Leu
210 215 220

Gly Ile Ala Thr Lys Leu Ile Asp Val Ala Arg Glu Asn Ile Val Tyr
225 230 235 240

Gly Glu Val Ile Pro Arg Tyr Gln Val Ala Trp Ser Gln Pro Thr Asp
245 250 255

Ser Gly Gly Lys Leu Ala Ser Lys Tyr Asn Gly Ile Met His Lys Ser
260 265 270

Gly Lys Leu Leu Leu Pro Val Tyr Ile
275 280

<210> 58
<211> 260
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 131

<400> 58

Met Gly Ser Ile Asn Ser Gln Lys Ala Gln Lys Ile Gln Ser Ile Leu
1 5 10 15

Ala Leu Pro Ser Asn Phe Lys Lys Ile Thr Cys Ser Thr Cys Asp Met
20 25 30

Thr Tyr Asn Pro His Ile Ser Gln Asp Lys Leu Leu His Asn Lys Tyr
35 40 45

His Thr Asn Phe Ile Asn Gly Ile Pro Trp Asn Tyr Lys Thr Asp Asn
50 55 60

Asp Val Leu Ile Ile Glu Asn Phe Thr Leu Val Glu Thr Pro Lys Leu
65 70 75 80

Asn Ser Thr Gly Lys Ser Leu Lys Leu Thr Lys Thr Arg Gln Thr Phe
85 90 95

Lys Gly Ser Ile Ile Cys Ile Asn Lys Ser Asn Lys Arg His Ile Gln
100 105 110

Lys Val Glu Leu Leu Leu Asn Met Val Asn Gln Glu Leu Asn Ala Ser
115 120 125

Gln Asp Ser Gly Gln Trp Lys Lys Pro Glu Phe Asp Arg Ser Lys Ala
130 135 140

Phe Val Ile Ile Ile Asp Ser Lys Ala Ile Gly Leu Cys Thr Thr Asp
145 150 155 160

Thr Ile Gln Pro Asp Gln Gly Arg Trp Met Ile His Lys Thr Gln Ser
165 170 175

Ile Val Pro Asn Gln Ile Asn Lys Asn Val Val Ile Gly Ile Ser Arg
180 185 190

Ile Trp Ile Ser Arg Lys Trp Arg Gln Tyr Gly Leu Gly Lys Lys Leu
195 200 205

Leu Asn Val Val Leu Lys Asn Ser Ile Tyr Ser Val Gln Leu Leu Lys

210 215 220

Asn Gln Val Ala Phe Ser Gln Pro Ser Phe Ser Gly Gly Met Leu Ala
225 230 235 240

Lys Ser Phe Asn Gly Val Lys His Lys Ser Gly Glu Met Leu Leu Pro
245 250 255

Val Tyr Ile Glu
260

<210> 59
<211> 620
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 132

<400> 59

Met Leu Asn Gly Glu Asp Phe Val Glu His Asn Asp Ile Leu Ser Ser
1 5 10 15

Pro Ala Lys Ser Arg Asn Val Thr Pro Lys Arg Val Asp Pro His Gly
20 25 30

Glu Arg Gln Leu Arg Arg Ile His Ser Ser Lys Lys Asn Leu Leu Glu
35 40 45

Arg Ile Ser Leu Val Gly Asn Glu Arg Lys Asn Thr Ser Pro Asp Pro
50 55 60

Ala Leu Lys Pro Lys Thr Pro Ser Lys Ala Pro Arg Lys Arg Gly Arg
65 70 75 80

Pro Arg Lys Ile Gln Glu Glu Leu Thr Asp Arg Ile Lys Lys Asp Glu
85 90 95

Lys Asp Thr Ile Ser Ser Lys Lys Lys Arg Lys Leu Asp Lys Asp Thr
100 105 110

Ser Gly Asn Val Asn Glu Glu Ser Lys Thr Ser Asn Asn Lys Gln Val
115 120 125

Met Glu Lys Thr Gly Ile Lys Glu Lys Arg Glu Arg Glu Lys Ile Gln
130 135 140

Val Ala Thr Thr Thr Tyr Glu Asp Asn Val Thr Pro Gln Thr Asp Asp
145 150 155 160

Asn Phe Val Ser Asn Ser Pro Glu Pro Pro Glu Pro Ala Thr Pro Ser
165 170 175

Lys Lys Ser Leu Thr Thr Asn His Asp Phe Thr Ser Pro Leu Lys Gln
180 185 190

Ile Ile Met Asn Asn Leu Lys Glu Tyr Lys Asp Ser Thr Ser Pro Gly
195 200 205

Lys Leu Thr Leu Ser Arg Asn Phe Thr Pro Thr Pro Val Pro Lys Asn
210 215 220

Lys Lys Leu Tyr Gln Thr Ser Glu Thr Lys Ser Ala Ser Ser Phe Leu
225 230 235 240

Asp Thr Phe Glu Gly Tyr Phe Asp Gln Arg Lys Ile Val Arg Thr Asn
245 250 255

Ala Lys Ser Arg His Thr Met Ser Met Ala Pro Asp Val Thr Arg Glu
260 265 270

Glu Phe Ser Leu Val Ser Asn Phe Phe Asn Glu Asn Phe Gln Lys Arg
275 280 285

Pro Arg Gln Lys Leu Phe Glu Ile Gln Lys Lys Met Phe Pro Gln Tyr
290 295 300

Trp Phe Glu Leu Thr Gln Gly Phe Ser Leu Leu Phe Tyr Gly Val Gly
305 310 315 320

Ser Lys Arg Asn Phe Leu Glu Glu Phe Ala Ile Asp Tyr Leu Ser Pro
325 330 335

Lys Ile Ala Tyr Ser Gln Leu Ala Tyr Glu Asn Glu Leu Gln Gln Asn
340 345 350

Lys Pro Val Asn Ser Ile Pro Cys Leu Ile Leu Asn Gly Tyr Asn Pro
355 360 365

Ser Cys Asn Tyr Arg Asp Val Phe Lys Glu Ile Thr Asp Leu Leu Val
370 375 380

Pro Ala Glu Leu Thr Arg Ser Glu Thr Lys Tyr Trp Gly Asn His Val
385 390 395 400

Ile Leu Gln Ile Gln Lys Met Ile Asp Phe Tyr Lys Asn Gln Pro Leu
405 410 415

Asp Ile Lys Leu Ile Leu Val Val His Asn Leu Asp Gly Pro Ser Ile
420 425 430

Arg Lys Asn Thr Phe Gln Thr Met Leu Ser Phe Leu Ser Val Ile Arg
435 440 445

Gln Ile Ala Ile Val Ala Ser Thr Asp His Ile Tyr Ala Pro Leu Leu
450 455 460

Trp Asp Asn Met Lys Ala Gln Asn Tyr Asn Phe Val Phe His Asp Ile
465 470 475 480

Ser Asn Phe Glu Pro Ser Thr Val Glu Ser Thr Phe Gln Asp Val Met

485 490 495

Lys Met Gly Lys Ser Asp Thr Ser Ser Gly Ala Glu Gly Ala Lys Tyr
500 505 510

Val Leu Gln Ser Leu Thr Val Asn Ser Lys Lys Met Tyr Lys Leu Leu
515 520 525

Ile Glu Thr Gln Met Gln Asn Met Gly Asn Leu Ser Ala Asn Thr Gly
530 535 540

Pro Lys Arg Gly Thr Gln Arg Thr Gly Val Glu Leu Lys Leu Phe Asn
545 550 555 560

His Leu Cys Ala Ala Asp Phe Ile Ala Ser Asn Glu Ile Ala Leu Arg
565 570 575

Ser Met Leu Arg Glu Phe Ile Glu His Lys Met Ala Asn Ile Thr Lys
580 585 590

Asn Asn Ser Gly Met Glu Ile Ile Trp Val Pro Tyr Thr Tyr Ala Glu
595 600 605

Leu Glu Lys Leu Leu Lys Thr Val Leu Asn Thr Leu
610 615 620

<210> 60
<211> 600
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 133

<400> 60

Met Ser His Ser Asn Ala Leu Pro Asn Ser Pro Phe Arg Ser Pro Lys
1 5 10 15

Lys Gln Arg Met Glu Val Ile Gly Pro Leu Asn Ala Ser Arg Phe Ser
20 25 30

Phe Ser Pro Val Lys Thr Pro Pro His Gly Arg Ala Gly Leu Ser Ser
35 40 45

Pro Glu Lys Arg Leu Val Lys Asp Leu Asp Lys Ala Arg Lys Arg Ala
50 55 60

Asn Asn Ser Leu Tyr Asn Arg Leu Met Asp Glu Tyr Leu Asp Thr Asp
65 70 75 80

Asp Tyr Leu Asp Glu Gln Asp Arg Ile Leu Ala Asp Arg Ile Ile Lys
85 90 95

Gln Ser Arg Gly Glu Pro Asp Glu Val Asn Tyr Gly Ser Asp Val Glu
100 105 110

Leu Glu Ile Asp Leu Thr Gln Gln Arg Arg Thr Arg Arg Arg Glu Lys
115 120 125

Lys Val Val Tyr Ser Ser Asp Ser Ser Asn Glu Tyr Glu Asp Thr Gly
130 135 140

Met Pro Glu Glu Ser Ser Ser Glu Glu Glu Glu Ala Asp Asp Asp Asp
145 150 155 160

Gly Asn Val Glu Phe Val Tyr Gly Pro Pro Lys Glu Arg Lys Thr Ser
165 170 175

Leu Ser Ser Ser Pro Pro Thr Val Lys Pro Thr Val Arg Arg Thr Lys
180 185 190

Arg Gly Arg Pro Ser Lys Ser Glu Leu Val Leu Gly Gln Ile Lys Ser
195 200 205

Ile Phe His Gln Asp Asp Val Leu Phe Ser Thr Asp Arg Lys Thr Phe
210 215 220

Thr Pro Thr Lys Pro Thr Ala Ala Lys Lys Pro Val Ser Asn Tyr Leu
225 230 235 240

Thr Ser Ile Phe Asp Gln Asn Phe Asp Arg Ser Lys Val Pro Ser Leu
245 250 255

Ser Gly Ile Pro Lys Ser Thr Asn Thr His Glu Glu Lys Lys Thr Phe
260 265 270

Val Pro Leu Pro Ile Pro Thr Leu Asp Ala Asp Gly Asn Ile Thr Asp
275 280 285

Lys Glu Tyr Ile Ser Lys Tyr Phe Asp Gly Val Asp Pro Ala Lys Phe
290 295 300

Lys Glu Gly Arg Phe Val Asp Glu Lys Val Phe Tyr Leu Glu Gly Pro
305 310 315 320

Glu Gly Tyr Phe Glu Gln Gln Thr Thr Arg Val Lys Gln Ser Gly Asn
325 330 335

Ser Leu Thr Ala Leu Ala Pro Gln Ile Glu Tyr Lys Asp Phe Ala Arg
340 345 350

Leu Val Lys Leu Gly Asp Asn Leu Ser Phe Gln Arg Lys Arg His Leu
355 360 365

Phe Glu Leu His Lys Tyr Ile Tyr His Gln Trp Cys Phe Glu Met Ser
370 375 380

Gln Gly Phe Asn Leu Asn Phe Tyr Gly Val Gly Ser Lys Ile Asp Leu
385 390 395 400

Leu Arg Asp Phe Ala Thr Asn Tyr Phe Gly Ile Trp Trp Glu Asn Val

405 410 415

Val His Ala Asp Leu Pro Lys Val Leu Val Val Asn Gly Phe Asn Pro
420 425 430

Ser Ile Asn Ile Lys Lys Leu Ile Leu Glu Ile Ala Ser Ile Leu Leu
435 440 445

Pro Asn Glu Leu Tyr Pro Lys His Ile Ala Gly Thr Val Pro Phe Val
450 455 460

Val Asp Tyr Leu Asn Asn His Arg Leu Pro Cys Gly Ser Ile Gly Phe
465 470 475 480

His Lys Pro Lys Ile Leu Leu Ile Ile His Asn Leu Asp Gly Glu Val
485 490 495

Phe Arg Val Asp Lys Thr Gln Thr Leu Leu Ser Gln Leu Met Thr Leu
500 505 510

Pro Glu Val Trp Ala Met Ser Ser Thr Asp His Ile Asn Ala Ser Leu
515 520 525

Leu Trp Asp Leu Ser Lys Val Lys Asn Leu Asn Phe Ile Trp His Asn
530 535 540

Leu Thr Thr Tyr Ala Thr Tyr Gln Arg Glu Thr Ser Phe Arg Asp Val
545 550 555 560

Ile Ser Leu Gly Lys Ser Lys Lys Phe Val Gly Gly Leu Gly Ala Lys
565 570 575

Tyr Val Leu Arg Ser Leu Thr Asp Asn His Arg Asn Leu Tyr Arg Glu
580 585 590

Leu Leu Ile Ala Gln Leu Asp Lys
595 600

<210> 61
<211> 577
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: Q13416

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 134

<400> 61

Met Ser Lys Pro Glu Leu Lys Glu Asp Lys Met Leu Glu Val His Phe
1 5 10 15

Val Gly Asp Asp Asp Val Leu Asn His Ile Leu Asp Arg Glu Gly Gly
20 25 30

Ala Lys Leu Lys Lys Glu Arg Ala Gln Leu Leu Val Asn Pro Lys Lys
35 40 45

Ile Ile Lys Lys Pro Glu Tyr Asp Leu Glu Glu Asp Asp Gln Glu Val
50 55 60

Leu Lys Asp Gln Asn Tyr Val Glu Ile Met Gly Arg Asp Val Gln Glu
65 70 75 80

Ser Leu Lys Asn Gly Ser Ala Thr Gly Gly Gly Asn Lys Val Tyr Ser
85 90 95

Phe Gln Asn Arg Lys His Ser Glu Lys Met Ala Lys Leu Ala Ser Glu
100 105 110

Leu Ala Lys Thr Pro Gln Lys Ser Val Ser Phe Ser Leu Lys Asn Asp
115 120 125

Pro Glu Ile Thr Ile Asn Val Pro Gln Ser Ser Lys Gly His Ser Ala
130 135 140

Ser Asp Lys Val Gln Pro Lys Asn Asn Asp Lys Ser Glu Phe Leu Ser
145 150 155 160

Thr Ala Pro Arg Ser Leu Arg Lys Arg Leu Ile Val Pro Arg Ser His
165 170 175

Ser Asp Ser Glu Ser Glu Tyr Ser Ala Ser Asn Ser Glu Asp Asp Glu
180 185 190

Gly Val Ala Gln Glu His Glu Glu Asp Thr Asn Ala Val Ile Phe Ser
195 200 205

Gln Lys Ile Gln Ala Gln Asn Arg Val Val Ser Ala Pro Val Gly Lys
210 215 220

Glu Thr Pro Ser Lys Arg Met Lys Arg Asp Lys Thr Ser Asp Leu Val
225 230 235 240

Glu Glu Tyr Phe Glu Ala His Ser Ser Ser Lys Val Leu Thr Ser Asp
245 250 255

Arg Thr Leu Gln Lys Leu Lys Arg Ala Lys Leu Asp Gln Gln Thr Leu
260 265 270

Arg Asn Leu Leu Ser Lys Val Ser Pro Ser Phe Ser Ala Glu Leu Lys
275 280 285

Gln Leu Asn Gln Gln Tyr Glu Lys Leu Phe His Lys Trp Met Leu Gln
290 295 300

Leu His Leu Gly Phe Asn Ile Val Leu Tyr Gly Leu Gly Ser Lys Arg
305 310 315 320

Asp Leu Leu Glu Arg Phe Arg Thr Thr Met Leu Gln Asp Ser Ile His

325 330 335

Val Val Ile Asn Gly Phe Phe Pro Gly Ile Ser Val Lys Ser Val Leu
340 345 350

Asn Ser Ile Thr Glu Glu Val Leu Asp His Met Gly Thr Phe Arg Ser
355 360 365

Ile Leu Asp Gln Leu Asp Trp Ile Val Asn Lys Phe Lys Glu Asp Ser
370 375 380

Ser Leu Glu Leu Phe Leu Leu Ile His Asn Leu Asp Ser Gln Met Leu
385 390 395 400

Arg Gly Glu Lys Ser Gln Gln Ile Ile Gly Gln Leu Ser Ser Leu His
405 410 415

Asn Ile Tyr Leu Ile Ala Ser Ile Asp His Leu Asn Ala Pro Leu Met
420 425 430

Trp Asp His Ala Lys Gln Ser Leu Phe Asn Trp Leu Trp Tyr Glu Thr
435 440 445

Thr Thr Tyr Ser Pro Tyr Thr Glu Glu Thr Ser Tyr Glu Asn Ser Leu
450 455 460

Leu Val Lys Gln Ser Gly Ser Leu Pro Leu Ser Ser Leu Thr His Val
465 470 475 480

Leu Arg Ser Leu Thr Pro Asn Ala Arg Gly Ile Phe Arg Leu Leu Ile
485 490 495

Lys Tyr Gln Leu Asp Asn Gln Asp Asn Pro Ser Tyr Ile Gly Leu Ser
500 505 510

Phe Gln Asp Phe Tyr Gln Gln Cys Arg Glu Ala Phe Leu Val Asn Ser
515 520 525

Asp Leu Thr Leu Arg Ala Gln Leu Thr Glu Phe Arg Asp His Lys Leu
530 535 540

Ile Arg Thr Lys Lys Gly Thr Asp Gly Val Glu Tyr Leu Leu Ile Pro
545 550 555 560

Val Asp Asn Gly Thr Leu Thr Asp Phe Leu Glu Lys Glu Glu Glu Glu
565 570 575

Ala

<210> 62
<211> 385
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 135

<400> 62

Met Ser Ser Val Asn Ala Asn Gly Gly Tyr Thr Lys Pro Gln Lys Tyr
1 5 10 15

Val Pro Gly Pro Gly Asp Pro Glu Leu Pro Pro Gln Leu Ser Glu Phe
20 25 30

Lys Asp Lys Thr Ser Asp Glu Ile Leu Lys Glu Met Asn Arg Met Pro
35 40 45

Phe Phe Met Thr Lys Leu Asp Glu Thr Asp Gly Ala Gly Gly Glu Asn
50 55 60

Val Glu Leu Glu Ala Leu Lys Ala Leu Ala Tyr Glu Gly Glu Pro His
65 70 75 80

Glu Ile Ala Glu Asn Phe Lys Lys Gln Gly Asn Glu Leu Tyr Lys Ala
85 90 95

Lys Arg Phe Lys Asp Ala Arg Glu Leu Tyr Ser Lys Gly Leu Ala Val
100 105 110

Glu Cys Glu Asp Lys Ser Ile Asn Glu Ser Leu Tyr Ala Asn Arg Ala
115 120 125

Ala Cys Glu Leu Glu Leu Lys Asn Tyr Arg Arg Cys Ile Glu Asp Cys
130 135 140

Ser Lys Ala Leu Thr Ile Asn Pro Lys Asn Val Lys Cys Tyr Tyr Arg
145 150 155 160

Thr Ser Lys Ala Phe Phe Gln Leu Asn Lys Leu Glu Glu Ala Lys Ser
165 170 175

Ala Ala Thr Phe Ala Asn Gln Arg Ile Asp Pro Glu Asn Lys Ser Ile
180 185 190

Leu Asn Met Leu Ser Val Ile Asp Arg Lys Glu Gln Glu Leu Lys Ala
195 200 205

Lys Glu Glu Lys Gln Gln Arg Glu Ala Gln Glu Arg Glu Asn Lys Lys
210 215 220

Ile Met Leu Glu Ser Ala Met Thr Leu Arg Asn Ile Thr Asn Ile Lys
225 230 235 240

Thr His Ser Pro Val Glu Leu Leu Asn Glu Gly Lys Ile Arg Leu Glu
245 250 255

Asp Pro Met Asp Phe Glu Ser Gln Leu Ile Tyr Pro Ala Leu Ile Met
260 265 270

Tyr Pro Thr Gln Asp Glu Phe Asp Phe Val Gly Glu Val Ser Glu Leu

275 280 285

Thr Thr Val Gln Glu Leu Val Asp Leu Val Leu Glu Gly Pro Gln Glu
290 295 300

Arg Phe Lys Lys Glu Gly Lys Glu Asn Phe Thr Pro Lys Lys Val Leu
305 310 315 320

Val Phe Met Glu Thr Lys Ala Gly Gly Leu Ile Lys Ala Gly Lys Lys
325 330 335

Leu Thr Phe His Asp Ile Leu Lys Lys Glu Ser Pro Asp Val Pro Leu
340 345 350

Phe Asp Asn Ala Leu Lys Ile Tyr Ile Val Pro Lys Val Glu Ser Glu
355 360 365

Gly Trp Ile Ser Lys Trp Asp Lys Gln Lys Ala Leu Glu Arg Arg Ser
370 375 380

Val
385

<210> 63
<211> 300
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 136

<400> 63

Met Ser Lys Ile Glu Pro Val Thr Glu Lys Glu Glu Glu Tyr Val Ser
1 5 10 15

Glu Trp Asp Arg Arg Arg Tyr Val Pro Lys Ala Gly Glu Pro Glu Leu
20 25 30

Pro Pro Gln Leu Ser Glu Phe Ser Asn Lys Thr Thr Asp Glu Val Ile
35 40 45

Glu Glu Leu Asn Arg Leu Pro Phe Phe Met Thr Leu Asp Glu Thr Asp
50 55 60

Gly Asp Gly Gly Glu Asn Val Asn Leu Glu Ala Leu Lys Ser Leu Ala
65 70 75 80

Tyr Glu Gly Asp Pro Asp Glu Ile Ala Ser Asn Phe Lys Asn Gln Gly
85 90 95

Asn Asn Cys Tyr Lys Phe Lys Lys Tyr Lys Asp Ala Ile Ile Phe Tyr
100 105 110

Thr Lys Gly Leu Glu Val Asn Cys Asp Val Asp Ala Ile Asn Ser Ala
115 120 125

Leu Tyr Leu Asn Arg Ala Ala Cys Asn Leu Glu Leu Lys Asn Tyr Arg
130 135 140

Arg Cys Ile Glu Asp Cys Lys Lys Val Leu Met Leu Asp Glu Lys Asn
145 150 155 160

Ile Lys Ala Cys Phe Arg Ser Gly Lys Ala Phe Phe Ala Ile Glu Lys
165 170 175

Tyr Asp Glu Ala Ile Lys Val Leu Glu Tyr Gly Leu Asn Ile Glu Pro
180 185 190

Glu Asn Lys Asp Leu Gln Lys Leu Leu Gln Gln Val Gln Lys Arg Gln
195 200 205

Glu Thr Leu Ala Gln Ile Lys Ala Lys Lys Ala Gln Glu Glu Glu Gln
210 215 220

Glu Arg Leu Lys Asn Ile Val Leu Glu Asn Ser Ile Lys Leu Arg His
225 230 235 240

Ile Glu Ile Val Lys Ser Ser Ser Pro Pro Glu Val Leu Lys Thr Ala
245 250 255

Lys Ile Arg Leu Glu Asp Pro Lys Asp Tyr Gln Ser Gln Leu Ile Phe
260 265 270

Pro Ala Met Ile Leu Tyr Pro Thr Thr Asp Glu Phe Asp Phe Ile Ala
275 280 285

Glu Ile Ser Glu Leu Thr Thr Pro Leu Glu Leu Leu
290 295 300

<210> 64
<211> 356
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: NP_004614

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 137

<400> 64

Met Glu Gln Pro Gly Gln Asp Pro Thr Ser Asp Asp Val Met Asp Ser
1 5 10 15

Phe Leu Glu Lys Phe Gln Ser Gln Pro Tyr Arg Gly Gly Phe His Glu
20 25 30

Asp Gln Trp Glu Lys Glu Phe Glu Lys Val Pro Leu Phe Met Ser Arg
35 40 45

Ala Pro Ser Glu Ile Asp Pro Arg Glu Asn Pro Asp Leu Ala Cys Leu
50 55 60

Gln Ser Ile Ile Phe Asp Glu Glu Arg Ser Pro Glu Glu Gln Ala Lys
65 70 75 80

Thr Tyr Lys Asp Glu Gly Asn Asp Tyr Phe Lys Glu Lys Asp Tyr Lys
85 90 95

Lys Ala Val Ile Ser Tyr Thr Glu Gly Leu Lys Lys Lys Cys Ala Asp
100 105 110

Pro Asp Leu Asn Ala Val Leu Tyr Thr Asn Arg Ala Ala Ala Gln Tyr
115 120 125

Tyr Leu Gly Asn Phe Arg Ser Ala Leu Asn Asp Val Thr Ala Ala Arg
130 135 140

Lys Leu Lys Pro Cys His Leu Lys Ala Ile Ile Arg Gly Ala Leu Cys
145 150 155 160

His Leu Glu Leu Ile His Phe Ala Glu Ala Val Asn Trp Cys Asp Glu
165 170 175

Gly Leu Gln Ile Asp Ala Lys Glu Lys Lys Leu Leu Glu Met Arg Ala
180 185 190

Lys Ala Asp Lys Leu Lys Arg Ile Glu Gln Arg Asp Val Arg Lys Ala
195 200 205

Asn Leu Lys Glu Lys Lys Glu Arg Asn Gln Asn Glu Ala Leu Leu Gln
210 215 220

Ala Ile Lys Ala Arg Asn Ile Arg Leu Ser Glu Ala Ala Cys Glu Asp
225 230 235 240

Glu Asp Ser Ala Ser Glu Gly Leu Gly Glu Leu Phe Leu Asp Gly Leu

245 250 255

Ser Thr Glu Asn Pro His Gly Ala Arg Leu Ser Leu Asp Gly Gln Gly
260 265 270

Arg Leu Ser Trp Pro Val Leu Phe Leu Tyr Pro Glu Tyr Ala Gln Ser
275 280 285

Asp Phe Ile Ser Ala Phe His Glu Asp Ser Arg Phe Ile Asp His Leu
290 295 300

Met Val Met Phe Gly Glu Thr Pro Ser Trp Asp Leu Glu Gln Lys Tyr
305 310 315 320

Cys Leu Ile Ile Trp Arg Ser Thr Leu Arg Met Arg Thr Gly Gln Asn
325 330 335

Tyr Thr Gly Cys Leu Pro Arg Ala Pro Cys Tyr Arg Phe Tyr Ser Thr
340 345 350

Arg Gly Thr Leu
355

<210> 65
<211> 167
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 138

<400> 65

Met Ser Thr Ile Pro Ser Glu Ile Ile Asn Trp Thr Ile Leu Asn Glu
1 5 10 15

Ile Ile Ser Met Asp Asp Asp Asp Ser Asp Phe Ser Lys Gly Leu Ile
20 25 30

Ile Gln Phe Ile Asp Gln Ala Gln Thr Thr Phe Ala Gln Met Gln Arg
35 40 45

Gln Leu Asp Gly Glu Lys Asn Leu Thr Glu Leu Asp Asn Leu Gly His
50 55 60

Phe Leu Lys Gly Ser Ser Ala Ala Leu Gly Leu Gln Arg Ile Ala Trp
65 70 75 80

Val Cys Glu Arg Ile Gln Asn Leu Gly Arg Lys Met Glu His Phe Phe
85 90 95

Pro Asn Lys Thr Glu Leu Val Asn Thr Leu Ser Asp Lys Ser Ile Ile
100 105 110

Asn Gly Ile Asn Ile Asp Glu Asp Asp Glu Glu Ile Lys Ile Gln Val
115 120 125

Asp Asp Lys Asp Glu Asn Ser Ile Tyr Leu Ile Leu Ile Ala Lys Ala
130 135 140

Leu Asn Gln Ser Arg Leu Glu Phe Lys Leu Ala Arg Ile Glu Leu Ser
145 150 155 160

Lys Tyr Tyr Asn Thr Asn Leu
165

<210> 66
<211> 184
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 139

<400> 66

Met Ser Glu Asp Lys Leu Gln Lys Leu Gln Asp Ser Gly Leu Val Asp
1 5 10 15

Trp Ala Val Phe Ser Glu Ile Val Thr Met Asp Glu Asp Glu Glu Gly
20 25 30

Phe Ser Lys Ser Leu Val Glu Val Phe Val Ser Gln Val Glu Glu Thr
35 40 45

Phe Glu Glu Ile Asp Lys Tyr Leu Lys Glu Lys Asn Leu Glu Lys Leu
50 55 60

Ser Ser Ser Gly His Phe Leu Lys Gly Ser Ala Ala Ala Leu Gly Leu
65 70 75 80

Thr Lys Ile Ser Asn Gln Cys Glu Arg Ile Gln Asn Tyr Gly His Lys
85 90 95

Ile Asn Phe Asp Asn Phe Gln Leu Glu Asp Ile Lys Thr Lys Gly Asp
100 105 110

Ser Ala Val Ser Ala Glu Asn Val Ala Val Asn Asp Gly Glu Thr Asn
115 120 125

Pro Glu Asn Gly Ser Asn Gly Asn Glu Thr Ser Asn Asn Lys Thr Asn
130 135 140

Thr Ser Asn Ile Pro Asp Glu Ser Ser Asp Asp Phe Trp Ile Ala Leu
145 150 155 160

Ile Glu Asp Ala Leu Ala Lys Ala Arg Asp Gly Phe Asp Gln Ser Arg
165 170 175

Arg Ala Leu Asp Glu Tyr Tyr Glu
180

<210> 67

<211> 240
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: CAA78727

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 140

<400> 67

Thr Asp Lys Leu Ser Asn Met Gln Lys Asp Leu Glu Asn Ser Asn Ala
1 5 10 15

Lys Leu Gln Glu Lys Ile Gln Glu Leu Lys Ala Asn Glu His Gln Leu
20 25 30

Ile Thr Leu Lys Lys Asp Val Asn Glu Thr Gln Lys Lys Val Ser Glu
35 40 45

Met Glu Gln Leu Lys Lys Gln Ile Lys Asp Gln Ser Leu Thr Leu Ser
50 55 60

Lys Leu Glu Ile Glu Asn Leu Asn Leu Ala Gln Glu Leu His Glu Asn
65 70 75 80

Leu Glu Glu Met Lys Ser Val Met Lys Glu Arg Asp Asn Leu Arg Arg
85 90 95

Val Glu Glu Thr Leu Lys Leu Glu Arg Asp Gln Leu Lys Glu Ser Leu
100 105 110

Gln Glu Thr Lys Ala Arg Asp Leu Glu Ile Gln Gln Glu Leu Lys Thr
115 120 125

Ala Arg Met Leu Ser Lys Glu His Lys Glu Thr Val Asp Lys Leu Arg

130 135 140

Glu Lys Ile Ser Glu Lys Thr Ile Gln Ile Ser Asp Ile Gln Lys Asp
145 150 155 160

Leu Asp Lys Ser Lys Asp Glu Leu Gln Lys Lys Ile Gln Glu Leu Gln
165 170 175

Lys Lys Glu Leu Gln Leu Leu Arg Val Lys Glu Asp Val Asn Met Ser
180 185 190

His Lys Lys Ile Asn Glu Met Glu Gln Leu Lys Lys Gln Phe Glu Pro
195 200 205

Asn Tyr Leu Cys Lys Cys Glu Met Asp Asn Phe Gln Leu Thr Lys Lys
210 215 220

Leu His Glu Ser Leu Glu Glu Ile Arg Ile Val Ala Lys Glu Arg Asp
225 230 235 240

<210> 68
<211> 93
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 141

<400> 68

Met Ser Phe Leu Gly Phe Gly Gly Gly Gln Pro Gln Leu Ser Ser Gln
1 5 10 15

Gln Lys Ile Gln Ala Ala Glu Ala Glu Leu Asp Leu Val Thr Asp Met
20 25 30

Phe Asn Lys Leu Val Asn Asn Cys Tyr Lys Lys Cys Ile Asn Thr Ser
35 40 45

Tyr Ser Glu Gly Glu Leu Asn Lys Asn Glu Ser Ser Cys Leu Asp Arg
50 55 60

Cys Val Ala Lys Tyr Phe Glu Thr Asn Val Gln Val Gly Glu Asn Met
65 70 75 80

Gln Lys Met Gly Gln Ser Phe Asn Ala Ala Gly Lys Phe
85 90

<210> 69
<211> 91
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 142

<400> 69

Met Phe Gly Leu Gly Gly Thr Thr Pro Gln Ile Ser Ser Gln Gln Lys
1 5 10 15

Leu Gln Ala Ala Glu Ala Glu Leu Asp Met Val Thr Gly Met Phe Asn
20 25 30

Ala Leu Val Ser Gln Cys His Thr Lys Cys Ile Asn Lys Ser Tyr Asn
35 40 45

Glu Ala Asp Ile Ser Lys Gln Glu Ser Leu Cys Leu Asp Arg Cys Val
50 55 60

Ala Lys Tyr Phe Glu Thr Asn Val Gln Val Gly Glu Asn Met Gln Lys
65 70 75 80

Leu Gly Gln Ser Gly Gln Phe Met Gly Arg Arg
85 90

<210> 70
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> human genbank accession #: NP_036588

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 143

<400> 70

Met Asp Pro Leu Arg Ala Gln Gln Leu Ala Ala Glu Leu Glu Val Glu
1 5 10 15

Met Met Ala Asp Met Tyr Asn Arg Met Thr Ser Ala Cys His Arg Lys
20 25 30

Cys Val Pro Pro His Tyr Lys Glu Ala Glu Leu Ser Lys Gly Glu Ser
35 40 45

Val Cys Leu Asp Arg Cys Val Ser Lys Tyr Leu Asp Ile His Glu Arg
50 55 60

Met Gly Lys Lys Leu Thr Glu Leu Ser Met Gln Asp Glu Glu Leu Met
65 70 75 80

Lys Arg Val Gln Gln Ser Ser Gly Pro Ala
85 90

<210> 71
<211> 600
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 144

<400> 71

Met Thr Thr Glu Asp Pro Asp Ser Asn His Leu Ser Ser Glu Thr Gly
1 5 10 15

Ile Lys Leu Ala Leu Asp Pro Asn Leu Ile Thr Leu Ala Leu Ser Ser
20 25 30

Asn Pro Asn Ser Ser Leu His Ser Pro Thr Ser Asp Glu Pro Val Pro
35 40 45

Glu Ser Ala Gly Lys Ala Asp Thr Ser Ile Arg Leu Glu Gly Asp Glu
50 55 60

Leu Glu Asn Lys Thr Lys Lys Asp Asn Asp Lys Asn Leu Lys Phe Leu
65 70 75 80

Lys Asn Lys Asp Ser Leu Val Ser Asn Pro His Glu Ile Tyr Gly Ser
85 90 95

Met Pro Leu Glu Gln Leu Ile Pro Ile Ile Leu Arg Gln Arg Gly Pro
100 105 110

Gly Phe Lys Phe Val Asp Leu Asn Glu Lys Glu Leu Gln Asn Glu Ile
115 120 125

Lys Gln Leu Gly Ser Asp Ser Ser Asp Gly His Asn Ser Glu Lys Lys
130 135 140

Asp Thr Asp Gly Ala Asp Glu Asn Val Gln Ile Gly Glu Asp Phe Met
145 150 155 160

Glu Val Asp Tyr Glu Asp Lys Asp Asn Pro Val Asp Ser Arg Asn Glu
165 170 175

Thr Asp His Lys Thr Asn Glu Asn Gly Glu Thr Asp Asp Asn Ile Glu
180 185 190

Thr Val Met Thr Gln Glu Gln Phe Val Lys Arg Arg Arg Asp Met Leu
195 200 205

Glu His Ile Asn Leu Ala Met Asn Glu Ser Ser Leu Ala Leu Glu Phe
210 215 220

Val Ser Leu Leu Leu Ser Ser Val Lys Glu Ser Thr Gly Met Ser Ser
225 230 235 240

Met Ser Pro Phe Leu Arg Lys Val Val Lys Pro Ser Ser Leu Asn Ser
245 250 255

Asp Lys Ile Pro Tyr Val Ala Pro Thr Lys Lys Glu Tyr Ile Glu Leu
260 265 270

Asp Ile Leu Asn Lys Gly Trp Lys Leu Gln Ser Leu Asn Glu Ser Lys
275 280 285

Asp Leu Leu Arg Ala Ser Phe Asn Lys Leu Ser Ser Ile Leu Gln Asn
290 295 300

Glu His Asp Tyr Trp Asn Lys Ile Met Gln Ser Ile Ser Asn Lys Asp
305 310 315 320

Val Ile Phe Lys Ile Arg Asp Arg Thr Ser Gly Gln Lys Leu Leu Ala
325 330 335

Ile Lys Tyr Gly Tyr Glu Asp Ser Gly Ser Thr Tyr Lys His Asp Arg
340 345 350

Gly Ile Ala Asn Ile Arg Asn Asn Ile Glu Ser Gln Asn Leu Asp Leu
355 360 365

Ile Pro His Ser Ser Ser Val Phe Lys Gly Thr Asp Phe Val His Ser
370 375 380

Val Lys Lys Phe Leu Arg Val Arg Ile Phe Thr Lys Ile Glu Ser Glu
385 390 395 400

Asp Asp Tyr Ile Leu Ser Gly Glu Ser Val Met Asp Arg Asp Ser Glu
405 410 415

Ser Glu Glu Ala Glu Thr Lys Asp Ile Arg Lys Gln Ile Gln Leu Leu
420 425 430

Lys Lys Ile Ile Phe Glu Lys Glu Leu Met Tyr Gln Ile Lys Lys Glu
435 440 445

Cys Ala Leu Leu Ile Ser Tyr Gly Val Ser Ile Glu Asn Glu Asn Lys
450 455 460

Val Ile Ile Glu Leu Pro Asn Glu Lys Phe Glu Ile Glu Leu Leu Ser
465 470 475 480

Leu Asp Asp Asp Ser Ile Val Asn His Glu Gln Asp Leu Pro Lys Ile
485 490 495

Asn Asp Lys Arg Ala Asn Leu Met Leu Val Met Leu Arg Leu Leu Leu
500 505 510

Val Val Ile Phe Lys Lys Thr Leu Arg Ser Arg Ile Ser Ser Pro His
515 520 525

Gly Leu Ile Asn Leu Asn Val Asp Asp Asp Ile Leu Ile Ile Arg Pro
530 535 540

Ile Leu Gly Lys Val Arg Phe Ala Asn Tyr Lys Leu Leu Leu Lys Lys
545 550 555 560

Ile Ile Lys Asp Tyr Val Leu Asp Ile Val Pro Gly Ser Ser Ile Thr
565 570 575

Glu Thr Glu Val Glu Arg Glu Gln Pro Gln Glu Asn Lys Asn Ile Asp

580 585 590

Asp Glu Asn Ile Thr Lys Leu Asn
595 600

<210> 72
<211> 587
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 145

<400> 72

Met Val Glu Lys Gln Phe Asn Ile Asp Leu Glu Leu Asn Asp Thr Gly
1 5 10 15

His Ile Asp Pro Phe Leu Gln Asp Glu Tyr Val Cys Phe Leu Thr Leu
20 25 30

Leu Val Phe Leu Val Leu Phe Phe Ser Leu Leu Thr Leu Pro Arg Asp
35 40 45

Lys Leu Lys Leu Glu Glu Leu Ile Pro Arg Ile Phe Glu Arg Lys Ser
50 55 60

Phe Leu Asn Val Thr Glu Asp Ser Leu Arg Lys Glu Ile Asp Asn Ser
65 70 75 80

Leu Lys Ile Ser Glu Glu Asp Ala Leu Asp Thr Glu Glu Ser Arg Glu
85 90 95

Asp Thr Val Glu Ala Asp Gln Gln Glu Val Phe Asn Lys His Lys Phe
100 105 110

Glu Leu Ser Lys Asn Ile Asn Asn Ala Leu Asn Glu Thr Gln Leu Ser
115 120 125

Leu Asp Phe Val Ser Leu Leu Ile Ser Ser Val Lys Pro Ser Leu Ala
130 135 140

Lys Ser Thr Ile Ser Pro His Leu Ser Lys Phe Val Lys Pro Thr Ser
145 150 155 160

Leu Asn Ser Asp Arg Leu Gly Gln Asp Ser Asn Asp Asn Gln Glu Ser
165 170 175

Lys Ala Thr Asp Ser Phe Gly Gln Gly Trp Lys Leu Glu Ser Leu Gly
180 185 190

Lys Ile Thr Asp Leu Phe Arg Glu Ala Ser Thr Asn Leu Asn Asp Gln
195 200 205

Val Ile Lys Glu Arg Arg Tyr Trp Asn Met Ile Asn Leu Val Leu Ala
210 215 220

Asn Asp Glu Val Leu Phe Arg Met Arg Asp Pro Gln Asn Asn Ala Arg
225 230 235 240

Ala Ile Gly Val Lys Tyr Gly Tyr Gly Asp Ser Gly Ser Asn Phe His
245 250 255

Asp Gln Gly Leu Ala Leu Leu Arg Lys Asp Asn Gln Thr Gly Glu Ile
260 265 270

Ser Phe His Pro Ile Ser Ser Ile Asn Asn Ala Lys Ile Val Glu Lys
275 280 285

Val Ser Arg Phe Ile Arg Val Lys Ile Leu Ser Gln Ile Asp Gly Asp
290 295 300

Tyr Met Leu Thr Gly Gln Ser Ile Phe Asn Phe Asp Phe Glu Lys Ser
305 310 315 320

Lys Gln Ser Ile Ile Asn Asp Ile Glu Lys Ala Arg Phe Phe Leu Phe
325 330 335

Glu Glu Asp Leu Phe His Gln Leu Ile Arg Glu Ala Lys Leu Leu Val
340 345 350

Asn Tyr Asn Val Ser Ile Ile Ser Asn Lys Ile Ile Ile Glu Ile Asn
355 360 365

Asn Ile Ile Ile Glu Ile Glu Ser Ile Val Tyr Asp Glu Leu Asn Glu
370 375 380

Glu Glu Leu Glu Asn Tyr Tyr Gln Asn Val Asn Glu Tyr Ser Thr Leu
385 390 395 400

His Asn Lys Lys Cys Gln Leu Ile Leu Asn Tyr Leu Lys Leu Met Leu
405 410 415

Cys Cys Tyr Tyr Lys Tyr Asn Leu Lys Leu Lys Gln Lys Val Pro Thr
420 425 430

Ala Leu Thr Lys Trp Lys Gln Ser Asn Ser His Pro Leu Ile Leu Arg
435 440 445

Pro Leu Val Gly Asn Met Arg His Glu Leu Asn Leu Leu Asn Met Lys
450 455 460

Ser Val Leu Asp Arg Leu Met His Ala His Glu Ser Glu Leu Ser Tyr
465 470 475 480

Ser Lys Leu Asp Val Glu Lys Phe Ile Asn Leu Ala Thr Arg Ser Lys
485 490 495

Lys Gln Asn Pro Phe Gln Lys Ser Ile Glu Lys Pro Ile Ser Lys Phe
500 505 510

His Leu Val Leu Cys Asn Lys Thr Ser Asn Met Leu Asp Val Asn Ile

515 520 525

Gln Leu Asp Asn Tyr Glu Leu Phe Val Asn Leu Ile Ile Asn Met Thr
530 535 540

Ile Ile Arg Phe Glu Thr Glu His Asp Phe Lys Asn Asn Val Asn Gly
545 550 555 560

Ile Asn Val Leu Gln Leu Gly Phe Ser Asp Phe Asn Glu Ile Glu Glu
565 570 575

Cys Leu Asp Trp Ser Ile Gln Asn Phe Val Leu
580 585

<210> 73
<211> 888
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 146

<400> 73

Met Tyr Gly Ser Ala Arg Ser Val Gly Lys Val Glu Pro Ser Ser Gln
1 5 10 15

Ser Pro Gly Arg Ser Pro Arg Leu Pro Arg Ser Pro Arg Leu Gly His
20 25 30

Arg Arg Thr Asn Ser Thr Gly Gly Ser Ser Gly Ser Ser Val Gly Gly
35 40 45

Gly Ser Gly Lys Thr Leu Ser Met Glu Asn Ile Gln Ser Leu Asn Ala
50 55 60

Ala Tyr Ala Thr Ser Gly Pro Met Tyr Leu Ser Asp His Glu Asn Val
65 70 75 80

Gly Ser Glu Thr Pro Lys Ser Thr Met Thr Leu Gly Arg Ser Gly Gly
85 90 95

Arg Leu Pro Tyr Gly Val Arg Met Thr Ala Met Gly Ser Ser Pro Asn
100 105 110

Ile Ala Ser Ser Gly Val Ala Ser Asp Thr Ile Ala Phe Gly Glu His
115 120 125

His Leu Pro Pro Val Ser Met Ala Ser Thr Val Pro His Ser Leu Arg
130 135 140

Gln Ala Arg Asp Asn Thr Ile Met Asp Leu Gln Thr Gln Leu Lys Glu
145 150 155 160

Val Leu Arg Glu Asn Asp Leu Leu Arg Lys Asp Val Glu Val Lys Glu
165 170 175

Ser Lys Leu Ser Ser Ser Met Asn Ser Ile Lys Thr Phe Trp Ser Pro
180 185 190

Glu Leu Lys Lys Glu Arg Ala Leu Arg Lys Asp Glu Ala Ser Lys Ile
195 200 205

Thr Ile Trp Lys Glu Gln Tyr Arg Val Val Gln Glu Glu Asn Gln His
210 215 220

Met Gln Met Thr Ile Gln Ala Leu Gln Asp Glu Leu Arg Ile Gln Arg
225 230 235 240

Asp Leu Asn Gln Leu Phe Gln Gln Asp Ser Ser Ser Arg Thr Gly Glu
245 250 255

Pro Cys Val Ala Glu Leu Thr Glu Glu Asn Phe Gln Arg Leu His Ala
260 265 270

Glu His Glu Arg Gln Ala Lys Glu Leu Phe Leu Leu Arg Lys Thr Leu
275 280 285

Glu Glu Met Glu Leu Arg Ile Glu Thr Gln Lys Gln Thr Leu Asn Ala
290 295 300

Arg Asp Glu Ser Ile Lys Lys Leu Leu Glu Met Leu Gln Ser Lys Gly
305 310 315 320

Leu Ser Ala Lys Ala Thr Glu Glu Asp His Glu Arg Thr Arg Arg Leu
325 330 335

Ala Glu Ala Glu Met His Val His His Leu Glu Ser Leu Leu Glu Gln
340 345 350

Lys Glu Lys Glu Asn Ser Met Leu Arg Glu Glu Met His Arg Arg Phe
355 360 365

Glu Asn Ala Pro Asp Ser Ala Lys Thr Lys Ala Leu Gln Thr Val Ile
370 375 380

Glu Met Lys Asp Ser Lys Ile Ser Ser Met Glu Arg Gly Leu Arg Asp
385 390 395 400

Leu Glu Glu Glu Ile Gln Met Leu Lys Ser Asn Gly Ala Leu Ser Thr
405 410 415

Glu Glu Arg Glu Glu Glu Met Lys Gln Met Glu Val Tyr Arg Ser His
420 425 430

Ser Lys Phe Met Lys Asn Lys Ile Gly Gln Val Lys Gln Glu Leu Ser
435 440 445

Arg Lys Asp Thr Glu Leu Leu Ala Leu Gln Thr Lys Leu Glu Thr Leu
450 455 460

Thr Asn Gln Phe Ser Asp Ser Lys Gln His Ile Glu Val Leu Lys Glu

465 470 475 480

Ser Leu Thr Ala Lys Glu Gln Arg Ala Ala Ile Leu Gln Thr Glu Val
485 490 495

Asp Ala Leu Arg Leu Arg Leu Glu Glu Lys Glu Thr Met Leu Asn Lys
500 505 510

Lys Thr Lys Gln Ile Gln Asp Met Ala Glu Glu Lys Gly Thr Gln Ala
515 520 525

Gly Glu Ile His Asp Leu Lys Asp Met Leu Asp Val Lys Glu Arg Lys
530 535 540

Val Asn Val Leu Gln Lys Lys Ile Glu Asn Leu Gln Glu Gln Leu Arg
545 550 555 560

Asp Lys Glu Lys Gln Met Ser Ser Leu Lys Glu Arg Val Lys Ser Leu
565 570 575

Gln Ala Asp Thr Thr Asn Thr Asp Thr Ala Leu Thr Thr Leu Glu Glu
580 585 590

Ala Leu Ala Glu Lys Glu Arg Thr Ile Glu Arg Leu Lys Glu Gln Arg
595 600 605

Asp Arg Asp Glu Arg Glu Lys Gln Glu Glu Ile Asp Asn Tyr Lys Lys
610 615 620

Asp Leu Lys Asp Leu Lys Glu Lys Val Ser Leu Leu Gln Gly Asp Leu
625 630 635 640

Ser Glu Lys Glu Ala Ser Leu Leu Asp Leu Lys Glu His Ala Ser Ser
645 650 655

Leu Ala Ser Ser Asp Glu Ser Ser Lys Ala Gln Ala Glu Val Asp Arg
660 665 670

Leu Leu Glu Ile Leu Lys Glu Val Glu Asn Glu Lys Asn Asp Lys Asp
675 680 685

Lys Lys Ile Ala Glu Leu Glu Ser Leu Thr Ser Arg Gln Val Lys Asp
690 695 700

Gln Asn Lys Lys Val Ala Asn Leu Lys His Lys Glu Gln Val Glu Lys
705 710 715 720

Lys Lys Ser Ala Gln Met Leu Glu Glu Ala Arg Arg Arg Glu Asp Asn
725 730 735

Leu Asn Asp Ser Ser Gln Gln Leu Gln Val Glu Glu Leu Leu Met Ala
740 745 750

Met Glu Lys Val Lys Gln Glu Leu Glu Ser Met Lys Ala Lys Leu Ser
755 760 765

Ser Thr Gln Gln Ser Leu Ala Glu Lys Glu Thr His Leu Thr Asn Leu
770 775 780

Arg Ala Glu Arg Arg Lys His Leu Glu Glu Val Leu Glu Met Lys Gln
785 790 795 800

Glu Ala Leu Leu Ala Ala Ile Ser Glu Lys Asp Ala Asn Ile Ala Leu
805 810 815

Leu Glu Leu Ser Ser Ser Lys Lys Lys Thr Gln Glu Glu Val Ala Ala
820 825 830

Leu Lys Arg Glu Lys Asp Arg Leu Val Gln Gln Leu Lys Gln Gln Thr
835 840 845

Gln Asn Arg Met Lys Leu Met Ala Asp Asn Tyr Glu Asp Asp His Phe
850 855 860

Lys Ser Ser His Ser Asn Gln Thr Asn His Lys Pro Ser Pro Asp Gln
865 870 875 880

Asp Glu Glu Glu Gly Ile Trp Ala
885

<210> 74
<211> 900
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> GENBANK Accession Number:CAA96279.1

<400> 74
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cagatgatgt cgaaaggaat aggcgcatta tttacacagc aagaactcca aaaacaaatg 120

ggaatcgggt cgttaacaga cttgatgtcc attgtacagg aattgctaga caagaacttg 180

atcaaattag taaaacaaaa cgacgaatta aaatttcaag gtgtcttaga atctgaggcg 240

caaaagaaag ccaccatgtc ggctgaagag gcactggtat attcttatat cgaggctagc 300

ggtagagaag ggatatggtc caagactatc aaggcaagaa ccaatctcca tcagcatgta 360

gttcttaaat gcttgaagag tttagaatcc caaagatacg tgaagagtgt taagagtgta 420

aagtttccca caaggaaaat ctacatgttg tacagcttac aaccctctgt ggacatcaca 480

ggaggtccat ggttcacaga tggagagctg gatatagaat ttatcaatag tttattgact 540

attgtttgga ggttcatatc agagaacacc ttccctaatg gcttcaagaa tttcgaaaat 600

ggacccaaaa aaaacgtctt ttatgctcca aacgtaaaaa attactctac cacacaagaa 660

attttggaat ttattacagc ggcacaagtg gccaatgtcg agttaacccc ttcaaatatc 720

agatctttgt gtgaagtctt agtgtacgac gacaagctgg aaaaagtcac gcatgactgc 780

tatagagtga ccttagagag cattctacaa atgaaccaag gtgagggcga gccggaggca 840

ggtaataagg ctttggagga tgaagaagaa ttttccatct ttaactactt caagatgttt 900

<210> 75
<211> 993
<212> DNA
<213> Candida albicans

<400> 75
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ccaacttcca aactttttga tcaagatgaa ttacaaacac tatttgatat taaaaaggga 120

tcagaattaa tggaatattt acaagaatta gtcaatggta aatatgttaa aattagtaaa 180

atgggagatc aattaaaatt tcaaactgtt gctgaagaag aagccaaaaa agtatcgtca 240

atgtctgatg atgaagcaat gatttattct tatattgaag cttcaggtcg tgaagggatt 300

tggactaaaa ccattaaagc taaaactaat ttacatcaac atattgttca aaaatgttta 360

aaaaatttag aaaataatcg atacattaaa agtattaaat cagtgaaaca tccaacaaga 420

aaaatttata tgttgtataa tttacaacct agtattgatg ttactggtgg tccttggttt 480

actgattcag aattagatac tgaatttata gaaactttat tggaagtgtg ttggagattt 540

attgttggga aaaccatgta tataaaggat gaagaagctg ataatgaaga tataaatcca 600

cttcaaacaa catatcacaa tcatcatcca ggggtgaatt tggatcaact tgttgaattt 660

ataaacaata gtaatatcac cagtgttgag ttgggtatta atgatattag atcattatgt 720

gatgtgctaa tctatgacga tagaatagaa gaagttggtg ggaatcaaga aaatagtggg 780

atttttaaag ctacttggca aagtataata gataaaggta acactatttt gcaaaataat 840

tatcaggatt tgaaaaatgt tgtttctgaa gattgtttta attatttaca acaaaatcaa 900

tcagatttta gtgtttttca atataaatct actattcaag atcttcaaga tgaatcggat 960

ctagtgtatt tagatagctg gataaatgaa taa 993

<210> 76
<211> 2203
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human GENBANK Accession Number: U93869

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<223> n is unknown

<220>
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<222> (1661)..(1661)
<223> n is unknown

<400> 76
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cgaaatagaa aacaggatta tagaattatg tcaccagttc cctcatggaa tcacagacca 180

agtaattcag aatgaaatgc ctcaatatag aagcccagca gcgggcagta gcatcaatag 240

gttgttgtct atgggtcagt tggatctctt aaggagcaat acgggccttt tatatagaat 300

aaaggactct cagaatgctg gtaaaatgaa gggatccgat aaccaagaaa aactagtata 360

tcaaatcata gaggatgcag gaaataaagg aatatggagc agagatatcc gctataaaag 420

taatttgcca ttaacagaaa tcaacaaaat tctgaagaat ctggaaagta aaaagcttat 480

caaagctgtt aagtctgtag cagcctcaaa aaagaaggtg tatatgctct ataacctgca 540

gccagaccgg tctgtgactg gtggagcctg gtacagtgac caggattttg aatctgaatt 600

tgtagaggtg cttaaccaac agtgttttaa attcctacag tccaaggcag aaacagcacg 660

agaaagcaaa cagaacccaa tgatacaaag aaatagttca tttgcctcat cacatgaagt 720

gtggaaatat atctgcgaat tgggaatcag taaggtagag ttatccatgg aagacattga 780

aaccatcctg aatacactca tttatgatgg aaaagtggag atgacgatta ttgcctgcaa 840

aagaaggcac agttggcagt gtagatggac acatgaaact gtacagggca gtcaatccaa 900

tcatccctcc cacaggtttg gtccgggcca ccctgtggac tctgccccgg tttttgatga 960

ctgccacgaa ggtggtgaga tttcaccatc taactgtatt tacatgacag agtggctcga 1020

attttaatag agagctatga actttattga cattttgcaa atgaagttac ttagggagca 1080

gataatttaa ttcatgatgg aacacgaaat ctccttgaaa gcaaacttca caataatgga 1140

cgtagacttg ctgctatgaa aacatatttt ttttatttat gaagactaaa tttatattgg 1200

taaaatagcc agtagaatat gaaagaaata aggttagtag tgaaattcat tcttcaataa 1260

ataaaacact ttgaaactcc ggaggaccac atctttcaag acttctgatg ggcgaagccc 1320

ccggcttcaa aacacgacaa ggaagtggtc tatttcgatg aatggacaat ttgaaaagat 1380

gccaacatac ccgtatttac caagtactat gataatggct agagtataaa aatgttcttt 1440

ttaaagttat ttattaagtt cttcattgga cgcttttttt tatatctggt tcactaccac 1500

cattttctgt ttcctacttt ctcagtggtt tcattgaaaa gaaattagaa ggggttaaag 1560

gcaggaatag caaagagtgc aaacttgggg tatgactggg ggagagtgga acatgccttt 1620

tccgcacaat attaattcct ttttgtatca gaaaggnnct nttaggagtt atgctaccat 1680

acttacttca aacccaatga ctactgtcaa ggtcatattt tcagtacata aatactatca 1740

ttttcattct aaagaatatt ttcactgttc cttctttctt aaagtcttat gtttcactct 1800

ttaactcaaa tgtattcttt gttagaattt accctagatt cttatttaat gtctgcagta 1860

gactgaatgt ttgtgtgccc ccagaattct aatgttgaaa tctcatttcc aatgtgatgg 1920

tatttggagg tggggctttt ggtaagtgat aggtcaggag agtaacagcg ctcatgaatg 1980

ggattagtgc ccttatataa agagacccag agagctccat cacccccttct gccatgtgaa 2040

agggagaaga caaacatcca cgaaccagga agtgggtcct caccagaaaa caaatctgta 2100

agcaccttga tcttggactt cccagcctcc agaattgtga gaaataaatt tctgttgttg 2160

attttttttt tttttttt ttttttttt ttttttttt ttt 2203

<210> 77
<211> 588
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> GENBANK Accession Number: CAA96194.1

<400> 77
atgtccgggt cgttaaaatc tctagacaag aaaatagcta aaagaaggca ggtgtataag 60

cccgtgctag acaatccgtt cacaaacgaa gcacatatgt ggccgcgcgt gcatgatcag 120

ccattgattt ggcagctgct gcaatcctct atcataaata agttgattca cattcaatcg 180

aaggagaact acccttggga gctgtataca gatttcaatg aaattgtgca gtatttgagc 240

ggcgctcacg gaaacagcga cccagtatgt ctatttgtgt gcaataagga ccctgatgta 300

ccgcttgtgc tcttgcagca aatcccgcta ttatgctata tggcgcccat gacggttaaa 360

ctggtgcagt tgcccaagag tgccatggat accttcaagt cggtttctaa atatggaatg 420

ctgctgctgc ggtgcgacga tagggtcgac aagaaattcg tatcgcagat ccagaagaac 480

gttgatctgc ttcagtttcc ctggttaaat gctatcaagt atcggcccac atctgtcaag 540

ctgttgaaaa ctacagtgcc aattgtctcg aagaagaggc aaaagtag 588

<210> 78
<211> 663
<212> DNA
<213> Candida albicans

<400> 78
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tcatcatcac tcaagtctca ggaagcaaag agaaaacaag ttttccgtcc aattctcgat 120

aactcattta cacaatcaaa ccaatggcca tttatagaac caactattgc aaacgatatt 180

gttgatctac tagaagtatt gctaaaaatg caagactcta catttaaata ccgtgggttt 240

aatccaactg tgtctgctct tgaaaaacaa gcagctgcta atcgtggtat acataaaaat 300

gcttgtgtac aaataaagta tgtatttgtg tgcaagtacg atatatcccc agcaacgctc 360

acaaatgtgt ttcctacgtt gtgtttcacg gcgtcaaaaa gtgctgaaga tcgggttaag 420

ctaatccagt taccaagagg aagtctagaa cggttatcga aagcacttgg ggtagataga 480

gttggtatat ttggtctaac taaagatact gaaggggcac aaccgttatt tgatcttata 540

aatgaaaatg tcaaagatat tgaagctcct tggctagact gtattttccg tgaggagatg 600

gtatttaatc aacctaacac aaagcatgtg gcaagtactg taggtagaaa gaaaaacaag 660

tag 663

<210> 79
<211> 960
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> GENBANK Accession Number: CAA82141.1

<400> 79
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tctgccccgg tgatcgcacc cgctaaagtt ggacagaaga agaccaatga cacagtgatt 120

actatagatg gaaacactag gaagaggacg gcctccgaac gtgcgcaaga aaacactttg 180

aactctgcga aaaatcctgt gttagtggat atcaagaaag aagctgggag caatagctct 240

aatgctattt cattagatga cgacgatgac gacgaagatt ttggtagctc tccttcaaaa 300

aaagtaaggc ctggctctat tgctgcagcc gctttacaag caaatcaaac agatatttcc 360

aagagtcacg attcttcaaa gttgctttgg gcgactgaat acattcaaaa gaaaggtaag 420

cccgttttgg tgaatgagtt attggactac ttgtcaatga aaaaagatga caaggttatt 480

gagcttttaa aaaaattaga tagaatagag tttgacccca agaaggggac tttcaaatac 540

ctttccacct acgatgtcca ttccccttcg gaactgctga agttgttacg ttcacaagta 600

acattcaaag gtatttcctg caaagacttg aaagacggtt ggccacaatg cgatgaaacg 660

attaaccaac tggaggaaga cagcaaaatt ttggtgttaa gaactaaaaa ggataaaact 720

ccaagatacg tttggtataa cagcggtggt aacttgaaat gtattgacga ggagtttgtt 780

aaaatgtggg aaaatgtgca attaccgcaa tttgcagaat tgccaagaaa gctgcaagat 840

ttaggtctaa agcctgctag tgtcgatcct gctactatca aaagacaaac aaagagagtt 900

gaagttaaaa agaagagaca aagaaagggt aagattacta acactcatat gaccggtatc 960

<210> 80
<211> 855

<212> DNA
<213> Candida albicans

<400> 80
atgtccgact tatcagctca actttcagct tttaagaata agatcaaaag tggaccatcg 60

gtgattgttc ctagaaaggc aacttttact caatctccat catcaccatt atcatcatca 120

accacaacaa caacactgaa gaatgacgcc aatgtgaaga agagatcaac gacggattca 180

gtaacccgag tattgaagaa acaaaaggca aatatgggag aaatgacggg atcacattta 240

tcgacacaat tacaccttgc tgttgaatat atcaaggaac atgaccaacc aatatcggtg 300

gagaagttgc agaattattt atcatttgat atatcacata ctttattgcc attattgaat 360

gaaattgatc gagtgaaata cgacgaatct aagggtacat tggaatatgt ttcattgcat 420

aatattcgta gtagtgatga tttattggaa tttttgagac gtcaaaccac attcaagggc 480

acttccgtaa aagaattaaa agatggttgg gctggttgtg ttgccgctat agacgaatta 540

gaatcacaag gcaaaatttt ggtgttgcgt aacaagaagg aaaatgctcc aagattagta 600

tgggctaata atggtggtga gttgggttat attgacacag aattcaagga tatgtgggat 660

caagtgaaat tgccggaacc agatgtattg tatcagaaat tattggatca aggattgaaa 720

cctacgggag ctgatcctaa tttgatcaaa aagcaaccac aacaaaagga aaagaaacaa 780

aagaaagcaa gaagaggaaa gattacaaat acacatatga aaggtatttt gaaggattat 840

tctcaattag tttga 855

<210> 81
<211> 1500
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human GENBANK Accession Number: NM_002095.1

<400> 81
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gcaggcgggg gcgctgacga gaagcaggaa gagggtgcag tgccggcgtg ggcggccggc 180

cgaggcggag gcgcaggaag ggggcggcga gtcgtgcgag gctgcccttc tcactcagca 240

ttatggatcc aagcctgttg agagaaaggg agctgttcaa aaaacgagct ctttctactc 300

ctgtagtaga aaaacgttca gcatcttctg agtcatcatc atcatcgtca aagaagaaga 360

aaacaaaggt agaacatgga ggatcgtcag gctctaaaca aaattctgat catagcaatg 420

gatcatttaa cttgaaagct ttgtcaggaa gctctggata taagtttggt gttcttgcta 480

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atgaaatttt ggatgaaaca caacatttag atattggact caagcagaaa caatggctaa 600

tgactgaggc tttagtcaac aatcccaaaa ttgaagtaat agatgggaag tatgctttca 660

agcccaagta caacgtgaga gataagaagg ccctacttag gctcttagat cagcatgacc 720

agcgaggatt aggaggaatt cttttagaag acatagaaga agcactgccc aattcccaga 780

aagctgtcaa ggctttgggg gaccagatac tatttgtaaa tcgtcccgat aagaagaaaa 840

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ggaggagtgt cactgtagat tccatggacg aggagaaaat tgaagaatat ctgaagcgac 960

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aaaagcctgc ttcacagaaa aagcgacgct ttaagactca taacgaacac ttggctggag 1080

tgctgaagga ttactctgac attacttcca gcaaataggg aacagttttg ccctggaaca 1140

gagttacaga tacacaatca agagtgttct tgctgatgct cggggtctga agactgtctt 1200

cctatctgct tcttgcggct gaggagagga gcagttcagt ttacaaaaca agtgcaaatt 1260

accaaactca aagcttattt gagtagaatg ggctcatggg caatgtgatg ttccctgtta 1320

accttctgtt actccctggg agaaaggcgc tgagcgtggc atgcaggtgt ctttgctgtg 1380

tttttctcca cttctaaatg gttcctggtt cctttcttcc tcgtttgtta ctttagagca 1440

agtttgccca tagtcttgaa tgcaatattt gtttattcca aaagaacata tttataataa 1500

<210> 82
<211> 1560

<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> GENBANK Accession Number: CAA96830.1

<400> 82
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aacggtggta ctgttgaatc tgtcgtagac gagctggcta gtttgtttga tagtgtttcg 180

agagatacgc ttgcaaatgt tgttcaaaca gcctttttcg cattagaagc tctgcaacag 240

ggagaaagtg ctgaaaatat tgtttccaaa attagaatga tgaatgcgca aagcttggga 300

caatcggata tcgcacaaca gcaacaacag caacaacaac aacagcaacc agacatcgcg 360

caacagcaac ctcaacagca acctcaacag caacctcaac agcaacctca acagcaacct 420

caacagcaac ctcaacagca acctcaacag caacctcaac agcaacctca acttcaacca 480

cttcagccac aactagggac ccagaatgca atgcagacag atgctcctgc aactccatcc 540

cccatatcag cctttttccgg cgttgttaac gctgcagctc cccctcagtt tgcgcctgta 600

gataacagcc aaaggttcac tcaacgtggc ggaggcgccg ttggaaagaa tcgtagaggt 660

ggtcgcggtg ggaaccgtgg aggacgcaac aataattcca cacgttttaa tccgttagca 720

aaagcacttg gaatggcggg tgagagtaat atgaacttca ctccaaccaa gaaagagggg 780

cgttgcagat tgtttcctca ctgtcctctt ggtagatcat gcccacatgc acacccaact 840

aaggtatgta atgaatatcc aaattgtcca aagcctcccg gaacttgtga gtttttacat 900

ccaaatgaag atgaagagtt gatgaaggaa atggaaagaa ctcgtgaaga atttcaaaaa 960

agaaaagctg atttattggc ggcaaaaagg aaaccggtac aaactggtat cgttctgtgt 1020

aaatttgggg ctctgtgttc caatccatca tgcccatttg gtcatccaac accagcaaat 1080

gaagatgcga aagtcattga tctaatgtgg tgtgacaaga atttgacatg tgataatcct 1140

gagtgtagaa aggcccactc ttcattgtcg aagatcaagg aagtaaaacc aataagccag 1200

aagaaagcag ctccacctcc ggttgaaaag tccttagaac aatgtaagtt cggtacgcac 1260

tgcaccaata aacgttgcaa atatagacat gctcgttctc atattatgtg ccgtgaagga 1320

gcaaactgta ctagaattga ttgtttattt ggccatccaa ttaatgaaga ttgtagattt 1380

ggtgtcaatt gtaagaatat ttactgtcta ttcagacatc ctccaggcag agtacttccg 1440

gaaaagaaag gcgctgcacc caattcaaac gttcctacca atgaaaggcc atttgcattg 1500

ccagaaaacg caataattga aaatgctcct ccgcaaacca gttttacgca ccaagaacaa 1560

<210> 83
<211> 1296
<212> DNA
<213> Candida albicans

<400> 83
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atacaaaggc gtttcaataa accggctgat gatgccgtag atattgctga ctatatcatc 120

tacttgattg tggcaaaaaa gagcgaacaa gaaatagtcg cagaagtcaa agatattgct 180

gacatatcta ttgatgttgg gtttattggg gatgtttatc tggaaatcag aaagttggaa 240

gtaaaatata atcaacctcc tgctgcagtg gaggaagctt ctcaacctca acaagaacag 300

caacagcaat ctcaagcttc tgtagtggct ccacaaattc ctattggtcc taagaaacaa 360

ttaactgagg aagagaagat tgcccttcga agtcaaagat ttggaactac tactagattg 420

agtgggcgag gtggacgtgg tggtataact aaaactagaa ccgatttcag aaatgggcac 480

aataataaga acttcctaga ccctaaaaaa ttagaccaaa taatttctgg tgccaataat 540

ggggctatta agtttgtacc actcccacca aaaggtagat gtccagattt cccatattgt 600

aagaatcaga attgtgaaaa agctcatcca acaaaaaact gtttcaacta cccggattgc 660

cctaacccac cgggaacatg taattttttg catccggatc aagaccaaga gttgattgct 720

aaattagaaa catctaaaaa agaatttgaa gaaaagaaaa agaatcaact tatggtcaaa 780

caaggctcat gtaaatatgg tttgaaatgt gctaaagaaa attgtccatt tgctcaccca 840

acaccagcta atcctgaatc tggtaagatt gaaactttgg aatggtgtcc acaaggtaag 900

aattgtcaag atagaaattg tactaaatca catccacctc cacctacggc aaactcagaa 960

aaattattat cagctgctga cttggcattg gaacaatgta aatttggttc acaatgtact 1020

aatctcaaat gtccaagaag acatgcaact tcggctgtgc catgtcgtgc tggtgctgaa 1080

tgtagaagag tcgattgtac attttcccat ccattgaaag aaccatgccg ttttggaaca 1140

aaatgtacaa ataaagtgtg tatgtaccaa catcctgaag gaagaactat tgcctctcac 1200

acttggacca aggatggtag tggcaataat aacagtacct caaatcgatc atttgctgtt 1260

tctgaagatc agattatgga acaagttgct caatag 1296

<210> 84
<211> 680
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human GENBANK Accession Number: AF155107.1

<400> 84
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agtactggcc tgcttgtaaa aatggggatg agtgtgccta ccatcacccc atctcaccct 180

gcaaagcctt ccccaattgt aaatttgctg aaaaatgttt gtttgttcac ccaaattgta 240

gatacggaaa tgaactgaaa tatgatgcaa agtgtactaa accagattgt cccttcactc 300

atgtgagtag aagaattcca gtactgtctc caaaaccagt tgcaccacca gcaccacctt 360

ccagtagtca gctctgccgt tacttccctg cttgtaagaa gatggaatgt cccttctatc 420

atccaaaaca ttgtaggttt aacactcaat gtacaagacc ggactgcaca ttctaccatc 480

ccaccattaa tgtcccacca cgacatgcct tgaaatggat tcgacctcaa accagcgaat 540

agcacccagt cctgcctggc agaagatcat gcagtttgga agttttcatg tctgatgaaa 600

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<210> 85
<211> 1140
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> GENBANK Accession Number:CAA88520.1

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agtgagctat cacatagcct tccgtcgcct agccagataa aatcaaccgc acatgtatct 180

tcaactcaca atgatgcggc aggtaatacg gatgattctg ttcttcctaa aaatgtatca 240

cccacaacta atttgagagt tgaaagtaat ggagatacaa acaatatgtt ctctagccct 300

gctggactag ctctaccaaa aaaggatgat aaaaaaaaaa acaagggtac gagtaaagca 360

gattctaaag atggcaaagc atccaactcc tcaggacaga atgcacaaca acaatcagac 420

ccaaataaaa tgcaagatgt cctttttcc gcaggtatcg atgttaggga ggaggaggct 480

cttctaaatt catctattaa tgcctcaaaa tcccaagttc aaacaaataa cgttaagatc 540

cccaaccatt taccattcct tcacccggaa caagtttcca attatatgag gaaagtcgga 600

aaagagcaaa acttcaacct gacccctaca aagaatcctg aaattttgga catgatgtca 660

agtgcctgcg aaaactatat gagagatatc ctaacaaatg ccattgtcat ctcccgacat 720

agaagaaaag cagtcaagat aaattctggt agaagaagtg aagtttctgc ggctttaaga 780

gccattgcac taattcaaaa aaaagaagaa gaaaggcgtg tgaaaaaaag aattgcgttg 840

ggactcgaga aggaagatta tgaaaataag attgattccg aagagacgtt acacagagca 900

tcgaacgtta cggctggcct tagagcaggt agtaaaaaac agtatggttg gctaacttca 960

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acggctagag gagaaagtgg gctaaagttt agagaagcta gagaggagcc tggtatagta 1080

atgagggatt tactctttgc tctcgaaaat aggcgcaaca gcgttcagac tattatttca 1140

<210> 86
<211> 1119
<212> DNA
<213> Candida albicans

<400> 86
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actaccacgg aaaaccagag ctcatgggag tctgacttta atagtttacc agtggaatta 180

ctacaaactg aaacaaatgg tacatcacca gcaccagcac cagcaacacc gatcgatacc 240

accaatgcat caagcacaaa ggaacgtgat caggatactt ctaaattaaa tgacgcgatt 300

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cctccatttc tacacaatta ccatttagct gcctttattg ataaagtggc taaacaaaat 480

ggaattcaac agaatttctt aatggatggt gagatgttgg aattaatttc agctgcttgt 540

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ggaatacctg ttattaataa gaagtcagga agtagttcag ttccaagatc agaaatttca 660

aaagaattga gaagcttggc cttaaaacaa aaggaaatgg aagagaaacg agtgaataaa 720

agagtgatgt tggggttgga aaaaagcacc aaagacgcat ccaaaaatga cgaaaatggt 780

gaatcaaaag ctggtgctga agaaacatta catcgtgcag caaatgctac agctgcaatg 840

atgactatga atcccgggag aaagaaatat agttggatga cttcaagtgc tacagcaggc 900

ggtgggtcag actttggtaa atcaagtggt ggctcatcaa aggactcggg aaaacaccaa 960

agtcctatta tttcagtacg tggtgataat ggccttaggt ttagagaaat aaggtcaggt 1020

aattccatta ttatgaaaga tttgttaggc gcaattgaag atgaaaaaat gggtacgaga 1080

aatgctgtaa taaaaggata tgcaaaattg aaagattaa 1119

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<211> 2307
<212> DNA

<213> Homo sapiens

<220>
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<223> Human GENBANK Accession Number: Y11354.1

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gggccgcagc gcccgggccc cccctcaccg cgccgccccc ttgtccccgc agggcccgcg 360

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gcgcccccgg cggcgcagac cctggcggcc agcggcccgg ccagcacggc ggccagcatg 1140

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acagagacag cagctaatgt gaaagagctc gtgcagaatt tactggatgg aaaaatagaa 1920

gcagaagatt tcacaagcag gttataccga gaacttaatt cttcacctca accttacctt 1980

gtgcctttcc tgaagaggag cttacccgcc ttgagacagc tgacccccga ctccgcggcc 2040

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accagtgccc tccagccccc tgtgctcagc ctcacgcagc ccacgcaggt cggcgtcggc 2220

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cggcccccgc aggtgacgtt gacgcag 2307

<210> 88
<211> 555
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> GENBANK Accession Number: CAA82029.1

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ttcgtacagc tttttaatcc aaacaactgc agaataatat ttaatgctac ccccttcgcg 180

caagcaacag tttttctgca aatgtggcaa aaccaggtcg tacaaacaca acatgcccta 240

acaggagtag actatcacgc tattccggga tccggcacgt tgatatgcaa cgtcaattgc 300

aaagtcagat tcgacgaaag cggcagagac aagatggggc aagacgcgac tgttcccatt 360

caaccaaata acactgggaa cagaaatcga cccaacgata tgaacaagcc aagacctcta 420

tggggtccat attttggcat ttccctgcag ctgatcatcg acgaccgcat atttagaaat 480

gattttaatg gtgtaatatc ggggtttaac tataacatgg tttacaaacc cgaggattct 540

ctgctaaaaa tttag 555

<210> 89
<211> 540
<212> DNA
<213> Candida albicans

<400> 89
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ctgtacacac agccaacatc acaaccattc cccaacgttg aatcgtatgc cactcagtta 120

ggatcaaact taaagcggtc aagtgcaatt atagtgaacg gccagcctat tataccgagc 180

ccacaagaag actgtaaatt acaattccaa aagaaatggt tacaaactcc gttatcgtca 240

caccaattga caagttacga tgggcattta attccaggca cggggacctt tgtcgttcat 300

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tggtttggag tcgacgtcaa tttggttgtt gacgaaaacg ttatgcaaga tggagagatt 480

ataaatagta tggattatag atttacctat gtacctaacg atagcattat aaaagtataa 540

<210> 90
<211> 720
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> GENBANK Accession Number: CAA97636.1

<400> 90
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ctggtctcac tggagaaaac agttaagcaa tatgcagaac atttaaacag atataaagaa 180

gatactaatg cagaggaaat tgatcctaag ttcgctaatc gactagcaac tttaacacag 240

gatctgcacg actttactgc caagtttaag gatttaaaac aatcctacaa cgaaaataat 300

tccagaactc agttgtttgg ctcaggagca tcgcatgtta tggactccga taaccccttt 360

agtacatcag agaccatcat gaataaaagg aacgttggtg gtgcgagtgc aaatggtaaa 420

gagggctcta gcaacggtgg gggactaccg ttgtaccaag ggctacaaaa ggaacagtct 480

gttttcgaaa ggggtaacgc tcaattagat tacattctag aaatgggcca acaatcattc 540

gaaaatatag tggaacaaaa caaaatttta tccaaggtac aagatagaat gtcaaatggc 600

ctaagaacat tgggtgtttc ggaacaaact atcacctcta tcaataaacg ggtgttcaaa 660

gataaactag tcttttggat cgcgttaatt ctcttgatca taggtattta ttatgtgttg 720

<210> 91
<211> 483
<212> DNA
<213> Candida albicans

<400> 91
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taactgcatt caggaaaact atcgaagaat atgatgattt attggaagta aatgtctatg 180

atacatctga taccatagat gagggtagat tagatatatt caatccagat ttaaatgaat 240

acactctgaa atatgatact ttaaataagc tacgtgagtt tcttctccat caagctaata 300

aacaagaatt attaggagaa ggacacttat caccaacagc aacagcagca ttggatcgac 360

atcatcagat aatccgtatg aatctagctc aaatccatct caacaacaac aacagcaatt 420

acaagatgaa caaaacacca tgtcttatag agaaggatta tatcatgaaa agaattctct 480

aga 483

<210> 92
<211> 1560
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human GENBANK Accession Number: NM_003569.1

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ggcccagagg atctcttcta acatccagaa gatcacacag tgttctgtgg aaatacaaag 180

aactctgaat caacttggaa cacctcaaga ttcacctgaa ttgaggcaac agttgcaaca 240

gaagcagcag tatactaacc agcttgccaa agaaacagat aagtacatta aagagtttgg 300

atctctgccc accaccccca gtgaacagcg tcaaaggaaa atacagaagg atcgcttagt 360

ggcagagttc acaacatcac tgacaaactt ccagaaggtc cagaggcagg ctgctgagcg 420

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tatcaggcaa cttgaagctg atattatgga tattaatgaa atatttaaag atttgggaat 660

gatgattcat gaacaaggag atgtaataga tagcatagaa gccaatgtgg aaaatgcaga 720

ggtgcacgtt cagcaagcaa atcagcagct gtcaagggca gcagattatc agcgcaaatc 780

cagaaaaacc ctgtgcatca tcattcttat ccttgtcatt ggagttgcga ttatcagtct 840

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taaattatgt aggaagattc ctgtaatcat gtttttttaa ttattattt aaagctattg 960

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<210> 93
<211> 720
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature
<223> GENBANK Accession Number: CAA85038.1

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agatgtgacc atcctgttac gttaggtatg gatctaacct cactaagtaa aatcctacgt 240

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ttattatttg aggataccaa gaaagaccgt atagccgaat actctctgaa attgatggat 360

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tcttccgaat tctctaaaat tgttcgtgac ttgtcccaat tgagtgattc tattaatatc 480

atgatcacca aagaaacaat aaagtttgta gctgacggtg atatcggatc aggttcagtc 540

ataataaaac cattcgtgga tatggaacat cctgaaacaa gcatcaaact tgaaatggat 600

caacctgtcg acttgacgtt cggagctaaa tatttattgg acatcattaa gggctcctcc 660

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<210> 94
<211> 780
<212> DNA
<213> Candida albicans

<400> 94
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gatgattctc gtgtattatt agtttcatta ttaattggtc aaacttcttt cagtgaatat 180

agatgtgaca gagacgttac attaggtatt gacttggaaa gtttcagtaa gattatcaaa 240

tctgctaaca atgaagattt cttgaccctt ttagctgaag attcaccaga tcaaataatg 300

gctattcttg aagaaaaaca aaaagagaaa atcagtgaat attctttaaa attaatggat 360

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agtagtgatt ttgctaaact tgtgagggat ttgaaaaatt taagtgaatc tttacgtgtt 480

gttgttacta aagattccgt caagtttaca tctgaaggtg attctggttc cggaagtgtt 540

atcttgaaac cttacaccaa cttgaaaaat gaaagagaaa gtgtcactat tagtttagat 600

gacccagttg atttgacttt tggtttgaaa tacttgaatg atattgtgaa ggcagctaca 660

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atgcaatctg gaggttattt gagattctac ttggcaccaa aattcgatga tgatgagtag 780

<210> 95
<211> 1200
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human GENBANK Accession Number: GI:181271

<400> 95
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gttcgaggcg cgcctggtcc agggctccat cctcaagaag gtgttggagg cactcaagga 180

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cgccggcaat gaagatatca ttacactaag ggccgaagat aacgcggata ccttggcgct 420

agtatttgaa gcaccaaacc aggagaaagt ttcagactat gaaatgaagt tgatggattt 480

agatgttgaa caacttggaa ttccagaaca ggagtacagc tgtgtagtaa agatgccttc 540

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attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720

accagttcaa ctaacttttg cactgaggta cctgaacttc tttacaaaag ccactccact 780

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aaagtccaaa gtctgatctg gtctagttaa cctagaagta ttttgtctc ttagaaatac 1140

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<210> 96
<211> 1500
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> misc_feature

<223> GENBANK Accession Number: CAA88556.1

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ctagaagaac aattgagtga tgaatttgat agtgatggtg aaattattga aattgatggc 180

gatgatgaga ttaatgacga agatgacctt aggaaaaagc aagaagaagc tgaaacttta 240

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atgtctcgtc cattagggcc agatgaagtc cttgaggctg atcccactgt ttatgaaatg 360

ctacataatg tcaatatgcc atggccatgc ttgacattag atgtcattcc agatacacta 420

ggttctgaac gtagaaacta tccacagtct attttgttga ccacggctac tcaatcttcc 480

aggaaaaagg agaatgaact aatggttcta gcactttcta atttagcgaa aacacttttg 540

aaagacgata atgaaggtga agatgatgaa gaggatgatg aagatgatgt ggatccagtc 600

attgagaatg aaaatatacc attgagagat acaaccaata gattaaaggt ttctcctttt 660

gccatttcta atcaagaggt gttaaccgct acaatgagcg aaaatggtga tgtttatata 720

tacaatctag ctccacaaag caaagctttt tccacaccag gttatcagat tccgaagtct 780

gctaagcgtc ctattcacac tgtaaaaaat catgggaatg ttgaaggcta cgggttggat 840

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ggatgtgatg gatatataag gatttgggac acaagatcaa aaaaacataa acctgctatc 1080

tctgttaaag cttctaatac tgacgtaaat gtcataagtt ggagtgataa aattggttac 1140

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ccaagtaatg ctgacgccgt ccaaccggtt gctcaatatg acttccataa gggagccatt 1260

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gccgaaacaa aagagctaca agaaattcca ccacaattat tgtttgttca ctggcaaaag 1440

gaagttaaag atgtcaaatg gcataagcaa atcccaggtt gtttagtaag taccggtact 1500

<210> 97
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<302> Molecular cloning, structure ande expression of the yeast proliferating cell nuclear antigen gene
<303> Nucleic Acids Research
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<307> 1990
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<301> Almendral, Huebsch, Blundell, MacDonald-Bravo and Bravo
<302> Cloning and sequence of the human nuclear protein cyclin: Homology with DNA-binding protein
<303> Proc. Natl. Acad. Sci. U.S.A.
<304> 84
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<307> 1987
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<309> 1993-04-27

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aaagaaaatg tcaaaaaagt tgatttttca ggaaatacta ttggtattga agcatcaaaa 180

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<213> Candida albicans

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ttatcttcag aatctacatt acaagatttt ttaaataata ataaattttt tgttgattcc 240

ataaaacata atcatggtaa tcaaatattt gatttgaatg gtcaaggtca atctcctcat 300

acattatgga tagggtgtag tgattcaaga gcaggtgatc aatgtttagc tacattacca 360

ggagaaatat ttgttcatag aaacattgct aatatagtca atgccaatga tataagtagt 420

caaggggtta tacaatttgc tattgatgta ttaaaagtga aaaaaatcat tgtttgtggt 480

catactgatt gtggtggtat ttgggcatca ttatcaaaga aaaaaattgg tggtgtttta 540

gatttatggt taaatccagt tagacatatt cgtgctgcta atttaaaatt attagaagaa 600

tataatcaag atcctaaatt aaaggccaaa aaattggctg aattaaatgt catttcttct 660

gtaacagcat tgaaaagaca tcctagtgct agtgttgcat taaagaagaa tgaaattgaa 720

gtttggggga tgttatatga tgtggcaact ggttatttat ctcaagtaga gattcctcaa 780

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ctgcatggac gtaaatggtc gccgaattgg ggttctatag tatacacaga gcgaaaccat 240

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gataagtcga atggtgaagt ccgagccatg acggagataa tgacactagt gaataacgag 420

ctgaatgcgc cacacgatga gaatgtcatt tggaacagta ccacagaaga aaaaggcaaa 480

gcgtttgtat acataagaaa tgacagggcg gtcggaataa taattataga gaacctttat 540

gggggcaatg gtaaaacatc tagtcgtgga cgttggatgg tttatgattc tagaagattg 600

gtacagaatg tgtaccccga ttttaagatt ggcatatcga gaatttgggt gtgcaggaca 660

gcaaggaagt tgggtatcgc aaccaaattg attgacgttg caagagaaaa tattgtttac 720

ggtgaagtta ttcctaggta ccaggtagca tggtcgcaac ccacagacag cggtggaaaa 780

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gataaattac tacataacaa ataccacaca aatttcatca atggaatacc ctggaattat 180

aaaactgata atgatgtttt aataattgag aattttacat tagttgaaac cccgaaattg 240

aattccacgg ggaaatcatt aaagctgaca aaaacgcgtc agacatttaa aggttctata 300

atttgtataa ataaatccaa caaacgacat atacaaaaag tggaactact attaaacatg 360

gtgaatcaag agttgaatgc tagtcaagat tcaggacaat ggaagaaacc tgaatttgat 420

agaagtaaag catttgtgat aataatagac agtaaggcca ttggattatg cacaacagat 480

acaattcaac ctgatcaagg aaggtggatg atacataaaa cacaatctat agtacctaat 540

cagattaata aaaatgttgt cattggaatt tcaagaatat ggataagtcg gaaatggaga 600

caatatggat taggtaaaaa acttttaaat gttgttttga aaaattctat ttacagtgtg 660

caattattga agaatcaagt tgcctttagt caaccaagtt ttagtggtgg aatgttggca 720

aaatcattca atggggtgaa acataaaagt ggtgaaatgt tgttacccgt atatattgaa 780

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gaaaaaatac aggtagcgac cacaacatat gaagataatg tgactccaca aactgatgat 480

aattttgtat caaattcacc cgagccacca gaacctgcaa caccatctaa gaagtcttta 540

accactaatc atgattttac ttcgccccta aagcaaatta taatgaataa tttaaaagaa 600

tataaagact caacctcccc aggtaaatta accttgagta gaaattttac tccaacccct 660

gtaccgaaaa ataaaaagct ctaccaaact tcggaaacca agtcagcaag ctcgtttttg 720

gatacttttg aaggatattt cgaccaaaga aaaattgtca gaactaatgc gaagtcaagg 780

cacaccatgt caatggcacc tgacgttacc agagaagagt tttccctagt atcaaacttt 840

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gctccgctcc tctgggacaa catgaaggcc caaaactaca actttgtctt tcatgatatt 1440

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catctctgtg ccgctgattt tattgcttct aatgagatag ctctaaggtc gatgcttaga 1740

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cccaaatcaa ccaacacgca tgaagagaag aaaacgtttg tgccgcttcc tattcccacc 840

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cataaatgga tgctgcaatt acaccttggg ttcaacattg tgctttatgg tttgggttct 1140

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